PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 9/12, 15/10, 15/54

A2

(11) International Publication Number: WO 98/22575

(43) International Publication Date: 28 May 1998 (28.05.98)

(21) International Application Number: PCT/US97/21347

(22) International Filing Date: 21 November 1997 (21.11.97)

(30) Priority Data:

60/031,626	22 November 1996 (22.11.96)	US
60/061,953	14 October 1997 (14.10.97)	US

(71) Applicants *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). UNIVERSITY OF WISCONSIN [US/US]; 1300 University Avenue, Madison, WI 53706 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: DILLON, Patrick, J. [US/US]; 7508 Boxberry Terrace, Gaithersburg, MD 20879 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). WELCH, Rodney, A. [US/US]; 410 Ridge Street, Madison, WI 53705 (US).

(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005-3934 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

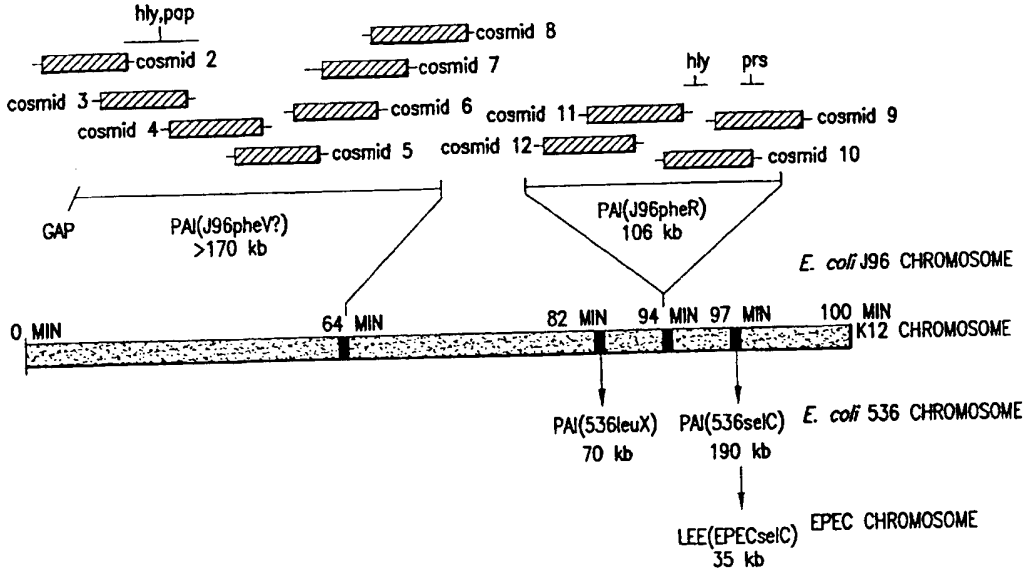
Without international search report and to be republished upon receipt of that report.

With an indication in relation to a deposited microorganism furnished under Rule 13bis separately from the description.

Date of receipt by the International Bureau:

20 March 1998 (20.03.1998)

(54) Title: THERMOSTABLE POLYMERASES HAVING ALTERED FIDELITY



(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.

\SDOCID <WO_ _9822575A2 I >

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	**ES**	Spain	**LS**	Lesotho	**SI**	Slovenia
AM	Armenia	**FI**	Finland	**LT**	Lithuania	**SK**	Slovakia
AT	Austria	**FR**	France	**LU**	Luxembourg	**SN**	Senegal
AU	Australia	**GA**	Gabon	**LV**	Latvia	**SZ**	Swaziland
AZ	Azerbaijan	**GB**	United Kingdom	**MC**	Monaco	**TD**	Chad
BA	Bosnia and Herzegovina	**GE**	Georgia	**MD**	Republic of Moldova	**TG**	Togo
BB	Barbados	**GH**	Ghana	**MG**	Madagascar	**TJ**	Tajikistan
BE	Belgium	**GN**	Guinea	**MK**	The former Yugoslav Republic of Macedonia	**TM**	Turkmenistan
BF	Burkina Faso	**GR**	Greece			**TR**	Turkey
BG	Bulgaria	**HU**	Hungary	**ML**	Mali	**TT**	Trinidad and Tobago
BJ	Benin	**IE**	Ireland	**MN**	Mongolia	**UA**	Ukraine
BR	Brazil	**IL**	Israel	**MR**	Mauritania	**UG**	Uganda
BY	Belarus	**IS**	Iceland	**MW**	Malawi	**US**	United States of America
CA	Canada	**IT**	Italy	**MX**	Mexico	**UZ**	Uzbekistan
CF	Central African Republic	**JP**	Japan	**NE**	Niger	**VN**	Viet Nam
CG	Congo	**KE**	Kenya	**NL**	Netherlands	**YU**	Yugoslavia
CH	Switzerland	**KG**	Kyrgyzstan	**NO**	Norway	**ZW**	Zimbabwe
CI	Côte d'Ivoire	**KP**	Democratic People's Republic of Korea	**NZ**	New Zealand		
CM	Cameroon			**PL**	Poland		
CN	China	**KR**	Republic of Korea	**PT**	Portugal		
CU	Cuba	**KZ**	Kazakstan	**RO**	Romania		
CZ	Czech Republic	**LC**	Saint Lucia	**RU**	Russian Federation		
DE	Germany	**LI**	Liechtenstein	**SD**	Sudan		
DK	Denmark	**LK**	Sri Lanka	**SE**	Sweden		
EE	Estonia	**LR**	Liberia	**SG**	Singapore		

3NSDOCID <WO _ 9822575A2 I >

Nucleotide Sequence of *Escherichia coli* Pathogenicity Islands

Background of the Invention

Field of the Invention

The present invention relates to novel genes located in two chromosomal regions within *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs).

Related Background Art

Escherichia coli (*E. coli*) is a normal inhabitant of the intestine of humans and various animals. Pathogenic *E. coli* strains are able to cause infections of the intestine (intestinal *E. coli* strains) and of other organs such as the urinary tract (uropathogenic *E. coli*) or the brain (extraintestinal *E. coli*). Intestinal pathogenic *E. coli* are a well established and leading cause of severe infantile diarrhea in the developing world. Additionally, cases of newborn meningitis and sepsis have been attributed to *E. coli* pathogens.

In contrast to non-pathogenic isolates, pathogenic *E. coli* produce pathogenicity factors which contribute to the ability of strains to cause infectious diseases (Mühldorfer, I. and Hacker, J., *Microb. Pathogen.* 16:171-181 1994). Adhesions facilitate binding of pathogenic bacteria to host tissues. Pathogenic *E. coli* strains also express toxins including haemolysins, which are involved in the destruction of host cells, and surface structures such as O-antigens, capsules or membrane proteins, which protect the bacteria from the action of phagocytes or the complement system (Ritter, *et al.*, *Mol. Microbiol.* 17:109-212 1995).

The genes coding for pathogenicity factors of intestinal *E. coli* are located on large plasmids, phage genomes or on the chromosome. In contrast to intestinal *E. coli*, pathogenicity determinants of uropathogenic and other extraintestinal *E. coli* are, in most cases, located on the chromosome. *Id.*

NSDOCID <WO 9822575A2_I_>

Large chromosomal regions in pathogenic bacteria that encode adjacently located virulence genes have been termed *pathogenicity islands* ("PAIs"). PAIs are indicative of large fragments of DNA which comprise a group of virulence genes behaving as a distinct molecular and functional unit much like an island within the bacterial chromosome. For example, intact PAIs appear to transfer between organisms and confer complex virulence properties to the recipient bacteria.

Chromosomal PAIs in bacterial cells have been described in increasing detail over recent years. For example, J. Hacker and co-workers described two large, unstable regions in the chromosome of uropathogenic *Escherichia coli* strain 536 as PAI-I and PAI-II (Hacker J., *et al.*, *Microbiol. Pathog.* 8:213-25 1990). Hacker found that PAI-I and PAI-II containing virulence regions can be lost by spontaneous deletion due to recombination events. Both of these PAIs were found to encode multiple virulence genes, and their loss resulted in reduced hemolytic activity, serum resistance, mannose-resistant hemagglutination, uroepithelial cell binding, and mouse virulence of the *E. coli.* (Knapp, S *et al.*, *J. Bacteriol.* 168:22-30 1986). Therefore, pathogenicity islands are characterized by their ability to confer complex virulence phenotypes to bacterial cells.

In addition to *E. coli,* specific deletion of large virulence regions has been observed in other bacteria such as *Yersinia pestis*. For example, Fetherston and co-workers found that a 102-kb region of the *Y. pestis* chromosome lost by spontaneous deletion resulted in the loss of many *Y. pestis* virulence phenotypes. (Fetherston, J.D. and Perry, R.D., *Mol. Microbiol.* 13:697-708 1994, Fetherston, *et al.*, *Mol. Microbiol.* 6:2693-704 1992). In this instance, the deletion appeared to be due to recombination within 2.2-kb repetitive elements at both ends of the 102-kb region.

It is possible that deletion of PAIs may benefit the organism by modulating bacterial virulence or genome size during infection. PAIs may also represent foreign DNA segments that were acquired during bacterial evolution that conferred important pathogenic properties to the bacteria. Observed flanking

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

INSDOCID: <WO___9822575A2 I >

repeats, as observed in *Y. pestis* for example, may suggest a common mechanism by which these virulence genes were integrated into the bacterial chromosomes.

Integration of the virulence genes into bacterial chromosomes was further elucidated by the discovery and characterization of a locus of enterocyte effacement (the LEE locus) in enteropathogenic *E. coli* (McDaniel, *et al.*, *Proc. Natl Acad. Sci.* (USA) 92:1664-8 1995). The LEE locus comprises 35-kb and encodes many genes required for these bacteria to "invade" and degrade the apical structure of enerocytes causing diarrhea. Although the LEE and PAI-I loci encode different virulence genes, these elements are located at the exact same site in the *E. coli* genome and contain the same DNA sequence within their right-hand ends, thus suggesting a common mechanism for their insertion.

Besides being found in enteropathogenic *E. coli*, the LEE element is also present in rabbit diarrheal *E. coli*, *Hafnia alvei*, and *Citrobacter freundii* biotype 4280, all of which induce attaching and effacing lesions on the apical face of enterocytes. The LEE locus appears to be inserted in the bacterial chromosome as a discrete molecular and functional virulence unit in the same fashion as PAI-I, PAI-II, and *Yersinia* PAI.

Along these same lines, a 40-kb *Salmonella typhimurium* PAI was characterized on the bacterial chromosome which encodes genes required for *Salmonella* entry into nonphagocytic epithelial cells of the intestine (Mills, D.M., *et al.*, *Mol. Microbiol.* 15:749-59 1995). Like the LEE element, this PAI confers to *Salmonella* the ability to invade intestinal cells, and hence may likewise be characterized as an "invasion" PAI.

The pathogenicity islands described above all possess the common feature of conferring complex virulence properties to the recipient bacteria. However, they may be separated into two types by their respective contributions to virulence. PAI-I, PAI-II, and the *Y. pestis* PAI confer multiple virulence phenotypes, while the LEE and the *S. typhimurium* "invasion" PAI encode many genes specifying a single, complex virulence process.

It is advantageous to characterize closely-related bacteria that contain or do not contain the PAI by the isolation of a discrete molecular and functional unit

INSDOCID <WO__9822575A2_I_>

on the bacterial chromosome. Since the presence versus the absence of essential virulence genes can often distinguish closely-related virulent versus avirulent bacterial strains or species, experiments have been conducted to identify virulence loci and potential PAIs by isolating DNA sequences that are unique to virulent bacteria (Bloch, C.A., *et al.*, *J Bacteriol.* 176:7121-5 1994, Groisman, E.A., *EMBO J.* 12:3779-87 1993).

At least two PAIs are present in *E. coli* J96. These PAIs, PAI IV and PAI V are linked to tRNA loci but at sites different from those occupied by other known *E. coli* PAIs. Swenson *et al., Infect. and Immun. 64*:3736-3743 (1996).

The era of true comparative genomics has been ushered in by high through-put genomic sequencing and analysis. The first two complete bacterial genome sequences, those of *Haemophilus influenzae* and *Mycoplasma genitalium* were recently described (Fleischmann, R.D., *et al.*, *Science 269*:496 (1995); Fraser, C.M., *et al.*, *Science 270*:397 (1995)). Large scale DNA sequencing efforts also have produced an extensive collection of sequence data from eukaryotes, including *Homo sapiens* (Adams, M.D., *et al.*, *Nature* 377:3 (1995)) and *Saccharomyces cerevisiae* (Levy, J., *Yeast 10*:1689 (1994)).

The need continues to exist for the application of high through-put sequencing and analysis to study genomes and subgenomes of infectious organisms. Further, a need exists for genetic markers that can be employed to distinguish closely-related virulent and avirulent strains of a given bacteria.

Summary of the Invention

The present invention is based on the high through-put, random sequencing of cosmid clones covering two pathogenic islands (PAIs) of uropathogenic *Escherichia coli* strain J96 (O4:K6; *E. coli* J96). PAIs are large fragments of DNA which comprise pathogenicity determinants. PAI IV is located approximately at 64 min (near *pheV*) on the *E. coli* chromosome and is greater than 170 kilobases in size. PAI V is located at approximately 94 min (at *phe*R) on the *E. coli* chromosome and is approximately 106 kb in size. These PAIs

NSDOCID <WO 9822575A2 I >

differ in location from the PAIs described by Hacker and colleagues for uropathogenic strain 536 (PAI I, 82 minutes {*sel*C} and PAI II, 97 minutes {*leu*X}).

The location of the PAIs relative to one another and the cosmid clones covering the J96 PAIs is shown in Figure 1. The present invention relates to the nucleotide sequences of 142 fragments of DNA (contigs) covering the PAI IV and PAI V regions of the *E. coli* J96 chromosome. The nucleotide sequences shown in SEQ ID NOs: 1 through 142 were obtained by shotgun sequencing eleven *E. coli* J96 subclones, which were deposited in two pools on September 23, 1996 at the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, and given accession numbers 97726 (includes 7 cosmid clones covering PAI (IV) and 97727 (includes 4 cosmid clones covering PAI V). The deposited sets or "pools" of clones are more fully described in Example 1. In addition, *E. coli* strain J96 was also deposited at the American Type Culture Collection on September 23, 1996, and given accession number 98176.

Three hundred fifty-one open reading frames have been thus far identified in the 142 contigs described by SEQ ID NOs: 1 through 142. Thus, the present invention is directed to isolated nucleic acid molecules comprising open reading frames (ORFs) encoding *E. coli* J96 PAI proteins, and fragments of said nucleic acid molecules.

The present invention also relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of *E. coli* J96 PAI proteins. Further embodiments include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an *E. coli* J96 PAI ORF described herein, and fragments of said nucleic acid molecules.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention and fragments thereof, host cells containing the recombinant vectors, as well as methods for

NSDOCID <WO 9822575A2 I_>

making such vectors and host cells for *E. coli* J96 PAI protein production by recombinant techniques.

The invention further provides isolated polypeptides encoded by the *E. coli* J96 PAI ORFs or fragments of said ORFs. It will be recognized that some amino acid sequences of the polypeptides described herein can be varied without significant effect on the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope-bearing portion is an immunogenic or antigenic epitope useful for raising antibodies.

The invention further provides a vaccine comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*, such as strain J96.

The invention also provides a method of eliciting a protective immune response in an animal comprising administering to the animal the above-described vaccine.

The invention further provides a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for one or more of:

(a) polynucleic acids encoding an open reading frame listed in Tables 1-4 or a fragment of said polynucleic acid;

(b) full length or mature polypeptides encoded for by an open reading frame listed in Tables 1-4; or

3NSDOCID <WO 9822575A2 I >

(c) antibodies specific to polypeptides encoded for by an open reading frame listed in Tables 1-4.

The invention further provides a nucleic acid probe for the detection of the presence of one or more *E. coli* PAI nucleic acids (nucleic acids encoding one or more ORFs as listed in Tables 1-4) in a sample from an individual comprising one or more nucleic acid molecules sufficient to specifically detect under stringent hybridization conditions the presence of the above-described molecule in the sample.

The invention also provides a method of detecting *E. coli* PAI nucleic acids in a sample comprising:

a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and

b) detecting the presence of the probe bound to an *E. coli* PAI nucleic acid.

The invention further provides a kit for detecting the presence of one or more *E. coli* PAI nucleic acids in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

The invention also provides a diagnostic kit for detecting the presence of pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antibodies.

The invention also provides a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antigens.

Brief Description of the Figures

Figure 1 is a schematic diagram of cosmid clones derived from *E. coli* J96 pathogenicity island and map positions of known *E. coli* PAIs (not drawn to scale). The gray bar represents the *E. coli* K-12 chromosome with minute demarcations of PAI junction points located above the bar. *E. coli* J96 overlapping cosmid clones are represented by hatched bars (overlap not drawn to

SDOCID: <WO__9822575A2 1 >

scale) with positions of *hly*, *pap*, and *prs* operons indicated above bar. The PAIs and estimated sizes are shown above and below the K-12 chromosome map.

Figure 2 is a block diagram of a computer system 102 that can be used to implement the computer-based systems of present invention.

Detailed Description of the Invention

The present invention is based on high through-put, random sequencing of a uropathogenic strain of *Escherichia coli*. The DNA sequences of contiguous DNA fragments covering the pathogenicity islands, PAI IV (also referred to as $PAI_{J96(pheV)}$) and PAI V (also referred to as $PAI_{J96(pheU)}$) from the chromosome of the *E. coli* uropathogenic strain, J96 (04:K6) were determined. The sequences were used for DNA and protein sequence similarity searches of the database.

The primary nucleotide sequences generated by shotgun sequencing cosmid clones of the PAI IV and PAI V regions of the *E. coli* chromosome are provided in SEQ ID NOs:1 through 142. These sequences represent contiguous fragments of the PAI DNA. As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system. The present invention provides the nucleotide sequences of SEQ ID NOs:1 through 142, or representative fragments thereof, in a form that can be readily used, analyzed, and interpreted by a skilled artisan. Within these 142 sequences, there have been thus far identified 351 open reading frames (ORFs) that are described in greater detail below.

As used herein, a "representative fragment" refers to *E. coli* J96 PAI protein-encoding regions (also referred to herein as open reading frames or ORFs), expression modulating fragments, and fragments that can be used to diagnose the presence of *E. coli* in a sample. A non-limiting identification of such representative fragments is provided in Tables 1 through 6, preferably in Tables 1 through 4. As described in detail below, representative fragments of the present invention further include nucleic acid molecules having a nucleotide sequence at least 95% identical, preferably at least 96%, 97%, 98%, or 99%

NSDOCID <WO 9822575A2 I >

identical, to an ORF identified in Tables 1 through 6, or more preferably Tables 1 through 4.

As indicated above, the nucleotide sequence information provided in SEQ ID NOs:1 through 142 was obtained by sequencing cosmid clones covering the PAIs located on the chromosome of *E. coli* J96 using a megabase shotgun sequencing method. The sequences provided in SEQ ID NOs:1 through 142 are highly accurate, although not necessarily a 100% perfect, representation of the nucleotide sequences of contiguous stretches of DNA (contigs) which include the ORFs located on the two pathogenicity islands of *E. coli* J96. As discussed in detail below, using the information provided in SEQ ID NOs:1 through 142 and in Tables 1 through 6 together with routine cloning and sequencing methods, one of ordinary skill in the art would be able to clone and sequence all "representative fragments" of interest including open reading frames (ORFs) encoding a large variety of *E. coli* J96 PAI proteins. In rare instances, this may reveal a nucleotide sequence error present in the nucleotide sequences disclosed in SEQ ID NOs: 1 through 142. Thus, once the present invention is made available (i.e., once the information in SEQ ID NOs: 1 through 142 and in Tables 1 through 6 is made available), resolving a rare sequencing error would be well within the skill of the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler™ can be used as an aid during visual inspection of nucleotide sequences.

Even if all of the rare sequencing errors were corrected, it is predicted that the resulting nucleotide sequences would still be at least about 99.9% identical to the reference nucleotide sequences in SEQ ID NOs: 1 through 142. Thus, the present invention further provides nucleotide sequences that are at least 99.9% identical to the nucleotide sequence of SEQ ID NOs: 1 through 142 in a form which can be readily used, analyzed and interpreted by the skilled artisan. Methods for determining whether a nucleotide sequence is at least 99.9% identical to a reference nucleotide sequence of the present invention are described below.

WSDOCID <WO_ 9822575A2_I_>

Nucleic Acid Molecules

The present invention is directed to isolated nucleic acid fragments of the PAIs of *E. coli* J96. Such fragments include, but are not limited to, nucleic acid molecules encoding polypeptides, nucleic acid molecules that modulate the expression of an operably linked ORF (hereinafter expression modulating fragments (EMFs)), and nucleic acid molecules that can be used to diagnose the presence of *E. coli* in a sample (hereinafter diagnostic fragments (DFs)).

By "isolated nucleic acid molecule(s)" is intended a nucleic acid molecule, DNA or RNA, that has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells, purified (partially or substantially) DNA molecules in solution, and nucleic acid molecules produced synthetically. Isolated RNA molecules include *in vitro* RNA transcripts of the DNA molecules of the present invention.

In one embodiment, *E. coli* J96 PAI DNA can be mechanically sheared to produce fragments about 15-20 kb in length, which can be used to generate an *E. coli* J96 PAI DNA library by insertion into lambda clones as described in Example 1 below. Primers flanking an ORF described in Tables 1 through 6 can then be generated using the nucleotide sequence information provided in SEQ ID NOs: 1 through 142. The polymerase chain reaction (PCR) is then used to amplify and isolate the ORF from the lambda DNA library. PCR cloning is well known in the art. Thus, given SEQ ID NOs: 1 through 142, and Tables 1 through 6, it would be routine to isolate any ORF or other representative fragment of the *E. coli* J96 PAI subgenomes. Isolated nucleic acid molecules of the present invention include, but are not limited to, single stranded and double stranded DNA, and single stranded RNA, and complements thereof.

Tables 1 through 6 herein describe ORFs in the *E. coli* J96 PAI cosmid clone library.

NSDOCID <WO_ 9822575A2 I >

Tables 1 and 3 list, for PAI IV and PAI V, respectively, a number of ORFs that putatively encode a recited protein based on homology matching with protein sequences from an organism listed in the Table. Tables 1 and 3 indicate the location of ORFs (i.e., the position) by reference to its position within the one of the 142 *E. coli* J96 contigs described in SEQ ID NOs: 1 through 142. Column 1 of Tables 1 and 3 provides the Sequence ID Number (SEQ ID NO) of the contig in which a particular open reading frame is located. Column 2 numerically identifies a particular ORF on a particular contig (SEQ ID NO) since many contigs comprise a plurality of ORFs. Columns 3 and 4 indicate an ORF's position in the nucleotide sequence (contig) provided in SEQ ID NOs: 1 through 142 by referring to start and stop positions in the contig sequence.

One of ordinary skill in the art will appreciate that the ORFs may be oriented in opposite directions in the *E. coli* chromosome. This is reflected in columns 3 and 4. For these ORFs, the sense strand is complementary to the actual sequence given. The corresponding sense-strand of the ORF must be read as the 5'-3' complement of the antisense strand actually shown in the Sequence Listing, wherein the location is specified 3'-5'.

Column 5 provides a database accession number to a homologous protein identified by a similarity search of public sequence databases (*see*, infra). Column 6 describes the matching protein sequence and the source organism is identified in brackets. Column 7 of Tables 1 and 3 indicates the percent similarity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 of Tables 1 and 3 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. The concepts of percent identity and percent similarity of two polypeptide sequences are well understood in the art and are described in more detail below. Identified genes can frequently be assigned a putative cellular role category adapted from Riley (*see*, Riley, M., *Microbiol. Rev. 57*:862 (1993)). Column 9 of Tables 1 and 3 provides the nucleotide length of the open reading frame.

NSDOCID <WO 9822575A2 I_>

Tables 2 and 4, below, provide ORFs of *E. coli* J96 PAI IV and PAI V, respectively, that did not elicit a homology match with a known sequence from either *E. coli* or another organism. As above, the first column in Tables 2 and 4 provides the contig in which the ORF is located and the second column numerically identifies a particular ORF in a particular contig. Columns 3 and 4 identify an ORF's position in one of SEQ ID NOs: 1 through 142 by reference to start and stop nucleotides.

Tables 5 and 6, below, provide the *E. coli* J96 PAI IV ORFs and PAI V ORFs, respectively, identified by the present inventors that provided a significant match to a previously published *E. coli* protein. Columns 1-6 correspond to columns 1-6 appearing in Tables 1 and 3. Column 7 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 indicates the length of the high-scoring segment pair (HSP). Column 9 provides the nucleotide length of the open reading frame.

As used herein, "open reading frame" or "ORF" refers to the nucleotide sequences as described in Tables 1 through 6. In Tables 1 through 6, each ORF is designated by a nucleotide sequence start position and stop position according to numbering of contig nucleotides in the Sequence Listing provided (Contig ID = SEQ ID NO).

In a first embodiment, the invention comprises a nucleotide sequence described in Tables 1 through 4 which begins with the nucleotide following the last nucleotide of an upstream stop codon (first nucleotide of the "ORF"), an initiation codon, in-frame putative polypeptide-encoding sequence, and nucleotides of an in-frame stop codon.

In a second embodiment, the invention comprises a nucleotide sequence of Tables 1 through 4 which contains an initiation codon (*e.g.* a methionine or valine codon) on their 5' end and a stop codon on their 3' end. The sequences of this embodiment are present within the nucleotide sequence described in Tables 1 through 4 by start and stop position as numbered in the Sequence Listing. To

INSDOCID: <WO 9822575A2_I_>

determine the 5' start position of this embodiment, one simply reads 5' to 3' from the designated 5' end position until an initiation codon is found.

In a third embodiment, the invention comprises a nucleotide sequence of the second embodiment, except that the 3' stop codon is not present.

In a fourth embodiment, the invention comprises a nucleotide sequence encoding a putative protein which is a sequence of Tables 1 through 4 excluding sequence encoding amino acids subject to removal by post-translational processing and sequences 3' of the last codon coding for an amino acid present in the putative polypeptide (*e.g.*, sequences not containing the stop codon and encoding the mature form of the polypeptide).

Certain embodiments of the invention may therefore either include or exclude initiation codons for methionine or valine and either include or exclude the stop codon.

Further details concerning the algorithms and criteria used for homology searches are provided in the Examples below. A skilled artisan can readily identify ORFs in the *Escherichia coli* J96 cosmid library other than those listed in Tables 1 through 6, such as ORFs that are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

Isolated nucleic acid molecules of the present invention include DNA molecules having a nucleotide sequence substantially different than the nucleotide sequence of an ORF described in Tables 1 through 4, but which, due to the degeneracy of the genetic code, still encode a *E. coli* J96 PAI protein. The genetic code is well known in the art. Thus, it would be routine to generate such degenerate variants.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of an *E. coli* protein encoded by an ORF described in Table 1 through 4. Non-naturally occurring variants may be produced using art-known mutagenesis techniques and include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more

NSDOCID <WO 9822575A2_I_>

nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *E. coli* protein or portions thereof. Also especially preferred in this regard are conservative substitutions.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an ORF described in Tables 1 through 6, preferably 1 through 4. By a polynucleotide having a nucleotide sequence at least, for example, 95% identical to the reference *E. coli* ORF nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the ORF sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference ORF nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5′ or 3′ terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleotide sequence of an *E. coli* J96 PAI ORF can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). Bestfit uses the local homology algorithm of Smith and Waterman, *Advances in Applied Mathematics 2*: 482-489 (1981),

NSDOCID <WO 9822575A2 I >

to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

Preferred are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence of an *E. coli* J96 PAI ORF that encode a functional polypeptide. By a "functional polypeptide" is intended a polypeptide exhibiting activity similar, but not necessarily identical, to an activity of the protein encoded by the *E. coli* J96 PAI ORF. For example, the *E. coli* ORF [Contig ID 84, ORF ID 3 (84/3)] encodes a hemolysin. Thus, a "functional polypeptide" encoded by a nucleic acid molecule having a nucleotide sequence, for example, 95% identical to the nucleotide sequence of 84/3, will also possess hemolytic activity. As the skilled artisan will appreciate, assays for determining whether a particular polypeptide is "functional" will depend on which ORF is used as the reference sequence. Depending on the reference ORF, the assay chosen for measuring polypeptide activity will be readily apparent in light of the role categories provided in Tables 1, 3, 5 and 6.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of a reference ORF will encode a functional polypeptide. In fact, since degenerate variants all encode the same amino acid sequence, this will be clear to the skilled artisan even without performing a comparison assay for protein activity. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a functional polypeptide. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not

INSDOCID <WO 9822575A2 I >

likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid).

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science 247*:1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie, J.U. *et al., supra,* and the references cited therein.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated nucleic acid molecule having the nucleotide sequence of an *E. coli* J96 PAI ORF is intended fragments at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length that are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-500 nt in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequence of an *E. coli* J96 PAI ORF. By a fragment at least 20 nt in length, for example, is intended fragments that include 20 or more contiguous bases from the nucleotide sequence of an *E. coli* J96 PAI ORF. Since *E. coli* ORFs are listed in Tables 1 through 6 and the sequences of the ORFs have been provided within the contig sequences of SEQ ID NOs: 1 through 142, generating

NSDOCID <WO 9822575A2 I >

such DNA fragments would be routine to the skilled artisan. For example, restriction endonuclease cleavage or shearing by sonication could easily be used to generate fragments of various sizes from the PAI DNA that is incorporated into the deposited pools of cosmid clones. Alternatively, such fragments could be generated synthetically.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of an *E. coli* J96 PAI protein. Methods for determining such epitope-bearing portions are described in detail below.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide that hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, an ORF described in Tables 1 through 6, preferably an ORF described in Tables 1, 2, 3 or 4. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5 x SSC (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 x SSC at about 65°C.

By a polynucleotide that hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide (e.g., a *E. coli* ORF), for instance, a portion 50-500 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of an *E. coli* J96 PAI ORF.

JSDOCID: <WO 9822575A2 I >

By "expression modulating fragment" (EMF), is intended a series of nucleotides that modulate the expression of an operably linked, putative polypeptide-encoding region (encoding region). A sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments that induce the expression of an operably linked encoding region in response to a specific regulatory factor or physiological event. EMF sequences can be identified within the *E. coli* genome by their proximity to the encoding regions within ORFs described in Tables 1 through 6. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken 5′ from any one of the encoding regions of ORFs of Tables 1 through 6 will modulate the expression of an operably linked 3′ encoding region in a fashion similar to that found within the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to the fragments of the *E. coli* J96 PAI subgenome that are between two encoding regions herein described. Alternatively, EMFs can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site 5′ to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence that is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed

JSDOCID <WO 9822575A2 I >>

host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

By a "diagnostic fragment" (DF), is intended a series of nucleotides that selectively hybridize to *E. coli* sequences. DFs can be readily identified by identifying unique sequences within the *E. coli* J96 PAI subgenome, or by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format for amplification or hybridization selectivity.

Each of the ORFs of the *E. coli* J96 PAI subgenome disclosed in Tables 1 through 4, and EMFs found 5′ to the encoding regions of the ORFs, can be used in numerous ways as polynucleotide reagents. The sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of uropathogenic *E. coli* in a sample. This is especially the case with the fragments or ORFs of Table 2 and 4 which will be highly selective for uropathogenic *E. coli* J96, and perhaps other uropathogenic or extraintestinal strains that include one or more PAIs.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56*:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the

NSDOCID: <WO_ 9822575A2 I >

sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

Vectors and Host Cells

The present invention further provides recombinant constructs comprising one or more fragments of the *E. coli* J96 PAIs. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which, for example, an *E. coli* J96 PAI ORF is inserted. The vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the encoding region of an ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments (preferably an ORF) of the *E. coli* J96 PAIs described herein. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a

3NSDOCID <WO_ 9822575A2 I_>

lower eukaryotic host cell, such as a yeast cell, or the host cell can be a procaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)). Host cells containing, for example, an *E. coli* J96 PAI ORF can be used conventionally to produce the encoded protein.

Polypeptides and Fragments

The invention further provides isolated polypeptides having the amino acid sequence encoded by an *E coli* PAI ORF described in Tables 1 through 6, preferably Tables 1 through 4, or a peptide or polypeptide comprising a portion of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least two amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

It will be recognized in the art that some amino acid sequences of *E. coli* polypeptides can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

Thus, the invention further includes variations of polypeptides encoded for by ORFs listed in Tables 1 through 6 which show substantial pathogenic activity or which include regions of particular *E. coli* PAI proteins such as the protein portions discussed below. Such mutants include deletions, insertions,

NSDOCID <WO_ 9822575A2_I >

inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" amino acid substitutions will generally have little effect on activity.

Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

As indicated in detail above, further guidance concerning which amino acid changes are likely to be phenotypically silent (i.e., are not likely to have a significant deleterious effect on a function) can be found in Bowie, J.U., *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science 247:*1306-1310 (1990).

Thus, the fragment, derivative or analog of a polypeptide encoded by an ORF described in one of Tables 1 through 6, may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Of particular interest are substitutions of charged amino acids with another charged amino acid and with neutral or negatively charged amino acids. The latter results in proteins with reduced positive charge to improve the

NSDOCID <WO___9822575A2 I_>

characteristics of said proteins. The prevention of aggregation is highly desirable. Aggregation of proteins not only results in a loss of activity but can also be problematic when preparing pharmaceutical formulations, because they can be immunogenic. (Pinckard *et al., Clin Exp. Immunol. 2*:331-340 (1967); Robbins *et al., Diabetes 36*:838-845 (1987); Cleland *et al. Crit. Rev. Therapeutic Drug Carrier Systems 10*:307-377 (1993)).

The replacement of amino acids can also change the selectivity of binding to cell surface receptors. Ostade *et al., Nature 361*:266-268 (1993) describes certain mutations resulting in selective binding of TNF-α to only one of the two known types of TNF receptors. Thus, proteins encoded for by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6, and that bind to a cell surface receptor, may include one or more amino acid substitutions, deletions or additions, either from natural mutations or human manipulation.

As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 7).

TABLE 7. Conservative Amino Acid Substitutions

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

NSDOCID <WO__9822575A2_I_>

Amino acids in the proteins encoded by ORFs of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, *Science 244*:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as receptor binding or *in vitro*, or *in vitro* proliferative activity. Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al., J. Mol. Biol. 224*:899-904 (1992) and de Vos *et al. Science 255*:306-312 (1992)).

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the polypeptides can be substantially purified by the one-step method described in Smith and Johnson, *Gene 67*:31-40 (1988).

The polypeptides of the present invention include the polypeptide encoded by the ORFs listed in Tables 1-6, preferably Tables 1-4, as well as polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above, and also include portions of such polypeptides with at least 30 amino acids and more preferably at least 50 amino acids.

By "% similarity" for two polypeptides is intended a similarity score produced by comparing the amino acid sequences of the two polypeptides using the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) and the default settings for determining similarity. Bestfit uses the local homology algorithm of Smith and Waterman *(Advances in Applied Mathematics 2*:482-489, 1981) to find the best segment of similarity between two sequences.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a reference amino acid sequence of a polypeptide is intended

NSDOCID <WO 9822575A2 I >

that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of said polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence encoded by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6 can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The polypeptide of the present invention could be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art.

As described in detail below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting pathogenic protein expression as described below or as

NSDOCID <WO__9822575A2 I_>

agonists and antagonists capable of enhancing or inhibiting protein function of important proteins encoded by the ORFs of the present invention. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" protein binding proteins which are also candidate agonist and antagonist according to the present invention. The yeast two hybrid system is described in Fields and Song, *Nature 340*:245-246 (1989).

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen *et al., Proc. Natl. Acad. Sci. USA 81*:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R.A. (1983) Antibodies that react with predetermined sites on proteins. *Science 219*:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. Sutcliffe *et al.*,

NSDOCID <WO 9822575A2 I >

supra, at 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. Sutcliffe *et al.*, *supra*, at 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (e.g., about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. See, for instance, Wilson *et al.*, *Cell 37*:767-778 (1984) at 777. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods well known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are

WSDOCID <WO__9822575A2_I_>

considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks. Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides: specificity of antigen-antibody interaction at the level of individual amino acids. *Proc. Natl. Acad. Sci. USA 82*:5131-5135. This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten *et al.* (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously. Houghten *et al.*, *supra*, at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe *et al.*, *supra*; Wilson *et al.*, *supra*; Chow, M. *et al.*, *Proc. Natl. Acad. Sci. USA 82*:910-914; and Bittle, F. J. *et al.*, *J. Gen. Virol. 66*:2347-2354 (1985).

3NSDOCID <WO__ 9822575A2 I >

Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 μg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an enzyme-linked immunosorbent assay. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction

INSDOCID <WO__ 9822575A2_I_>

with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) on Peralkylated Oligopeptide Mixtures discloses linear C_1-C_7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

The entire disclosure of each document cited in this section on "Polypeptides and Peptides" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, *E. coli* PAI polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, e.g., for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins (EP A 394,827; Traunecker *et al.*, *Nature 331*:84-86 (1988)). Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other

3NSDOCID: <WO 9822575A2_I_>

molecules than the monomeric *E. coli* J96 PAI proteins or protein fragments alone (Fountoulakis *et al., J. Biochem 270*:3958-3964 (1995)).

Vaccines

In another embodiment, the present invention relates to a vaccine, preferably in unit dosage form, comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit a protective immune response in an animal to pathogenic *E. coli*. Antigens of *E. coli* J96 PAI IV and V may be obtained from polypeptides encoded for by the ORFs listed in Tables 1-6, particularly Tables 1-4, using methods well known in the art.

In a preferred embodiment, the antigens are *E. coli* J96 PAI IV or PAI V proteins that are present on the surface of pathogenic *E. coli*. In another preferred embodiment, the pathogenic *E. coli* J96 PAI IV or PAI V protein-antigen is conjugated to an *E. coli* capsular polysaccharide (CP), particularly to capsular polypeptides that are more prevalent in pathogenic strains, to produce a double vaccine. CPs, in general, may be prepared or synthesized as described in Schneerson *et al. J. Exp. Med. 152:*361-376 (1980); Marburg *et al. J. Am. Chem. Soc.* 108:5282 (1986); Jennings *et al., J. Immunol. 127:*1011-1018 (1981); and Beuvery *et al., Infect. Immunol. 40:*39-45 (1983). In a further preferred embodiment, the present invention relates to a method of preparing a polysaccharide conjugate comprising: obtaining the above-described *E. coli* J96 PAI antigen; obtaining a CP or fragment from pathogenic *E. coli*; and conjugating the antigen to the CP or CP fragment.

In a preferred embodiment, the animal to be protected is selected from the group consisting of humans, horses, deer, cattle, pigs, sheep, dogs, and chickens. In a more preferred embodiment, the animal is a human or a dog.

In a further embodiment, the present invention relates to a prophylactic method whereby the incidence of pathogenic *E. coli*-induced symptoms are

WSDOCID: <WO 9822575A2 I_>

decreased in an animal, comprising administering to the animal the above-described vaccine, wherein the vaccine is administered in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*. This vaccination method is contemplated to be useful in protecting against severe diarrhea (pathogenic intestinal *E. coli* strains), urinary tract infections (uropathogenic *E. coli*) and infections of the brain (extraintestinal *E. coli*). The vaccine of the invention is used in an effective amount depending on the route of administration. Although intra-nasal, subcutaneous or intramuscular routes of administration are preferred, the vaccine of the present invention can also be administered by an oral, intraperitoneal or intravenous route. One skilled in the art will appreciate that the amounts to be administered for any particular treatment protocol can be readily determined without undue experimentation. Suitable amounts are within the range of 2 micrograms of the protein per kg body weight to 100 micrograms per kg body weight.

The vaccine can be delivered through a vector such as BCG. The vaccine can also be delivered as naked DNA coding for target antigens.

The vaccine of the present invention may be employed in such dosage forms as capsules, liquid solutions, suspensions or elixirs for oral administration, or sterile liquid forms such as solutions or suspensions. Any inert carrier is preferably used, such as saline, phosphate-buffered saline, or any such carrier in which the vaccine has suitable solubility properties. The vaccines may be in the form of single dose preparations or in multi-dose flasks which can be used for mass vaccination programs. Reference is made to Remington's *Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, Osol (ed.) (1980); and *New Trends and Developments in Vaccines*, Voller *et al.* (eds.), University Park Press, Baltimore, MD (1978), for methods of preparing and using vaccines.

The vaccines of the present invention may further comprise adjuvants which enhance production of antibodies and immune cells. Such adjuvants include, but are not limited to, various oil formulations such as Freund's complete adjuvant (CFA), the dipeptide known as MDP, saponins (ex. *Quillajasaponin* fraction QA-21, U.S. Patent No. 5,047,540), aluminum hydroxide, or lymphatic

3NSDOCID <WO_ 9822575A2 I_>

cytokines. Freund's adjuvant is an emulsion of mineral oil and water which is mixed with the immunogenic substance. Although Freund's adjuvant is powerful, it is usually not administered to humans. Instead, the adjuvant alum (aluminum hydroxide) may be used for administration to a human. Vaccine may be absorbed onto the aluminum hydroxide from which it is slowly released after injection. The vaccine may also be encapsulated within liposomes according to Fullerton, U.S. Patent No. 4,235,877.

Protein Function

Each ORF described in Tables 1 and 3 possesses a biological role similar to the role associated with the identified homologous protein. This allows the skilled artisan to determine a function for each identified coding sequence. For example, a partial list of the *E. coli* protein functions provided in Tables 1 and 3 includes many of the functions associated with virulence of pathogenic bacterial strains. These include, but are not limited to adhesins, excretion pathway proteins, O-antigen/carbohydrate modification, cytotoxins and regulators. A more detailed description of several of these functions is provided in Example 1 below.

Diagnostic Assays

In another preferred embodiment, the present invention relates to a method of detecting pathogenic *E. coli* nucleic acid in a sample comprising:

a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and

b) detecting the presence of the probe bound to pathogenic *E. coli* nucleic acid.

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* nucleic acid in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

INSDOCID <WO 9822575A2 I >

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antibodies.

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antigens.

The present invention provides methods to identify the expression of an ORF of the present invention, or homolog thereof, in a test sample, using one of the antibodies of the present invention. Such methods involve incubating a test sample with one or more of the antibodies of the present invention and assaying for binding of the antibodies to components within the test sample.

In a further embodiment, the present invention relates to a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for a nucleic acid, protein, polypeptide-antigen or antibody specific to one of the ORFs described in Tables 1-4 herein from *E. coli* J96 PAI IV or V. Analysis of nucleic acid specific to pathogenic *E. coli* can be by PCR techniques or hybridization techniques (cf. *Molecular Cloning: A Laboratory Manual, second edition*, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989; Eremeeva *et al., J. Clin. Microbiol. 32*:803-810 (1994) which describes differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA).

Proteins or antibodies specific to pathogenic *E. coli* may be identified as described in *Molecular Cloning: A Laboratory Manual, second edition*, Sambrook *et al.*, eds., Cold Spring Harbor Laboratory (1989). More specifically, antibodies may be raised to *E. coli* J96 PAI proteins as generally described in *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988). *E. coli* J96 PAI-specific antibodies can also be obtained from infected animals (Mather, T. *et al.*, *JAMA 205*:186-188 (1994)).

BNSDOCID <WO_ 9822575A2_I >

In another embodiment, the present invention relates to an antibody having binding affinity specifically to an *E. coli* J96 PAI antigen as described above. The *E. coli* J96 PAI antigens of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, a peptide can be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well as fragments of these antibodies. The invention further includes single chain antibodies. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques, for example, such fragments include but are not limited to: the $F(ab')_2$ fragment; the Fab' fragments, Fab fragments, and Fv fragments.

Of special interest to the present invention are antibodies to pathogenic *E. coli* antigens which are produced in humans, or are "humanized" (i.e. non-immunogenic in a human) by recombinant or other technology. Humanized antibodies may be produced, for example by replacing an immunogenic portion of an antibody with a corresponding, but non-immunogenic portion (i.e. chimeric antibodies) (Robinson, R.R. *et al.*, International Patent Publication PCT/US86/02269; Akira, K. *et al.*, European Patent Application 184,187; Taniguchi, M., European Patent Application 171,496; Morrison, S.L. *et al.*, European Patent Application 173,494; Neuberger, M.S. et al., PCT Application WO 86/01533; Cabilly, S. *et al.*, European Patent Application 125,023; Better, M. *et al., Science 240*:1041-1043 (1988); Liu, A.Y. *et al., Proc. Natl. Acad. Sci. USA 84*:3439-3443 (1987); Liu, A.Y. *et al., J. Immunol. 139*:3521-3526 (1987); Sun, L.K. *et al., Proc. Natl. Acad. Sci. USA 84*:214-218 (1987); Nishimura, Y. *et al., Canc. Res. 47*:999-1005 (1987); Wood, C.R. *et al., Nature 314*:446-449 (1985)); Shaw *et al., J. Natl. Cancer Inst. 80*:1553-1559 (1988). General reviews of "humanized" chimeric antibodies are provided by Morrison, S.L. (*Science, 229*:1202-1207 (1985)) and by Oi, V.T. *et al., BioTechniques 4*:214 (1986)). Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones, P.T. *et al., Nature 321*:552-525 (1986); Verhoeyan *et al.*,

NSDOCID <WO_ 9822575A2_I_>

Science 239:1534 (1988); Beidler, C.B. *et al., J. Immunol. 141*:4053-4060 (1988)).

In another embodiment, the present invention relates to a hybridoma which produces the above-described monoclonal antibody. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "*Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*," Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al., J. Immunol. Methods 35*:1-21 (1980)).

In another embodiment, the present invention relates to a method of detecting a pathogenic *E. coli* antigen in a sample, comprising: a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and b) detecting the presence of said antibody bound to the antigen. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard, *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock *et al., Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands

INSDOCID: <WO__9822575A2 1 >

(1985); and *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is capable with the system utilized.

In another embodiment, the present invention relates to a method of detecting the presence of antibodies to pathogenic *E. coli* in a sample, comprising: a) contacting the sample with an above-described antigen, under conditions such that immunocomplexes form, and b) detecting the presence of said antigen bound to the antibody. In detail, the methods comprise incubating a test sample with one or more of the antigens of the present invention and assaying whether the antigen binds to the test sample.

In another embodiment of the present invention, a kit is provided which contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: i) a first container means containing an above-described antibody, and ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies. Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits.

NSDOCID: <WO_ 9822575A2_I_>

One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

Screening Assay for Binding Agents

Using the isolated proteins described herein, the present invention further provides methods of obtaining and identifying agents that bind to a protein encoded by an *E. coli* J96 PAI ORF or to a fragment thereof.

The method involves:

(a) contacting an agent with an isolated protein encoded by a *E. coli* J96 PAI ORF, or an isolated fragment thereof; and

(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques. For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by an ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide ligands, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides, In *Synthetic Peptides, A User's Guide*, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry 28*:9230-8 (1989).

3NSDOCID: <WO__9822575A2 I >

In addition to the foregoing, one class of agents of the present invention, can be used to control gene expression through binding to one of the ORF encoding regions or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed and selected. Targeting the encoding region or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF encoding region or multiple encoding regions that rely on the same EMF for expression control.

One class of DNA binding agents are those that contain nucleotide base residues that hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives having base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*: 1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56*:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Computer Related Embodiments

The nucleotide sequence provided in SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to the sequences provided in SEQ ID NOs: 1 through 142, can be "provided" in

VSDOCID <WO 9822575A2 I >

a variety of media to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, that contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NOs: 1 through 142, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NOs: 1 through 142. Such a manufacture provides the *E. coli* J96 PAI subgenomes or a subset thereof (e.g., one or more *E. coli* J96 PAI open reading frame (ORF)) in a form that allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *E. coli* J96 PAI subgenome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, one or more nucleotide sequences of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on

3NSDOCID: <WO 9822575A2_I_>

computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of dataprocessor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to SEQ ID NOs: 1 through 142, in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem. 17*:203-207 (1993)) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the *E. coli* J96 PAI subgenome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the *E. coli* J96 PAI subgenome and are useful in producing commercially important proteins such as enzymes used in modifying surface O-antigens of bacteria. A comprehensive list of ORFs encoding commercially important *E. coli* J96 PAI proteins is provided in Tables 1 through 6.

The present invention provides a DNA sequence - gene database of pathogenicity islands (PAIs) for *E. coli* involved in infectious diseases. This database is useful for identifying and characterizing the basic functions of new virulence genes for *E. coli* involved in uropathogenic and extraintestinal diseases. The database provides a number of novel open reading frames that can be selected for further study as described herein.

Selectable insertion mutations in plasmid subclones encoding PAI genes with potentially significant phenotypes for *E. coli* uropathogenesis and sepsis can

ISDOCID <WO 9822575A2_I_>

be isolated. The mutations are then crossed back into wild type, uropathogenic *E. coli* by homologous recombination to create wild-type strains specifically altered in the targeted gene. The significance of the genes to *E. coli* pathogenesis is assessed by *in vitro* assays and *in vivo* murine models of sepsis/peritonitis and ascending urinary tract infection.

New virulence genes and PAI sites in uropathogenic *E. coli* may be identified by the transposon signature-tagged mutagenesis system and negative selection of *E. coli* mutants avirulent in murine models of ascending urinary tract infection or peritonitis.

Epidemiological investigations of new virulence genes and PAIs may be used to test for their occurrence in the genomes of other pathogenic and opportunistic members of the Enterobacteriaceae.

One can choose from the ORFs included in SEQ ID NOs: 1 through 142, using Tables 1 through 6 as a useful guidepost for selecting, as candidates for targeted mutagenesis, a limited number of candidate genes within the PAIs based on their homology to virulence, export or regulation genes in other pathogens. For the large number of apparent genes within the PAIs that do not share sequence similarity to any entries in the database, the transposon signature-tagged mutagenesis method developed by David Holden's laboratory can be employed as an independent means of virulence gene identification.

Allelic knock-outs are constructed using different *pir*-dependent suicide vectors (Swihart, K.A. and R.A. Welch, *Infect. Immun. 58*:1853-1869 (1990)). In addition, two different animal model systems can be employed for assessment of pathogenic determinants. The initial identification of *E. coli* hemolysin as a virulence factor came from the construction of isogenic *E. coli* strains that were tested in a rat model of intra-abdominal sepsis (Welch, R.A. *et al., Nature (London) 294*:665-667 (1981)). The ascending UTI (Urinary Tract Infection) mouse model was also successfully performed with allelic knock-outs of the *hpmA* hemolysin of *Proteus mirabilis* (Swihart, K.A. and R.A. Welch, *Infect. Immun. 58*:1853-1869 (1990)).

3NSDOCID: <WO _ 9822575A2 I >

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *E. coli* J96 PAI subgenome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *E. coli* genome that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

NSDOCID: <WO 9822575A2_I_>

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the *E. coli* J96 PAI subgenome, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequence and the homologous *E. coli* J96 PAI sequence identified using a search means as described above, and an output means for outputting the identified homologous *E. coli* J96 PAI sequence. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *E. coli* J96 PAI subgenome possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the

3NSDOCID: <WO__9822575A2 I >

E. coli J96 PAI subgenomes. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) can be used to identify open reading frames within the *E. coli* J96 PAI subgenome A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

One application of this embodiment is provided in Figure 2. Figure 2 provides a block diagram of a computer system 102 that can be used to implement the present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114 once inserted in the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. Software for accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108 during execution.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

VSDOCID <WO_ 9822575A2 I_>

Experimental

Example 1: High Through-put Sequencing of Cosmid Clones Covering PAI IV and PAI V in E. coli J96

The complete DNA sequence of the pathogenicity islands, PAI IV and PAI V (respectively >170 kb and ~110 kb), from uropathogenic *E. coli* strain, J96 (04:K6) was determined using a strategy, cloning and sequencing method, data collection and assembly software essentially identical to those used by the TIGR group for determining the sequence of the *Haemophilus influenzae* genome (Fleischmann, R.D., *et al.*, *Science 269*:496 (1995)). The sequences were then used for DNA and protein sequence similarity searches of the databases as described in Fleischmann, *Id.*

The analysis of the genetic information found within the PAIs of *E. coli* J96 was facilitated by the use of overlapping cosmid clones possessing these unique segments of DNA. These cosmid clones were previously constructed and mapped (as further described below) as an overlapping set in the laboratory of Dr. Doug Berg (Washington University). A gap exists between the left portion of cosmid 2 and the end of the PAI IV that would represent the *phe*V junction to the *E. coli* K-12 genome.

Uropathogenic strain *E. coli* J96 (O4:K6) was used as a source of chromosomal DNA for construction of a cosmid library. *E. coli* K-12 DH5α and DH12 (Gibco/BRL, Gaithersburg, Md.) were used as hosts for maintaining cosmid and plasmid clones. The cosmid library of *E coli* J96 DNA was constructed essentially as described by Bukanow & Berg (*Mol. Microbiol 11*:509-523 (1994)). DNA was digested with *Sau*3AI under conditions that generated fragments with an average size of 40 to 50 kb and electrophoresed through 1% agarose gels. Fragments of 35 to 50 kb were isolated and cloned into Lorist 6 vector that had been linearized with *Bam*III and treated with bacterial alkaline phosphatase to block self-ligation. (Lorist 6 is a 5.2-kb moderate-copy-number cosmid vector with T7 and SP6 promoters close to the cloning site.) Cloned

NSDOCID <WO 9822575A2 I >

DNA was packaged in lambda phage particles *in vitro* by using a commercial kit (Amersham, Arlington Heights, IL) and cosmid-containing phage particles were used to transduce *E. coli* DH5α. Transductant colonies were transferred to 150 μL of Luria-Bertani broth supplemented with kanamycin in 96-well microtiter plates and grown overnight at 37°C with shaking. Two sets of clones, one for each PAI were ultimately assembled, as previously described (Swenson *et al.*, *Infection and Immunity 64*:3736-3743 (1996)), fully incorporated by reference herein).

The two sets of clones contain eleven sub-clones that were employed in the sequencing method described below. One set of four overlapping cosmid clones covers the *prs*-containing PAI V, ATCC Deposit No. 97727, deposited September 23, 1996. A second set of seven subclones covers much of the *pap*-containing PAI V, ATCC Deposit No. 97726, deposited September 23, 1996. See Figure 1.

A high through-put, random sequencing method (Fleischmann *et al.*, *Science 269*:496 (1995); Fraser *et al.*, *Science 270*:397 (1995)) was used to obtain the sequences for 142 (contigs) fragments of *E. coli* J96 PAIs. All clones were sequenced from both ends to aid in the eventual ordering of contigs during the sequence assembly process. Briefly, random libraries of ~ 2 kb clones covering the two J96 PAIs were constructed, ~ 2,800 clones were subjected to automated sequencing (~ 450 nt/clone) and preliminary assemblies of the sequences accomplished which result in 142 contigs for each of the two PAIs that total 95 and 135 kb respectively. The estimated sizes of the PAI IV and PAI V based on the overlapping cosmid clones are 1.7×10^5 and 1.1×10^5 bp respectively. The 142 sequences were assembled by means of the TIGR Assembler (Fleischmann *et al.*; Fraser *et al.*); Sutton *et al.*, *Genome Sci. Tech. 1*:9 (1995)). Sequence and physical gaps were closed using a combination of strategies (Fleischmann *et al.*; Fraser *et al.*). Presently the average depth of sequencing for each base assembled in the contigs is 6-fold. The tentative identity of many genes based on sequence homology is covered in Tables 1, 3, 5 and 6.

SUBSTITUTE SHEET (RULE 26)

Open reading frames (ORFs) and predicted protein-coding regions were identified as described (Fleischmann *et al.*; Fraser *et al.*) with some modification. In particular, the statistical prediction of uropathogenic *E. coli* J96 pathogenicity island genes was performed with GeneMark (Borodovsky, M. & McIninch, *J. Comput. Chem. 17*:123 (1993)). Regular GeneMark uses nonhomogeneous Markov models derived from a training set of coding sequences and ordinary Markov models derived from a training set of noncoding sequences. The ORFs in Tables 1-6 were identified by GeneMark using a second-order Markov model trained from known *E. coli* coding regions and known *E. coli* non-coding regions.

Among the important genes that are implicated in the virulence of *E. coli* J96 PAIs are adhesins, excretion pathway proteins, proteins that participate in alterations of the O-antigen in the PAIs, cytotoxins, and two-component (membrane sensor/DNA binding) proteins.

I. Adhesins. It is believed that the principal adhesin determinants involved in uropathogenicity that are present within PAIs of uropathogenic *E. coli* are the pili encoded by the *pap*-related operons (Hultgren *et al.*, *Infect. Immun. 50*:370-377 (1993), Stromberg *et al.*, *EMBO J 9*:2001-2010 (1990), High *et al.*, *Infect. Immun. 56*:513-517 (1988)) and the distantly related afimbrial adhesins (Labigne-Roussel *et al.*, *Infect. Immun. 46*:251-259 (1988)). The presence of two of these (*pap*, and *prs*) has been confirmed. In addition potential genes for five other adhesins including *sla* (described above), AIDA-I (diffuse adherence-DEAC), *hra* (heat resistant hemagglutinin-ETEC), *fha* (filamentous hemagglutinin- *Bordetella pertussis*) and the arg-gingipain proteinase of *Porphyromonas gingivalis* have been found.

II. Type II exoprotein secretion pathway. Highly significant statistics support the presence of multiple genes involved in the type II exoprotein pathway. Curiously, perhaps two different determinants appear to be present in PAI IV where one set of genes has the highest sequence similarity to *eps*-like genes (*Vibrio cholerae* Ctx export) and the other has greatest similarity to *exe* genes (*Aeromonas hydophilia* aerolysin and protease export). At present, the assembly of contigs involving these potential genes is incomplete. Thus, it is

NSDOCID <WO_ 9822575A2 I >

uncertain if two separate and complete determinants are present. However, it is clear that these genes are newly discovered and novel to pathogenic *E. coli* because the derived sequences do not have either the *bfp* or *hop* genes as the highest matches. The gene products that are the target of the type II export pathway are not evident at this time.

Within PAI IV there are sequences which suggest genes very similar to *secD* and *secF*. These two linked genes encode homologous products that are localized to the inner membrane and are hypothesized to play a late role in the translocation of leader-peptide containing proteins across the inner membrane of gram-negative bacteria. In addition, in each PAI, sequences are found that are reminiscent of the heat-shock htrA/degA gene that encodes a piroplasmic protease. They may perform endochaperone-like function as Pugsley *et al.* have hypothesized for different exoprotein pathways.

III. O-antigen/capsule/carbohydrate modification (Nod genes). J96 has the O4. The O-antigen portion of lipopolysaccharide is encoded by *rfb* genes that are located at 45 min. on the *E. coli* chromosome. We have found in both PAIs a cumulative total of five possible *rfb*-like genes which could participate alterations of the O-antigen in the PAIs. Overall these data suggest that PAIs provide the genetic potential for greater change of the cell surface for uropathogenic *E. coli* strains than what was previously known.

The apparent capsule type for strain J96 is a non-sialic acid K6-type. Sequence similarity "hits" were made in PAI IV region to two region-1 capsule genes, *kpsS* and *kpsE* involved in the stabilization of polysaccharide synthesis and polysaccharide export across the inner membrane. This is not altogether surprising based on the genetic mapping of the *kps* locus to *serA* at 63 minutes on the genome of the K1 capsular type of *E. coli*. This suggests that these *kps*-like genes either are participating in the K6-biosynthesis or perhaps are involved in complex carbohydrate export for other purposes.

An intriguing discovery are the hits made on genes involved in bacteria-plant interactions by *Rhizobium, Bradyrhizobium* and *Agrobacterium*. Four potential genes identified thus far share significant sequence similarity to genes

NSDOCID: <WO 9822575A2 I >

encoding products that modify lipo-oligosaccharides that influence nodule morphogenesis on legume roots. These are: ORF140, carbamyl phosphate synthetase; nodulation protein 1265; phosphate-regulatory protein; and an ORF at a plant-inducible locus in *Agrobacterium*. To date there are no descriptions in the literature of such gene products being utilized by human or animal bacterial pathogens for the purposes of modification or secretion of extracellular carbohydrate. However, the sequence similarity to the capsular region-2 genes and to lipooligosaccharide biosynthetic genes in *Rhizobium* spp has been recently noted by Petit (1995).

IV. Cytotoxins. Besides the previously known hemolysin and CNF toxins in the PAIs, in each PAI sequences similar to the *shlBA* operon (cosmid 5 and 12) were found for a cytolytic toxin from *Serratia marcescens* and *Proteus mirabilis*. Ironically, the *P. mirabilis* hemolysin (HpmA) member of this family of toxins was discovered by Uphoff and Welch (1990), but not thought to exist in other members of the Enterobacteriaceae (Swihart (1990)). A *shlB*-like transporter does also appear to be involved in the export of the filamentous hemagglutinin of *Bordetella pertussis* which was described above and a cell surface adhesin of *Haemophilus influenzae*. It has been demonstrated that cosmid #5 of *E. coli* J96 encodes an extracellular protein that is ~180 kDa and cross-reactive to polyclonal antisera to the *P. mirabilis* HpmA hemolysin. Thus, there is evidence suggesting there is new member of this family of proteins in extraintestinal *E. coli* isolates. In addition, there is also a hit on the FhaC hemolysin-like gene within the PAI V although its statistical significance for the sequence thus far available is only 0.0043.

V. Regulators. A common regulatory motif in bacteria are the two-component (membrane sensor/DNA binding) proteins. In numerous instances in pathogenic bacteria, external signals in the environment cause membrane-bound protein kinases to phosphorylate a cytoplasmic protein which in turn acts as either a negative or positive effector of transcription of large sets of operons. On cosmid 11 representing PAI V were found, in two different *Pst*I clones, sequences

NSDOCID: <WO _ 9822575A2 I >

for two-component regulators (similar probabilities for OmpR/ AIGB and separately RcsC, probabilities at the 10^{-22} level).

In addition, the phosphoglycerate transport system (*pgtA*, *pgtC*, and *pgtP*) including the *pgtB* regulator is present in PAI IV. This transport system which was originally described in *S. typhimurium* is not appreciated as a component of any pathogenic *E. coli* genome. The operon had been previously mapped at 49 minutes, near or within one of the *S. typhimurium* chromosome specific-loops not present in the K-12 genome. It should be noted that the *E. coli* K-12 glpT gene product is similar to pgtP gene product (37% identity), but the *E. coli* J96 genes are clearly homologs to the *pgt* genes and their linkage within the middle of PAI IV element (cosmid #4) is suspicious.

VI. Mobile genetic elements. There are numerous sequences that share similarity to genes found on insertion elements, plasmids and phages. The temperate bacteriophage P4 inserts within tRNA loci in the *E. coli* chromosome. The hypothesis was made that PAIs are the result of bacteriophage P4-virulence gene recombination events (Blum *et al., Infect. Immun. 62*:606-614 (1994). Data supporting this hypothesis was found during our sequencing with the identification of P4-like sequences in each of the PAIs (cosmids 7 and 9). This is a very important preliminary result which supports the hypothesis that PAIs can be identified by common sequence or genetic elements. However, there are indications that multiple mobile genetic elements involved in the evolution of the J96 PAIs. Conjugal plasmid-related sequences may also be present at two different locations (F factor and Rl plasmid). Sequences for multiple transposable elements are present that are likely to have originated from different bacterial genera (Tnl000, IS630, IS911, IS100, IS21, IS 1203, IS5376 (*B. stearothermophflus*) and RHS). Of particular interest is IS100, which was originally identified in *Yersinia pestis* (Fetherston *et al., Mol. Microbiol. 6*:2693-2704 (1992)). The presence of IS100 is significant because it has been associated with the termini of a large chromosomal element encoding pigmentation and some aspect of virulence in *Y. pestis*. This element undergoes spontaneous deletions similar to the PAIs from *E. coli* 536 (Fetherston *et al., Mol. Microbiol.*

NSDOCID <WO _ 9822575A2_I_>

6:2693-2704 (1992)) and appears to participate in plasmid-chromosome rearrangements. This element was not previously known to be in genera outside of *Yersinia*.

The discovery of the apparent *att* site for bacteriophage P2 in the PAIs is interesting. P2 acts as a helper phage for the P4 satellite phage. The P2 *att* site is at 44 min in the K-12 genome. The significance of this hit is unknown at present, but may be explained as either a cloning artifact (some K-12 fragments in the *Pst* I library of cosmid 5) or evidence of some curious chromosomal-P4/P2 phage history. It may indicate that the J96 PAIs are composites of multiple smaller PAIs.

Example 2: Preparation of PCR Primers and Amplification of DNA

Various fragments of the sequenced *E. coli* J96 PAIs, such as those disclosed in Tables 1 through 6 can be used, in accordance with the present invention, to prepare PCR primers. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers are useful during PCR cloning of the ORFs described herein.

Example 3: Gene expression from DNA Sequences Corresponding to ORFs

A fragment of an *E. coli* J96 PAI (preferably, a protein-encoding sequence provided in Tables 1 through 6) is introduced into an expression vector using conventional technology (techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art). Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper

NSDOCID <WO _ 9822575A2 I >

protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Pat. No. 5,082,767, which is hereby incorporated by reference.

The following is provided as one exemplary method to generate polypeptide(s) from a cloned ORF of an *E. coli* J96 PAI whose sequence is provided in SEQ ID NOs: 1 through 142. A poly A sequence can be added to the construct by, for example, splicing out the poly A sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *E. coli* J96 PAI DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *E. coli* J96 PAI DNA and containing restriction endonuclease sequences for PstI incorporated into the 5′ primer and BglII at the 5′ end of the corresponding *E. coli* J96 PAI DNA 3′ primer, taking care to ensure that the *E. coli* J96 PAI DNA is positioned such that its followed with the poly A sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface.

Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *E. coli* J96 PAI DNA

NSDOCID <WO__9822575A2 I_>

sequence are injected into mice to generate antibody to the polypeptide encoded by the *E. coli* J96 PAI DNA.

If antibody production is not possible, the *E. coli* J96 PAI DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as a chimeric with, for example, ß-globin. Antibody to ß-globin is used to purify the chimeric. Corresponding protease cleavage sites engineered between the ß-globin gene and the *E. coli* J96 PAI DNA are then used to separate the two polypeptide fragments from one another after translation. One useful expression vector for generating ß-globin chimerics is pSG5 (Stratagene). This vector encodes rabbit ß-globin. Intron II of the rabbit ß-globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides may additionally be produced from either construct using *in vitro* translation systems such as In vitro Express™ Translation Kit (Stratagene).

Example 4

E. coli Expression of an E. coli J96 PAI ORF and protein purification

An *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified using PCR oligonucleotide primers designed from the nucleotide sequences flanking the selected ORF and/or from portions of the ORF's NH_2- or COOH-terminus. Additional nucleotides containing restriction sites to facilitate cloning are added to the 5′ and 3′ sequences, respectively.

The restriction sites are selected to be convenient to restriction sites in the bacterial expression vector pQE60. The bacterial expression vector pQE60 is used for bacterial expression in this example. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible

NSDOCID <WO__9822575A2 I >

promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin sold by QIAGEN, Inc., *supra*, and suitable single restriction enzyme cleavage sites. These elements are arranged such that a DNA fragment encoding a polypeptide may be inserted in such as way as to produce that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of an *E. coli* J96 PAI is amplified from the deposited cDNA clone using PCR oligonucleotide primers which anneal to the amino terminal sequences of the desired portion of the *E. coli* protein and to sequences in the deposited construct 3' to the cDNA coding sequence. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

The amplified *E. coli* J96 PAI DNA fragments and the vector pQE60 are digested with one or more appropriate restriction enzymes, such as SalI and XbaI, and the digested DNAs are then ligated together. Insertion of the *E. coli* J96 PAI DNA into the restricted pQE60 vector places the *E. coli* J96 PAI protein coding region, including its associated stop codon, downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described in Sambrook *et al., Molecular Cloning: a Laboratory Manual, 2nd Ed.;* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989). *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing an *E. coli* J96 PAI protein, is available commercially from QIAGEN, Inc., *supra*. Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from

NSDOCID <WO_ _9822575A2_I_>

resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 μg/ml) and kanamycin (25 μg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the laci repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH8. The cell debris is removed by centrifugation, and the supernatant containing the *E. coli* J96 PAI protein is dialyzed against 50 mM Na-acetate buffer pH6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. coli* J96 PAI protein. The purified protein is stored at 4°C or frozen at -80°C.

Example 5

Cloning and Expression of an E. coli J96 PAI protein in a Baculovirus Expression System

A *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified as above. The plasmid is digested with appropriate restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1%

NSDOCID <WO 9822575A2 I_>

agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.). This vector DNA is designated herein "V1".

Fragment F1 and the dephosphorylated plasmid V1 are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria are identified that contain the plasmid with the *E. coli* J96 PAI gene by digesting DNA from individual colonies using appropriate restriction enzymes and then analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing. This plasmid is designated herein pBac *E. coli J96*.

Five μg of the plasmid pBac *E. coli* J96 is co-transfected with 1.0 μg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA.), using the lipofection method described by Felgner *et al., Proc. Natl. Acad. Sci. USA 84*:7413-7417 (1987). 1 μg of BaculoGold™ virus DNA and 5 μg of the plasmid pBac *E. coli* J96 are mixed in a sterile well of a microliter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27°C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation is continued at 27°C for four days.

After four days the supernatant is collected and a plaque assay is. performed, as described by Summers and Smith, *supra.* An agarose gel with "Blue Gal" (Life Technologies Inc.) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies

SDOCID <WO 9822575A2_I_>

Inc., page 9-10). After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4°C. The recombinant virus is called V-*E. coli* J96.

To verify the expression of the *E. coli* gene Sf9 cells are grown in Grace's medium supplemented with 10% heat inactivated FBS. The cells are infected with the recombinant baculovirus V-*E. coli* J96 at a multiplicity of infection ("MOI") of about 2. Six hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc.). If radiolabeled proteins are desired, 42 hours later, 5 µCi of ^{35}S-methionine and 5 µCi ^{35}S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then they are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled). Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the mature protein and thus the cleavage point and length of the secretary signal peptide.

Example 6

Cloning and Expression in Mammalian Cells

Most of the vectors used for the transient expression of an *E. coli* J96 PAI gene in mammalian cells should carry the SV40 origin of replication. This allows the replication of the vector to high copy numbers in cells (e.g., COS cells) which express the T antigen required for the initiation of viral DNA synthesis. Any other mammalian cell line can also be utilized for this purpose.

A typical mammalian expression vector contains the promoter element, which mediates the initiation of transcription of mRNA, the protein coding

WSDOCID: <WO 9822575A2 I >

sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription can be achieved with the early and late promoters from SV40, the long terminal repeats (LTRS) from Retroviruses, e.g., RSV, 1HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter). Suitable expression vectors for use in practicing the present invention include, for example, vectors such as PSVL and PMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146) and pBC12MI (ATCC 67109). Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV I, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the gene can be expressed in stable cell lines that contain the gene integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful to develop cell lines that carry several hundred or even several thousand copies of the gene of interest. Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy *et al., Biochem J. 227*:277-279 (199 1); Bebbington *et al., Bio/Technology 10:*169-175 (1992)). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

The expression vectors pC1 and pC4 contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen *et al.,* Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart *et al., Cell 41*:521-530 (1985)). Multiple cloning sites, e.g., with the restriction enzyme

JSDOCID: <WO 9822575A2_I_>

cleavage sites BamHI, Xbal and Asp718, facilitate the cloning of the gene of interest. The vectors contain in addition the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene.

Example 6(a): Cloning and Expression in COS Cells

The expression plasmid, p *E. coli* J96HA, is made by cloning a cDNA encoding *E. coli* J96 PAI protein into the expression vector pcDNAI/Amp or pcDNAIII (which can be obtained from Invitrogen, Inc.).

The expression vector pcDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a cDNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson *et al., Cell 37:*767 (1984). The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pcDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding the *E. coli* J96 PAI protein is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The *E. coli* cDNA of the deposited clone is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *E. coli* J96 PAI protein in *E. coli.*

The PCR amplified DNA fragment and the vector, pcDNAI/Amp, are digested with appropriate restriction enzymes for the chosen primer sequences

3NSDOCID <WO 9822575A2 I >

and then ligated. The ligation mixture is transformed into *E. coli* strain SURE (available from Stratagene Cloning Systems, La Jolla, CA 92037), and the - transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the *E. coli* J96 PAI protein-encoding fragment.

For expression of recombinant *E. coli* J96 PAI protein, COS cells are transfected with an expression vector, as described above, using DEAE-DEXTRAN, as described, for instance, in Sambrook *et al., Molecular Cloning: a Laboratory Manual,* Cold Spring Laboratory Press, Cold Spring Harbor, New York (1989). Cells are incubated under conditions for expression of *E. coli* J96 PAI protein by the vector.

Expression of the *E. coli* J96 PAI - HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow *et al., Antibodies: A Laboratory Manual, 2nd Ed.;* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988). To this end, two days after transfection, the cells are labeled by incubation in media containing ^{35}S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson *et al.* cited above. Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 6(b): Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of an *E. coli* J96 PAI protein. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Acc. No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early

WSDOCID <WO _9822575A2 ! >

promoter. Chinese hamster ovary- or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies, Inc.) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented (see, e.g., Alt, F. W. *et al.*, 1978, *J. Biol. Chem. 253*:1357-1370, Hamlin, J. L. and Ma, C. 1990, *Biochim. et Biophys. Acta, 1097*:107-143, Page, M. J. and Sydenham, M.A. 1991, *Biotechnology 9*:64-68). Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains for expressing the gene of interest the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus (Cullen, *et al., Molecular and Cellular Biology,* March 1985:438-447) plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV) (Boshart *et al., Cell 41*:521-530 (1985)). Downstream of the promoter is BamHI restriction enzyme site that allows the integration of the gene. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β-actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLVI. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. coli* protein in a regulated way in mammalian cells (Gossen, M., & Bujard, H. 1992, *Proc. Natl. Acad. Sci. USA 89*: 5547-5551). For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the

3NSDOCID <WO 9822575A2 I >

chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

The DNA sequence encoding the complete *E. coli* J96 PAI protein including its leader sequence is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene.

The amplified fragment is digested with appropriate endonucleases for the chosen primers and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. 5 μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using lipofectin (Felgner *et al., supra).* The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methothrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nm, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM, 2 μM, 5 μM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μM. Expression

of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 7

Production of an Antibody to an E. coli J96 Pathogenicity Island Protein

Substantially pure *E. coli* J96 PAI protein or polypeptide is isolated from the transfected or transformed cells described above using an art-known method. The protein can also be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler and Milstein, *Nature 256*:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol. 70*:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis,

BNSDOCID <WO 9822575A2_I_>

L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than other molecules and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab. 33*:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall (*See* Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973)). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2nd ed., Rose and Friedman, (eds.), Amer. Soc. For Microbio., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample.

NSDOCID <WO 9822575A2 I >

INSDOCID <WO 9822575A2_I_>

TABLE 1 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
65	2	1902	1042	gi|1655838	ORFB; putative transposase [Yersinia pestis]	100	100	861
65	3	2096	1821	gi|467612	ORF1 [Yersinia pestis]	100	100	276
63	11	7856	9238	gi|154262	transporter protein pgtP [Salmonella typhimurium]	98	93	1383
65	4	2889	1915	gi|1655837	ORFA; putative transposase [Yersinia pestis]	97	96	975
138	1	2	172	gi|1208992	unknown [Escherichia coli]	97	78	171
64	6	4075	4338	gi|1143207	Description: IS630 insertion element; ORF5 protein; Method: conceptual translation supplied by author [Shigella sonnei]	92	92	264
67	1	1	273	gi|809648	ExeF gene product [Aeromonas hydrophila]	92	71	273
73	4	3029	2511	gi|799234	glucose-1-phosphate thymidylyltransferase [Escherichia coli]	92	86	519
73	5	3139	2996	gi|454900	rfbC gene product [Shigella flexneri]	92	92	144
64	5	3741	4088	gi|47542	ORF (343 AA) [Shigella sonnei]	91	85	348
73	3	2613	2242	gi|46985	glucose-1-phosphate thymidylyltransferase [Salmonella enterica]	91	82	372
90	1	1	366	gi|38826	ExeE gene product [Aeromonas hydrophila]	91	77	366
91	2	604	248	gi|609625	putative [Vibrio cholerae]	91	67	357
63	9	6301	5234	gi|858753	regulatory protein pgtB [Salmonella typhimurium]	89	84	1068
73	2	2179	1811	gi|294899	dTDP-6-deoxy-L-mannose-dehydrogenase [Shigella flexneri]	89	84	369
90	2	201	689	gi|38826	ExeE gene product [Aeromonas hydrophila]	89	80	489
95	2	1519	413	gi|581654	dTDP-glucose 4,6-dehydratase [Salmonella enterica]	88	81	1107
96	1	729	457	pir|S43483|S434	Orf104 homolog - Escherichia coli	88	72	273
63	6	4281	3019	gi|154255	phosphoglycerate transport system activator protein [Salmonella typhimurium]	87	79	1263
67	2	251	745	gi|609628	putative [Vibrio cholerae]	87	72	495
82	12	5254	4406	gi|1208992	unknown [Escherichia coli]	87	74	849
60	1	693	4	gi|609625	putative [Vibrio cholerae]	86	57	690
95	1	428	3	gi|508238	dTDP-6-deoxy-L-mannose-dehydrogenase [Escherichia coli]	85	74	426
64	7	4336	4731	gi|47542	ORF (343 AA) [Shigella sonnei]	84	81	396
80	8	2800	2582	gi|38832	ExeK gene product [Aeromonas hydrophila]	84	53	219
82	10	4380	3829	gi|1033137	ORF_o152 [Escherichia coli]	84	72	552

TABLE 1 (PAI IV)(CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
63	8	5399	4830	sp|P37433|PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-).	83	75	570
63	10	7572	6259	gi|154258	regulatory protein pgtC [Salmonella typhimurium]	83	78	1314
65	7	3351	3100	gi|1196999	unknown protein [Transposon Tn3411]	82	80	252
100	1	337	2	gi|41004	URF 2 [Escherichia coli]	82	64	336
138	2	109	429	gi|1033128	ORF_o273 [Escherichia coli]	80	62	321
74	4	1331	831	gi|38826	ExeE gene product [Aeromonas hydrophila]	79	62	501
63	7	4873	4256	sp|P37433|PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-).	78	72	618
70	13	5759	5529	gi|1773143	Hha protein [Escherichia coli]	78	58	231
91	3	1154	534	gi|609625	putative [Vibrio cholerae]	77	65	621
75	5	3524	3255	gi|463911	heat resistant agglutinin 1 [Escherichia coli]	76	62	270
63	1	2	667	gi|1574313	H. influenzae predicted coding region HI1472 [Haemophilus influenzae]	75	56	666
104	2	485	315	gi|530438	arabinose transport protein [Mycoplasma capricolum]	72	41	171
63	3	2180	1629	gi|622948	transposase [Escherichia coli]	71	60	552
63	12	9688	10005	sp|P39213|YI91_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN.	71	57	318
61	3	1283	876	gi|581535	ORF140 gene product [Rhizobium sp.]	70	54	408
84	3	2361	3437	gi|1772623	HecA [Erwinia chrysanthemi]	70	60	1077
91	1	300	4	gi|295430	epsE [Vibrio cholerae]	70	49	297
74	1	541	2	gi|609627	putative [Vibrio cholerae]	69	54	540
67	4	1297	1581	gi|151469	PilD-dependent protein [Pseudomonas aeruginosa]	68	50	285
84	1	578	1741	gi|1772622	HecB [Erwinia chrysanthemi]	68	54	1164
84	2	1698	2363	gi|1772622	HecB [Erwinia chrysanthemi]	67	48	666
63	2	1734	1393	gi|1323798	transposase [Plasmid pRL1063a]	65	46	342
71	1	1134	4	gi|397405	kpsE gene product [Escherichia coli]	65	36	1131
64	2	2828	1839	gi|310632	hydrophobic membrane protein [Streptococcus gordonii]	64	38	990
74	2	861	355	gi|148436	secretory component [Erwinia chrysanthemi]	64	54	507
66	1	556	2	gi|1235662	RfbC [Myxococcus xanthus]	62	39	555
70	6	3017	2814	gi|1657478	similar to E. coli ORF_o208 [Escherichia coli]	62	41	204

TABLE 1 (PAI IV)(CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
85	1	278	66	pir|A45253|A452	activator 1 37K chain - human	62	56	213
126	1	3	323	gi|1778562	hypothetical protein [Escherichia coli]	62	45	321
73	1	773	3	pir|S32879|S328	lipA protein - Neisseria meningitidis	61	46	771
96	2	796	644	gnl|PID|e276217	T03F6.f [Caenorhabditis elegans]	61	46	153
67	3	743	1312	gi|609629	putative [Vibrio cholerae]	60	43	570
70	10	4666	4292	gi|1657478	similar to E. coli ORF_o208 [Escherichia coli]	60	45	375
81	1	1	1179	gi|1591717	spore coat polysaccharide biosynthesis protein E [Methanococcus jannaschii]	60	44	1179
80	5	2563	1790	gi|609632	putative [Vibrio cholerae]	59	41	774
137	1	73	528	gi|1736670	Adhesin AIDA-I precursor. [Escherichia coli]	59	45	456
61	1	773	3	gi|1196968	unknown protein [Insertion sequence IS66]	58	41	771
63	5	2831	2178	gi|622948	transposase [Escherichia coli]	58	41	654
64	3	3568	2690	gi|1335913	unknown [Erysipelothrix rhusiopathiae]	57	36	879
64	1	1819	917	gi|153826	adhesin B [Streptococcus sanguis]	55	30	903
64	9	7008	6685	gi|152259	lcrB gene product [Rhizobium sp.]	55	42	324
70	14	6481	6753	pir|G42465|G424	hypothetical protein 88 - phage phi-R73	53	30	273
85	5	9317	1530	gi|144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	7788
64	8	5063	4806	gnl|PID|e264304	F53C11.6 [Caenorhabditis elegans]	51	27	258
80	9	3411	2761	gi|149309	pulJ [Klebsiella pneumoniae]	50	40	651
88	1	98	388	gi|156087	[Brugia malayi myosin heavy chain gene, complete cds.], gene product [Brugia malayi]	50	32	291
96	3	1127	687	gi|1196964	unknown protein [Plasmid Ti]	50	38	441
89	1	981	4	gi|57633	neuronal myosin heavy chain [Rattus rattus]	48	22	978
113	1	657	199	gi|147899	extragenic suppressor [Escherichia coli]	48	25	459
118	1	654	145	pir|S27564|S275	polysaccharide translocation-related protein - Escherichia coli	48	25	510
58	2	2101	4245	gi|1235662	RfbC [Myxococcus xanthus]	47	35	2145
87	1	595	134	gi|1235662	RfbC [Myxococcus xanthus]	42	28	462
85	2	1018	515	bbs|117606	glycine-rich protein, atGRP (clone atGRP-1) [Arabidopsis thaliana, C24, Peptide Partial, 210 aa] [Arabidopsis thaliana]	36	36	504
85	3	1779	973	bbs|157676	silk fibroin heavy chain (C-terminal) [Bombyx mori=silkworms, Peptide Partial, 633 aa] [Bombyx mori]	34	29	807

SUBSTITUTE SHEET (RULE 26) <WO 98/22575 A2 | >

NSDOCID <WO 9822575A2 | >

TABLE 2 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
58	1	1176	2120
61	2	54	560
63	4	1875	2639
64	4	3911	3627
65	6	3009	3239
65	12	6027	6683
66	2	1289	978
70	2	1418	861
70	3	1886	1476
70	4	2124	1900
70	5	2795	2220
70	7	3645	3259
70	8	4078	3680
70	9	4220	4513
70	11	4950	4498
70	12	4594	4866
70	15	6805	7449
70	16	9520	10806
73	7	3247	3666
74	3	720	1301
75	1	1	165
79	1	719	354
80	6	2108	2575
80	7	2831	2469
80	10	3223	3387
80	11	3541	3362
82	8	3313	4260
82	11	4340	5218
82	13	6090	5614
84	4	3487	3281
85	4	1485	2285
85	6	8373	9320
104	1	358	2
112	1	677	105
142	1	3	143
142	2	119	328

INSDOCID <WO 9822575A2 I >

TABLE 3 (PAI V)

Putative coding regions of novel *E. coli* PAI V proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
14	3	2826	3686	gi|1655838	ORFB; putative transposase [Yersinia pestis]	100	100	861
14	2	1837	2907	gi|1655837	ORFA; putative transposase [Yersinia pestis]	99	99	1071
3	9	7927	7595	gi|1657499	putative transposase for insertion sequence IS3 [Escherichia coli]	89	85	333
20	6	3462	4304	gi|1208992	unknown [Escherichia coli]	87	73	843
6	6	3541	3263	pir|S43483|S434	Orf104 homolog - Escherichia coli	81	62	279
20	3	1616	2332	gi|1033129	ORF_o233 [Escherichia coli]	80	61	717
9	1	1	681	gi|537112	ORF_o396 [Escherichia coli]	77	55	681
15	3	1899	1672	pir|S43483|S434	Orf104 homolog - Escherichia coli	75	55	228
20	9	4302	4880	gi|1552816	similar to E. coli ORF_o152 [Escherichia coli]	74	60	579
14	13	12972	15359	gi|1772623	HecA [Erwinia chrysanthemi]	70	60	2388
5	3	1112	1570	gi|1001717	regulatory components of sensory transduction system [Synechocystis sp.]	68	45	459
3	1	2572	1373	gi|849022	Lactate oxidase [Aerococcus viridans]	66	46	1200
3	8	6869	6498	gi|581535	ORF140 gene product [Rhizobium sp.]	66	45	372
6	5	3265	2951	gi|642184	F19C6.1 [Caenorhabditis elegans]	66	44	315
14	12	11775	12974	gi|1772622	HecB [Erwinia chrysanthemi]	66	50	1200
20	1	545	1450	gi|1033127	ORF_o289 [Escherichia coli]	66	45	906
57	1	696	124	gi|1772622	HecB [Erwinia chrysanthemi]	66	47	573
3	3	3320	3700	gi|431950	similar to a B.subtilis gene (GB: BACHEMEHY_5) [Clostridium pasteurianum]	65	34	381
5	7	4565	4239	sp|P39213|YI91_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN.	65	38	327
22	2	1651	557	gi|290430	adhesin [Escherichia coli]	64	48	1095
5	4	1455	1841	gi|1575577	DNA-binding response regulator [Thermotoga maritima]	61	47	387
14	11	11161	11937	gi|1772622	HecB [Erwinia chrysanthemi]	60	39	777
14	1	930	1700	gi|1657478	similar to E. coli ORF_o208 [Escherichia coli]	58	47	771
5	6	3834	3391	gi|155032	ORF B [Plasmid pEa34]	56	36	444
3	5	6500	5982	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	54	25	519
14	7	8429	8809	gi|1196729	unknown protein [Bacteriophage P4]	54	41	381

NSDOCID <WO 9822575A2 I >

TABLE 3 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
14	14	15191	21793	gi|144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	6603
14	16	21427	22671	bbs|117613	glycine-rich protein, atGRP (clone atGRP-4) [Arabidopsis thaliana, C24, Peptide Partial, 112 aa] [Arabidopsis thaliana]	52	39	1245
5	2	1004	381	gi|48518	HydC [Wolinella succinogenes]	51	34	624
5	5	1941	3311	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	51	21	1371
14	4	3968	5431	gi|1033120	ORF_o469 [Escherichia coli]	51	29	1464
32	1	481	227	gi|1673731	(AE000010) Mycoplasma pneumoniae, fructose-permease IIBC component; similar to Swiss-Prot Accession Number P20966, from E. coli [Mycoplasma pneumoniae]	50	41	255
20	17	7039	7284	gi|1123054	coded for by C. elegans cDNA CEESN53F; similar to protein kinases including CDC15 in yeast [Caenorhabditis elegans]	48	28	246

NSDOCID: <WO 9822575A2_I_>

TABLE 4 (PAI V)

Putative coding regions of novel *E. coli* PAI V proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	1	809	1165
3	2	3275	2640
3	6	6006	6425
3	7	6423	6833
4	1	3	455
5	1	501	4
6	1	2168	1749
6	2	2527	2114
6	3	2648	2331
6	4	3099	2626
14	5	7112	7699
14	6	7800	8507
14	8	9040	9624
14	10	10586	10846
14	15	21721	20921
15	1	575	826
15	2	850	1365
20	2	904	605
20	4	2330	3157
20	5	3139	3396
20	7	3812	3492
20	8	4373	3828
20	18	7282	7950
22	1	356	3
24	1	492	4

SUBSTITUTE SHEET (RULE 26) WO 98/22575 A2

TABLE 5 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
59	1	968	54	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	99	790	915
59	2	1551	805	emb|Y00529|ECPA	E. coli papC gene involved in formation of pap pili	99	518	747
59	3	1742	1494	emb|Y00529|ECPA	E. coli papC gene involved in formation of pap pili	99	182	249
61	4	1975	1220	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	100	69	756
63	13	10097	10480	gb|AE000133|	Escherichia coli from bases 263572 to 274477 (section 23 of 400) of the complete genome	91	216	384
65	1	886	671	gb|U06468|	Escherichia coli O111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	93	164	216
65	5	3218	2868	gb|U06468|	Escherichia coli O111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	85	285	351
65	8	4064	3216	gb|U06468|	Escherichia coli O111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	86	145	849
65	9	4939	4337	emb|Y00976|ECHN	E.coli hns gene for DNA-binding protein H-NS (5'-region)	96	53	603
65	10	4919	5266	emb|Y00976|ECHN	E.coli hns gene for DNA-binding protein H-NS (5'-region)	98	310	348
65	11	5206	5781	gb|AE000133|	Escherichia coli from bases 263572 to 274477 (section 23 of 400) of the complete genome	89	431	576
68	1	1575	1315	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	100	186	261
68	2	2468	1848	emb|X51704|ECPA	Escherichia coli papJ gene for PapJ protein	99	621	621
68	3	2232	2594	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	99	363	363
68	4	3212	2466	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	100	747	747
69	1	300	4	gb|M14040|	E.coli apt gene encoding adenine phosphoribosyl-transferase (APRT), complete cds	98	225	297
69	2	383	117	gb|M14040|	E.coli apt gene encoding adenine phosphoribosyl-transferase (APRT), complete cds	95	162	267
70	1	832	149	gb|U09857|	Escherichia coli 4787 o115:v165:f165 fimbrial regulatory f1652I, f1652B and f1652 A genes, complete cds	89	225	684
70	17	10799	11767	gb|AE000291|	Escherichia coli , asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	95	553	969
70	18	11809	11045	gb|AE000291|	Escherichia coli , asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	94	595	765
70	19	12022	15222	dbj|D90838|D908	E.coli genomic DNA, Kohara clone #348(44.5-44.9 min.)	89	2667	3201

TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
70	20	15316	16836	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	1488	1521
70	21	16722	17711	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	82	990
70	22	17426	16776	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	63	651
72	1	12	1061	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1024	1050
72	2	947	1285	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	96	261	339
73	6	4437	3205	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	392	1233
73	8	6177	4555	gb|U28377|	Escherichia coli K-12 genome; approximately 65 to 68 minutes	90	1133	1623
73	9	6835	6128	gb|AE000380|	Escherichia coli , glcB, glcG, glcD genes from bases 3112500 to 3126189 (section 270 of 400) of the complete genome	93	703	708
75	2	1553	1059	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	90	385	495
75	3	2579	1566	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	464	1014
75	4	3297	2743	gb|U07174|	Escherichia coli O9:H10:K99 heat resistant agglutinin 1 gene, complete cds	81	283	555
76	1	698	3	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	693	696
78	1	382	59	gb|AE000360|	Escherichia coli from bases 2885166 to 2897277 (section 250 of 400) of the complete genome	99	315	324
79	2	2620	1529	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1084	1092
79	3	2925	2587	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	97	322	339
79	4	3576	2923	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	654	654
80	1	376	83	gb|U05251|	Escherichia coli polysialic acid gene cluster region 3, promoter region	93	210	294
80	2	638	210	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	347	429
80	3	1246	710	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	96	388	537

SUBSTITUTE SHEET (RULE 26) <WO 9822575A2 I >

TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
80	4	1796	1182	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	397	615
82	1	1	567	emb|X74567|ECKP	E.coli K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	87	551	567
82	2	549	1157	emb|X74567|ECKP	E.coli K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	88	554	609
82	3	1500	1180	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	90	62	321
82	4	2163	1519	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	143	645
82	5	2594	2139	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	97	456	456
82	6	3000	2605	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	98	396	396
82	7	3463	3047	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	283	417
82	9	3831	3337	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	495
83	1	3	311	gb|AE000151|	Escherichia coli , ybaE, cof, mdlA, mdlB, glnK, amtB, tesB, ffs genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	99	207	309
83	2	176	433	gb|AE000151|	Escherichia coli , ybaE, cof, mdlA, mdlB, glnK, amtB, tesB, ffs genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	100	223	258
86	1	529	2	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	93	398	528
93	1	440	3	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	95	351	438
94	1	368	72	emb|X14180|ECGL	Escherichia coli glutamine permease glnHPQ operon	100	229	297
99	1	161	586	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	98	426	426
99	2	643	476	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	168	168
99	3	532	1092	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	537	561
99	4	1094	1396	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	274	303

NSDOCID <WO_ 9822575A2 I >

TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
102	1	527	3	emb|Y00529|ECPA	E. coli papC gene involved in formation of pap pili	100	427	525
102	2	762	373	emb|Y00529|ECPA	E. coli papC gene involved in formation of pap pili	99	333	390
105	1	377	3	gb|AE000480|	Escherichia coli from bases 4277211 to 4288813 (section 370 of 400) of the complete genome	100	343	375
107	1	2	397	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	390	396
107	2	406	966	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	549	561
110	1	148	2	emb|X56175|ECSE	Escherichia coli secD and secF genes for membrane proteins involved in protein export	99	143	147
110	2	312	40	gb|M63939|	E.coli tRNA-guanine-transglycosylase (tgt) gene, complete cds	100	125	273
115	1	501	325	gb|AE000459|	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	98	177	177
117	1	3	302	gb|AE000506|	Escherichia coli from bases 4584059 to 4594314 (section 396 of 400) of the complete genome	100	263	300
121	1	2	250	gb|M16202|	E.coli papH gene encoding a pilin-like protein	98	148	249
123	1	361	2	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	113	360
127	1	2	229	gb|AE000233|	Escherichia coli , racC, ydaD, sieB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	100	200	228
127	2	227	382	gb|AE000233|	Escherichia coli , racC, ydaD, sieB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	97	113	156
130	1	337	2	emb|X60200|ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	335	336
131	1	510	79	gb|M30198|	E.coli recQ gene complete cds, and pldA gene, 3' end	98	304	432
131	2	743	270	gb|M30198|	E.coli recQ gene complete cds, and pldA gene, 3' end	99	314	474
133	1	1	258	gb|AE000115|	Escherichia coli , yabF, kefC, folA, apaH, apaG, ksgA, pdxA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	98	237	258
133	2	192	350	gb|AE000115|	Escherichia coli , yabF, kefC, folA, apaH, apaG, ksgA, pdxA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	99	115	159
135	1	103	327	emb|X02143|ECPL	Escherichia coli K-12 pldA gene for DR-phospholipase A	97	178	225
135	2	152	409	emb|X02143|ECPL	Escherichia coli K-12 pldA gene for DR-phospholipase A	98	157	258

INSDOCID <WO 9822575A2 | >

TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
136	1	122	532	gb|AE000459|	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	97	237	411
140	1	576	244	gb|AE000291|	Escherichia coli , asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	89	329	333
141	1	445	2	gb|AE000291|	Escherichia coli , asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	77	432	444

SUBSTITUTE SHEET (RULE 26) <WO 9822575A2 I >

TABLE 6 (PAI V)

Putative coding regions of novel *E. coli* PAI V containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
3	4	6150	4855	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	91	129	1296
3	10	8214	7723	emb|X02311|ECIS	E.coli insertion sequence IS3	76	274	492
3	11	7867	8319	emb|Z11606|ECIS	E.coli DNA for insertion sequence IS3	80	378	453
3	12	8462	8157	emb|Z11606|ECIS	E.coli DNA for insertion sequence IS3	90	267	306
3	13	8487	8663	gb|L19084|	Escherichia coli RhsD genetic element; core protein (rhsD) gene, complete cds; complete ORF-D2; complete ORF-D3	96	112	177
4	2	1441	815	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	91	577	627
4	3	923	1372	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	448	450
4	4	2343	1324	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	244	1020
7	1	3	743	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	100	741	741
7	2	977	615	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	99	363	363
7	3	741	1214	emb|X51704|ECPA	Escherichia coli papJ gene for PapJ protein	98	459	474
8	1	438	4	emb|X60200|ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	435	435
10	1	1932	2426	emb|X61238|ECPR	E.coli prsEFG genes for F13 pili tip proteins	97	462	495
11	1	903	1550	gb|M10133|	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	452	648
12	1	2559	1531	gb|U82598|	Escherichia coli genomic sequence of minutes 9 to 12	100	1029	1029
12	2	1594	1860	emb|X13668|ECIS	E.coli insertion element 5 (IS5) DNA	100	267	267
12	3	1858	2235	gb|U95365|	Escherichia coli transposon IS5, transposase (is5B) gene, complete cds	99	354	378
13	1	93	1424	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	99	885	1332
14	9	9832	10515	gb|U09857|	Escherichia coli 4787 o115:v165:f165 fimbrial regulatory f1652I, f1652B and f1652 A genes, complete cds	92	225	684
16	1	1	375	gb|U07174|	Escherichia coli O9:H10:K99 heat resistant agglutinin 1 gene, complete cds	94	320	375
16	2	263	616	gb|U07174|	Escherichia coli O9:H10:K99 heat resistant agglutinin 1 gene, complete cds	98	283	354
17	1	282	4	emb|Y00529|ECPA	E. coli papC gene involved in formation of pap pili	98	240	279
17	2	410	174	emb|Y00529|ECPA	E. coli papC gene involved in formation of pap pili	100	168	237

NSDOCID <WO 9822575A2 I >

NSDOCID <WO 9822575A2 I >

TABLE 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
19	1	1	369	gb|AE000418|	Escherichia coli from bases 3550279 to 3561054 (section 308 of 400) of the complete genome	99	347	369
20	10	5401	4829	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	468	573
20	11	4874	5371	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	498
20	12	5245	5679	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	235	435
20	13	5732	6139	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	93	329	408
20	14	6316	5822	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	95	239	495
20	15	6048	6590	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	406	543
20	16	6569	7075	gb|AE000292|	Escherichia coli , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	136	507
20	19	8686	9915	gb|M67452|	Escherichia coli lysine decarboxylase (cadB, and cadC, complete cds, and cadA, 5' end) genes	98	1205	1230
20	20	10604	11938	gb|U14003|	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	1308	1335
20	21	11940	12368	gb|M76411|	E.coli cadA gene, 5' cds and cadB and cadC genes, complete cds	100	363	429
21	1	369	4	emb|X03391|ECPA	E. coli major pilu subunit genes genes papI, papB, papA and papH 5'-region	98	201	366
23	1	1	879	gb|U14003|	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	879	879
23	2	900	16	gb|U14003|	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	885	885
23	3	953	1186	emb|X77707|ECCY	E.coli ORF112, DIPZ and ORF191 genes	99	225	234
23	4	1223	2677	emb|X77707|ECCY	E.coli ORF112, DIPZ and ORF191 genes	97	1454	1455
25	1	536	171	emb|X60200|ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	164	366
25	2	1128	562	emb|X60200|ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	459	567
27	1	708	436	emb|X61239|ECPA	E.coli papABCDEFGHIJK genes for F13 P-pili proteins	100	252	273
28	1	309	4	emb|X77707|ECCY	E.coli ORF112, DIPZ and ORF191 genes	98	278	306
28	2	431	213	emb|X77707|ECCY	E.coli ORF112, DIPZ and ORF191 genes	96	150	219

TABLE 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
30	1	399	4	gb|M26893|	E.coli amidophosphoribosyltransferase (purF) gene, complete cds	98	295	396
31	1	706	170	emb|X56780|ECRR	E.coli terminator sequence of RNA G operon gene	99	513	537
37	1	2	400	gb|M63703|	E.coli pyruvate kinase type II (pykA) gene, complete cds	98	399	399
38	1	463	2	emb|X13463|ECGU	Escherichia coli gutM gene and gutR gene for activator and repressor proteins	99	363	462
42	1	413	3	gb|M64367|	Escherichia coli DNA recombinase (recG) gene, complete cds, spoU gene, 3' end, and gltS gene, 3' end	97	316	411
42	2	115	591	gb|M64367|	Escherichia coli DNA recombinase (recG) gene, complete cds, spoU gene, 3' end, and gltS gene, 3' end	98	266	477
46	1	2	277	emb|X77707|ECCY	E.coli ORF112, DIPZ and ORF191 genes	98	187	276
48	1	1	171	gb|AE000491|	Escherichia coli from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	162	171
48	2	105	464	gb|AE000491|	Escherichia coli from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	144	360
49	1	2	172	gb|U00800|	Escherichia coli cloning vector Pk184, complete sequence, kanamycin phosphotransferase (kan) and (lacZalpha) genes, complete cds	98	167	171
50	1	414	4	gb|AE000341|	Escherichia coli , glyA, hmpA, glnB, yfhA, yfhG genes from bases 2677406 to 2687636 (section 231 of 400) of the complete genome	99	411	411
52	1	2	307	emb|X60200|ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	284	306
53	1	280	41	gb|M36536|	E.coli htrA gene, complete cds	100	131	240
53	2	558	214	gb|M36536|	E.coli htrA gene, complete cds	99	315	345
54	1	9	263	gb|AE000381|	Escherichia coli from bases 3125914 to 3136425 (section 271 of 400) of the complete genome	94	111	255
55	1	1	675	gb|AE000179|	Escherichia coli , modA, modB, modC, ybhA, ybhE, ybhD genes from bases 794199 to 805132 (section 69 of 400) of the complete genome	98	332	675

NSDOCID: <WO 9822575A2 I >

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications recited herein are hereby incorporated by reference.

NSDOCID <WO_ 9822575A2 I >

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Human Genome Sciences, Inc.
9410 Key West Avenue
Rockville, Maryland 20850
United States of America

University of Wisconsin
1300 University Avenue
Madison, Wisconsin 53706
United States of America

APPLICANTS/INVENTORS: Dillon, Patrick J.
Choi, Gil H.
Welch, Rodney A.

(ii) TITLE OF INVENTION: Nucleotide Sequence of *Escherichia coli* Pathogenicity Islands

(iii) NUMBER OF SEQUENCES: 142

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Ave., N.W., Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
(B) FILING DATE: 22-NOV-1996 AND 14-OCT-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.074PC02/EKS/CBM

(vi) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

NSDOCID <WO 9822575A2 I >

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CNTANATTAG GCCTGCTNAA TGTATTTATA TCTAAAAAAA TTCGCATCCA AAAGGAATCC 60

AATCTGTACT GTTTTTTCTT GTGCTGACAT CTTCTTTTCC CTGGCTGGTA TGGCAAGTGA 120

CGGAGACAAG AGAAACGTTT TAAGCTCAGT TATCTCCGCC ATCACTTTCC ACGAATGACA 180

AGTAATTTTG CCTATTTTAA AACCATGCAA AAGGCAGGGT AAAAGGAGAA AATTCGATCG 240

AATCGATCGA CAAAATCGAT CATACATGAT GAAGATTTCT TATCGAATCC ATAAAAATAG 300

TGACAGCTAA CCGGCGTTGC AGGAACAGTC AGAAATGGGC GTTTGGGAAA GAGCCATAGC 360

ATACGTCGTC GCTGACATAG AGGAACTGTG CTTTGTTGAT AAGATCCTTT ATACGGCAAC 420

CAATCCACTG GACAAAAGAT GAACTACGTA ATCACCGGGT TCTCACTGAC GAAATACAGA 480

AGTTAATGAC ACAACTGTGC CATGCACCTT GTACAACAGC GGTGGAAAGC TCTCAGAACA 540

ATGGAATTGC AGAAAGGTGT TAAAACGATG AAAGCCTTCA TACCCAAATC GAATGTAAGA 600

ACGGCAGTAA AGACTGAATT GCGTAACCTT GCAGTAGCTC GAGTATTACA CTGCATAGTG 660

TGCAGGGTTA TCTCCCATCG AGAAAATATC GGCGCCAGCG AATAACGTCA CCTTAGATGT 720

AGCAGTTGCC AAATAGTGAC TCAAGGGCGG GCTTACCGCA TACACTGACA CTTAGCGGAT 780

CGACAGAATA TTATTAGCAG ATCATCACTG AACGCTACGT AATTATCGTA ATAAAGGCTT 840

TTTCTGGCTA CCAGGAAGAC CTGACATGGC TCTGCTCTGG AACCAGGCCG CAGGAAGCAT 900

CAATCTGGAG TTTATCAGCT ACTGGAATTC CGGTGTATTG GCAGCCCCTG ATAATCACCT 960

GACCCACGAA GAGCGCTCTG CTTTGCAGAA ACTCTGGGGC GGTTTGGAGA CAGGAGATGT 1020

AACGATTATA GGACGTTCTG ATGAAGTCCA TGATTTTACC TCCGCCTTAA TTAACTGTTT 1080

TCTTTCTGAA GAAGAAATTG TCTGGTGGCA ATCAGGTGGC ATTTTCCCGG ATCCTTGGCC 1140

CGCTAATATA TCCCGGCTGA ACTGACGATT AACGCGAT 1178

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCCTATTCA TTTTGCCATG ACGGGCGAAC TCCAGATAAA GGTTTTGAAA GTAATGAGAA 60

ATTATTAATT CATCCATGTT ACTGGCTTGG TTTGAATCTA AATCGTAATG CACTTGCTCC 120

AGAGGAAGCA GAGGAGATAA ATGACGAATA TGATATTAAT ATTATTTCAG ATAATTCAGC 180

WNSDOCID <WO 9822575A2_I >

CATTAGAAAT AAAACAATAG GTCAAATAAC TACTCATCTA GATCAGATAC CGATAGGAAA 240

TGAAGGTGCC ACTGAATTTG AACAATGGTG TTTAGACGCA CTAAGAATAG TATTTGCATC 300

CCACCTAACA GACATCAAGT CCCATCCAAA TGGTAACGCA GTTCAGAGAC GAGATATTAT 360

AGGCACCAAT GGTGGCAAAT CTGAWTTTTG GRAACGAGTA TTGGAGGACT ATAA 414

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGGATCTG GTACANTCCA CCCAGCGGCA TTATCCNGAA GGCAATATTT TTAAGGATTA 60

TTCGTCCACA AAATCAGTAC TGGAACCAGG CTCAAAAAAG GCTTTAACGT GACCTGCTNC 120

CATCTACAGT AGATGTACAA CCTGTTAAGT TAATTGAAAA TGGTGTTAAT CCGGTTGTTT 180

CTCCAGGGGT AGCAAGGGCC TTATTCGATA CAGTGGGTAA TGTTACTGTA AAATTACCAT 240

CATTCCCTGT GGTCACATTG CAGGTCTGAG CTACAACTTT GCCTGTAAAC GTAATTGTTC 300

CGTCATAGGC CATAGCTGAA CCAACAAACA CAGCAGAAAC AAATGTAGCC AATGCTATAA 360

CTTTTATTTT CATAAAATGA ATTCCTGTTT AATTCCGGTA TTGATCATTT GTTCAGCAAT 420

CATCCCCAAC AAAACAATCA TTTTCAAAAT GTTTTTACCG ATCGATAACC AGCACATGAT 480

AGATTGCACC TATCATGATT GCTAAAACGA TCGGGAAAAG CGATCAAAAA CCATATTTAT 540

TGTGTTGGTA ATGACAAAAG ATATGCTTTA CCCTGAAATG AGCGACCTAT TCATGAAAAT 600

ATGTAGGTCT GTATTTGATT ACTATCATTG CTATATTTCC ACTATCCAAT TTATATTTCA 660

TGATTAAAAT ATACCTTTTT ACACTATTAT TTATTTGTTG CAGCTTGCCT GGCTTTATCT 720

TATTCCGACT ATTTTATGGT AGATACAGAA TACAATTAAT TAAACTTATT TAAAGATTTT 780

ATAAATACCA TATTGGAGTT GACCGATAGA TACCTACTAA CAAGAGCAAT CACCACCACC 840

CCATGAGGTG TTTAGGAATA CAATCAATAA ACAACATCCA TGCCCGGCGA CGTACATACC 900

TGTTTGCTAT GATATCTGTT ACGCTACGCT TGCTAATTTA CTGAAACTCA GCATCTGTCG 960

ACGGAGATTC GTCCGGGCCC TGATACAACA AGGGCAAGAA AACCACCCGA AATACAGATA 1020

TTCTTATAAA AATGGATCAT ATTTCCATGT GCAAGTTCAG CTGGCATCGT CCAGAATGCG 1080

TGTCCAAGAA ATGAAGCAAA CACGGTATAC AGGCACAGAA TAATGCTCAC TGGCCGGGTG 1140

AAAAAGCCRA AAACAATCAT TAATGCTCCA ACGATTTCGA CAAGGACCAC TATTGCTGCA 1200

GTAATCGCCG GAAATATAAG CCCAAGAGAG GCCATTTTAT CGATAGTGCC AGTGAATGAT 1260

AGCAGCTTGG GAACGCCGGA TATCATATAA AGGCATGCCA GCATCAGACG GGCAAGGAGC 1320

AACAATGCCG ACGTGTAATT TCCCATATTA AAATACCTGA TTTTATCCAC TATCAATGCT 1380

CAGTCTCCTT GTTTCTGATA AAGCCCTGAG CCAAATCCTT AAGTGTACGA GCACCACTCA 1440

GTAACATTGC CGTCCTCAGC TCCGTCTTCA GGTGCTCAAT GACACTGGCA ACGCCCCCGA 1500

CACCACCTGC TGCGATGCCA TAAAGAACAG GACGTCCGAC CGCAACAGCC GTTGCCCCAA 1560

GAGAGATAGC CCTTACAACA TCAACCCCCC TGCGAATACC GCTGTCAAAA ATGACCGGAA 1620

CTTTGTGCCC GACTCTTGCA GCAACTTCCT GCAACTGGCT GATGGCAGAA GGAACACCAT 1680

CAATCTGGCG ACCACCATGA TTAGACACCT GGATGGCATC TGCTCCTGCA TCAATGGCGA 1740

CCACTGCATC CTCACCTCTG AGGATGCCCT TGACAATGAC TGGCAGCCCG GTGATTTTTT 1800

TTACAAACTC AATATCAGCC GGGGTCAGCT CAACTTTTTG GTTAAAAAAA TCACCTTTGC 1860

CACCGTAACG GGGGTCATGA TTACCGAACG TCGCTCCTGC AGGGAAAGGC GAGCTCATGC 1920

TGAGAAAAGC ATCACTTGTC CCGGGACCAA GCGCATCCGC TGTGATAATA ATGGCTGAAT 1980

AGCCTGCCGC TTTTGCACGC TCCAGTAAAC TTCGGGTCAC ACCAGCATCC GCGTTAAAAT 2040

ACAGCTGGAA CCATTTAGGT CCTTTACTGG CTTTTGCAAT ATCCTCCAGA GAGCGGTTGG 2100

ATGCCCCTGA TGATTCATAA AGTGCCCCGG CCTTTTCTGC ACCCGCTGCA GCAATCACCT 2160

CCCCTTCCGG ATGGACGAAC ATATGCGCGC CCATAGGTGC TATCAGCAGG GGATGTTCCA 2220

GATGATGGCC CAAAAGGTCA GTCCGGATAT CAATGCTGTG GGCAGCAACT CCACTGAGTC 2280

GGTGAGGTAA CAAAGGATAA TCACTGAANT GCCTGCGGTT CTCATGATAC GTCCACTCAT 2340

CTCCAGCACC ATGAGCAATA TATGCATACG CAGCTTCCGT CATCACATCT TTTGCTGAAG 2400

TCTYCAGTCT GTCCAGACTG ATGATATGAA GAGATTTGCT GGTCGATGTA TCAGCATGTC 2460

CAGACGTTTT ACTGATGATA TGTGCCGTTG AAGATGAGAT ATTTTTGGCA AGGGCCGGCG 2520

CAGTTGACAG CCTGCGGCAG ATATTCCTAA AACGGCATTC TGAATAAAAT TACGTCGGGA 2580

AAGAGGCATA ATAAGCTCCA TATATTATAA ATAAGCCAGG TCTCCCTGGC TTATAATGAT 2640

CATGCCACGC CCTGAAGCGG GTTGGTGTTG AAGGTATAAA GGAAAATTTT CCATTCACCA 2700

TTAATTTTAC TGAGGACAAA AACTTCACGG TTCAGGTCAA TAATGGTTTT CTGCTCTTTA 2760

AAGTTCGTTA CAACAGAACC CACATGGTGG TGAGTGCGGA CAACCGCGGT ATCTCCGTTG 2820

ATCCAGATAG AGTCAAACGC AAAATCGGTC TCAAACTTTT CACGCTTGAA CAGATCATCG 2880

TACTGCCCCT GGCGTTTTTC TGTATTGTCA GCCGTCAACT TATCATTCCA CTGGGAATAA 2940

CTTTCATCAG CAAACAGGCC CAGGATGGTT TTTGTATCCC CGGCATTCAG TGCGTTCTGA 3000

TACTTGATTA TCGTGTCATA CACGTTCTTC TGCTCAGTAG CAATCTTACT GTCTGTGGAG 3060

TATTTGAATG TACCGCCGGA TTGTTCAGGT GAGCTTTCCT TCTGTGCTGT CGACGATGAG 3120

GCAGCCAGAG CATTAGAGCC GAAAAGAAGG GATGATGCCA TGACTGCTGT TGCTATAAAA 3180

TGTTTCATAT ATTCTCCATC AGTTCTTCTG GGGATCTGTG GGCAGCATAT AGCGCTCATA 3240

CTATGCTGCT GTTTCAATAT TAGCGGCAGA CGTCAGCCTT ACCGCACTAC TTATTGGATA 3300

AGAATATCAA AAGTGACCGT GAAGTCAATT TTATCACAAC ACAGAAGGCC ACTATTTATG 3360

CCCAGAAAAT ATGAATCGTC CTCATCATGC ACGAAAGACT CGTAGTTGCA GCCCGGAAAA 3420

AACTGCCAGG ACACGACAGC AGATAGCCCG GGCAGCACTT GAGGAGTTCT CTGCACAAGG 3480

GTTCGCTCGC GCCACATNCA GCAATATCAG CAAGCGCGCA GGAGTAGCTA AAGGCACGGT 3540

ATATAACTAC TTCCCAACAA AGGAATTATT GTTTGAAGCG GTTCTGAAGG AGTTCATTGC 3600

TACCGTCCGT ACTGAACTGG AATCTTCCCC CCGCCGCAAC GGGGNAAACC GTAAAAGCCT 3660

ATCTGTTGAG AGTGATGTTA CCTGCCGTCA GGAAAATTGA CGACGCATCA ACAGGCAGAG 3720

CCAGAATAGC CCACCTGGTT ATGACAGAAG GGAGCCGGTT CCCGGTAATC GCTCAGGCTT 3780

ATTTACGGGA AATACATCAG CCACTACAGC AAGCCATGAC CCAACTGATT CAGGAAGCAG 3840

CATCAGCCGG AGAGTTAAAA GCAGAGCAAC TGCTCTGCKT CCCCTGTTTA TTGCTGGCTC 3900

CAAACTGGTT TGGCATGGTG TATAACGAAT TCTGAACCCG GCAGCACCGG TCAGTACAGG 3960

CGATCTTTTT GAAGCCGGAA TTGGTGCTTT TTTCCGATAG ACACATAACT GTCAGTATTA 4020

TGACCATGCC GTCAGGAGGA GGTATACCAG TGATACCCTG CCATGACCCG GTAACGTCTC 4080

CTGGCTGCCT TAAACCTGAA AGACCTGGCC CCACCACACT GCCGGTTACG CATCAAGATG 4140

CAGCAACCCT TGCATAAGGC TGTTTTGTGC AGAGGGCTAC CGGAAAGATA ATAACGTCAC 4200

AGCCCGTATG CATCAGATAA AACAGTGTAT TTTATCTGTC AGCAGTCACT GGAGCGGATT 4260

GTGGGGCGAG ATTCAGGTGC TGATACTGTA ACGACTCTGC GCCGCTGCTG CGGTAAAAGC 4320

GGCTGCCACC AGGCACGGTT ATCAGAGGAG GATGACCGTG TCCGCCCCTG GTGGTGATGA 4380

ACTCTCCATC ACAATCAATA ATGCCGCCGG GTGGATGAAG CAGACAGGGA TGGCAAGTCC 4440

CACTATCCCG GATAAAATGG GCTCTGGGCG CTCAGAAGAC CTGTGTGTCA GGCAGGGGTG 4500

AGAACGGTGA TGTTTTTTGT TGTCTGAAAG TCCAGCTCCA GCATTGCCTG CCAGCCTCAA 4560

GACTTCCGCT TTCTGCCCTT TCCGGCATTT TCTTCCGTTA CCATCATTCT GTTAATTCAG 4620

AGGCGTAGTA GTAGTAAACG TAATACATAT CCGGGAGGAT GAAGTCATCT AATCCTGCTC 4680

CCCGAATATC ATACAGCCAT TCCTGAGTGT GACTGCACCA TTTCCAATTA TGCAGTCTGT 4740

CCTCATCACA AAAATGTTGC AAGCAGTGCG GAGTCACGTT CCGTATTCAT GCCCTCTGCC 4800

AGATATTGAG CGGGGGAGAA ATGTGTAAGC GTCAACAGAG CGCCGTATTG ACACTTATTT 4860

ATCGGTGAAA ACTACGTTCC ATGGCAGCAG TTCGTCAACA CGGTTGGAGG GCCATTCCGG 4920

CAGTACGCTC AGGATATGGC GCAGATACGC TTCTGGATCG ATACCGTTCA ACCGACAGCT 4980

CCCGATTAGT CCGTACAGCA GAGCTCCGCG CTCGCCTCCA TGATCGTTGC CGAAGAACAT 5040

GTAATTCTTT TTCCCGAGAC AGACGGCACG AAGCGCTCTT TCTGCTGTGT TATTGTCCGC 5100

CTCCGCCAGA CCGTCATCAC TGTAATAACA GAGGGCGTCC CACTGATTCA GGACATAGCT 5160

GAACGCTTSR CCCAGTCTGG ATTTTTTCGA CAACGTGCCA TTCTTCTCCA CCATCCATTC 5220

ATGCAGCGAC GTCAGTAACG CTTTGCTTCG CTGCTGCCTG GCTGCAAGAC GTTCAGACTC 5280

CGGTAAGCCC CGTATTTCAT CMTCAATGGC GTACAGTTCA CTGATGCGCT TCAGAGCTTC 5340

TTCTGCCGTC GTACTTTTGC TGCTGATGTA TACATCGTGG ATTTTTCGCC GGGCATGGGC 5400

CCAGCACGCA ACTTCTGTCA GTGCACCACC TTCACGTTCG GCACTGAACA GCCGATCGTA 5460

ACCGCTGAAT GCATCCGCCT GCAGGATACC CCGGAAGGGA CGAAGGTGTT GTACCGGATG 5520

TTTTCCCTGC CTGTCTGGTG AGTAGGCGAA CCAGACCSCC GGTGGCTCTG ATGAGCCCGC 5580

ATTCCGGTCA TCCCSGACAT ACGTCCAGAT GCGTCCTGTT TTTGCCTTTT TTCTGCCCGG 5640

TGCCAGCACT TTTACTGGTA TGTCGTCAGT GTGAACCTTG CGGGTGTTCA TCACGTAACG 5700

GTACAGGGCA TCATTCAGCG GAGTCATTAA CTGGCAGCAC GCGTCAACCC AGTTGGAGAG 5760

TAATGCACGG CTCAGTTCGG CACCCTGTCG GGCAAAGATT TCACTCTGAC GATACAGTGG 5820

CAGGTGTTCG CAGTATTTTC CCGTTAACAC GCGGGCAAGT AATCCGGAGC CCGCGATGCC 5880

GCGCTCTATC GGGCGGGACG GCGCTGGCGC TTCAACTATA CAGTCACATT TTGTACAGGC 5940

TTTTTTTACC CGAACAGTGC GGATCACTTT CAGGGCGCTA CTCACCAGTT CCAGCTGCTC 6000

AGCACTAACT TCACCCAGAT AATCCAGCTC ACTGCCACAC TCCGGGCAAC AACTTTCTTC 6060

AGGCTCCAGG CGGTGTATTT CACGGGGAAG ATGTGCTGGT AACGGACGAC GATGACGTGA 6120

TTGTCGCAAC TGGCGGGGAA CTGCGGGTCA TCCTCACGCC CACTGTAACG ATCGCTTTCC 6180

TGTTCGCGTT GTTTCAGTTG GGCCTCAGCC TGTTCAACCT CACGCTGCAG TTTTTCAGAA 6240

CGGGTACCGA ACAGCATCCG GCGCAGTTTT TCTATCTGGG CCCTCAGATG TTCTATTTCC 6300

CGCTCCTCCT CTTCGATCTT TTCTTCGGCA CGTGCCARTG CAGAGCGCAG GAAGGCCTCC 6360

GTCTCTTCAA CCAGACTCAG TTGCTGATCT TTCTGACGGA GGGCTTCAGC CTGCTCAGAG 6420

AGTAGCCTTT CCAGCTCAGT GATACGAATG AGGTATTTCC GACTCATGAC CGTTTTTATA 6480

ATCCGGCCAT GACATTTTTA CAACATTGTC AGTGCATTAA GGCGGGATGT TTTGGGTTGA 6540

CGCCAGTCCA GTTTATCGAG GAGCATTGCC AGCTGCGAGC GGGTAATGGA TACCTTACCG 6600

TCACGCACCG CAGNCCAGAT AAACTGGCCT TCCTCCAGAC GTTTGGTGAA CAGGCACAGA 6660

CCATCAGCAT CAGCCCACAG GATTTTAATC GTGTCACCCC GTCGGCCGCG AAAGATAAAC 6720

AGGTGACCGG AGAAGGGGTT CTCATCCAGC ACATGTTGTA CCTGTTCACC CAGACCGTTG 6780

AAGGATTTAC GCATATCAGT AACGCCGGCA ACCAGCCAGA TTCGAGTGTC TGATGGGAGC 6840

GAGATCATCG TCCTCTCCCG GTCAGTTCAC GGATCAACAC CGTGAGCAGC TCTGGTGAAG 6900

GATTTTCCAG CGTCATGTTA CCGTGGCGGA ACTCAACTTT ACAGGAACTG GCACTGACTG 6960

TGCTTTGTGA AGGAGTGGAT AAAAGCGGAG TAAGAGCCGC CATAGGCTCT TTCTGCTCAT 7020

CAGGCGTTAT CTCAACAGGT AATAATTCAA CGCCAGCGCC AGAAGAGGTT GTTACCGGAA 7080

GACGCCGCGA TATACGCCCT TCGTTCTGCC AGAGCCTGAG CCATTTGAAC AGGAGGTTAT 7140

CATTGATATC GTGTTCCCTG GCAATACGGG CAACAGAGGC TCCTGGTTGT GAAGCCAGTT 7200

TAACCATTTG AAGTTTAAAC TCATTTGAAA ATGTTCTGCA GGGTTCTGCG GATAATATTT 7260

TCTGTTCCAT AACAGGTGTC CACTAGTTGA AAAAGTGGGC ACCTACGTTA CCAATACTGG 7320

CTTAATGGCT ACATACGGCG GTCAGTTTAC GCTTACAGAA ATGTAATGAA CACGTCCTAC 7380

CATTAACTGA AGAGCATGGT GACGGATGAA GGAAAAAGCA GGAGTGTGTG GTGCCTCACA 7440

GATTTCCGAC ATCATAGCTG TCAACGACGG ATGAAAAGCG GCTCTTCCGC AACTTGGGTG 7500

GAAGAAAATG GATGAAACTT TCTGGTGTGA GAACCTTAAG GAAACAACAT GTTGGGTGGA 7560

GCGGACAATC CAAATGGTGA ATTACCGTCT TATATCACTG GCGCTGACAT TCCGGGCGTC 7620

TTCTCCGCCA CAACGCCATT TGCAGTGCAT CACAGGCCAG TTGTGCTGTC ATTCGCGGTG 7680

ACATCGACCA GCCAATAACG GCGCGTGACC ACAGGTCGAT GACTACTGCG AGATACAACC 7740

AGCCCTCATC GGTACGCAAG TAMGTGATGT CACCCGCCCA MTTCTGGTTC GGAGCCTGGC 7800

GCTGAAGTTC CTGCTCCAGC AGATTCTCCA ATACGGGCAG GCCATGTGCA CGGTAGCTGA 7860

CCGGGCTGAA CTTCCGGCTG CTTTCGCCCG CAGCCCCTGA CGACGCAGGC TGGCGGCAAT 7920

GGTTTTAATA TTGAACTCCG GCATTTCGTC AGCAAGGCGG GGAGCACCGT ATCGCTGCTT 7980

TGCCTCAATG AATGCCTTAT GGACAGCGGC ATCGCAGGTG AGCCGAAACT GTTGGCGCAG 8040

GCTCATCTGG TGACGACGCC TGAGCCAGAC ATACCAGCCG CTGCGGGCAA CCCGAAGTAC 8100

ACGACACATC GCTTTGATGC TGAACTCTGC CCGATGATTT TCGATGAAGA CATACTTCAT 8160

TTCAGGCGCT TCGCGAAGTA TGTCGCGGCC TTTTGGAGGA TGGCCAGTTC CTCAGCCTGC 8220

TCCGCCAGTT GTCGTTTAAG GCGGACATTT TCAGCGGCCA GTTCGCTTTC GCGCTCTGAC 8280

GAACTCATTT GTTGCTGCTG TTTACTGCGC CAGGCATAAA GCTGAGATTC ATACAGGCTG 8340

AGTTCACGGG CTGCGGCGGC CACACCGATG CGTTCAGCGA GTTTCAGGGC TTCGTTACGA 8400

AATTCAGGCG TATGTTGTTT ACGGGGCTTC TTGCTGATTG ATACTGGTTT TGTCATGAGT 8460

CACCTCTGGT TGAGAGTTTA CTCACTTAGT CCTGTGTCCA CTATTGGTGG GTAAGATCAC 8520

TCAGCAACGT ATCAAAAGTC TGTAAAATCA TGGGCGTTTC GCGTGATACA TTTTATCGTT 8580

ACCGCGAACT GGTCGATGAA GGCGGTGTGG ATGCGCTGAT TAATCGTAGT GCCGCGCTCC 8640

TAACCTTAAG AACGTACCGA TGAGGCAACT GAACAGGCTG TTGTTGATTA CGCCGTCGCT 8700

TTCCCGGCAC ACGGTCAGCA CCGGACCAGC AAACAAGCTG CGTAAACAGG GC 8752

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

INSDOCID <WO 9822575A2 I >

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TGGTCAAAGA TGCAACTGCA TTTCGTCGCG GCTTTGCGGC AAATACTTAC ATCGCAGAAA 60

TACTGTGCGG AAATCTGCAT CCATTTCCAC TTGCTGTATG GCATAACTTT TCAGGCGGTC 120

CGGATACTGC CGAAGATTAT TATGCCACAT ACCACCCGTT ATGGGGGCAA TATCCGGAAG 180

CATTGCTGTT TGTAAACTGG CTCTATAATC ATTCCTCTGT GCTGCATGAA CGGGCAGAAA 240

TCATTAAATG CGCCGAAATG CTGATGCAGG AAGATGATTT CGAAATATGC GAAAGTATTT 300

TAAGACAGCA GGAGAAGTTG CGTGAAAGAA TTGATGAGAC GCTTTCTGAG AAAATTGTAC 360

AGAAATGCAG AAATATGAAT GGTGAATATG TCTGGCCCTG GATATTGCCG TTTTCAGCGG 420

CAGGCATGAA ACATACTGGC ATACAGTATC AGTAGATATT GCATTAGTGT ATCCTGCACA 480

CAAGTAATAA TTTATCCACC AATAATAACA CTGTTAATGT CCCCTTCCCC TGGTTGTCAG 540

CCAGGGGTTA TCTTCTGAAT ATTTCTTTTG AAAAGGATAA CACAATAAAT TATTTTTATG 600

AATTATCCCA TGGACTCATT AACACCCTTT CATAATGTTT TATTGTCAAA CACGTTATGG 660

CTGACATCAA AAAAAACCGG ATTTCCTCTG CCAGCGGGTA ATCACCTCCC CGGTGTTTTC 720

GGTTGGTCTG GTTACTCCTG TCTGGTTATT AGCAAGATAA TTGCTATAAA CAGTGGAAAA 780

CTCATCGTAC ATAATCTGGT GATGAACATT ACGCTTATTT TCCCTTGACC GGAAGAATCA 840

GAGGCTGCGG TTTCAGACTG TCTGCCGGTA CATTCCTCTC TCCGTTAAAA ACCATAATGG 900

GTTCATTATC TTCGTCTGTC AGTAGATTGA ATGGCGGTAT ATTTTCAGTA CGAATGCCGG 960

TCAGCCACTG AAAAATACCT GCGAAATGAC GGGCACTGAT TTTTCTGCTG ACGGACTGAT 1020

GAGACGTGAT GTCACTGGCG GTAATAATCA GGGGAACGCT GTAGCCTCCC TGCACATGAC 1080

CATCATGATG AACAGGATTA GCACTGTCGC TGACCGACAG CCCATGGTCA GAAAAGTAAA 1140

GCATGACGAA ATGACGGGAA TGCCGGCGAN GGATACCATC AAGCTGACCG AGAAAGTTAT 1200

CCAGTTTACT GATGCTGGCG AGGTAACAGG CAACCTTTCG GGGATACTGC TCCAGGTAAT 1260

GATTCGGCCA GGAGTGAAGC CGGTCACACG GGTTCGGATG AGACCCCATC ATGTGCAGGA 1320

ATATCACCTT CGGAGAGGAT TTATCCGCCA GCGCACGTTC TGTTTCCTGT AACAACAACA 1380

TGTCATCCGT TTTACGGGAA GCGAATGCSC TTTCTTGAGG AAAACGGTAT GCTCCGCATC 1440

AGAAGCAATA ACAGAGATGC GTGTGTCATG CTCTCCCAGT TTTCCCTGAT TGGATATCCA 1500

CCATGTGCTG TATCCTGCTT TTGCTGCCAG CGCCACCACG TTGTTGCCGG AATCAGGGTT 1560

CTGCTCATAG TCATAAATCA GTGTCCSGCT CAGGGAAGGT ACGGTACTGG CTGCTGCCGA 1620

TGTATAGCCG TCAATAAATA AACCGGGAGC TGTCATTCCA GCCACGGCGT GGTTGGCCAC 1680

GGGATAACCA TATACCGACA TATAATCCCT GCGCACACTC TCACCAGTGA CAATCACAAT 1740

CGTGTCATAT AACGGTGTTC CCCGGCCAGG ATTTTCCCAG TTGTCAGCCC CGTGCTGACT 1800

CAGTTGTTTA TAATGCTGCA TTTCACGCAA TGTGTCAGTT GTCCCCACAA CAGTTCCTTT 1860

AACCATCCGC AACGGCCAGC TGTTTACTGA GCATAATACG AACAGCAGCA GTGCCAGCCA 1920

GTTACGGTGA CCACGGCGGT GTGTTCGCCA GAAAATCACC ATGAATACCT GAATCGCGGC 1980

ACTGACCAGA AAATGATAAA CAGGAATCAT CCCGGTAAAC TCCGCTGCCT CATCAGTTGT 2040

GGTCTGCAGC AACGCGACAA TAAAACTGTT GTTGATTTTA CCGTACGTCA TACCGGCAGG 2100

CGCATACAGT GCACAACAGA ACAGAAATAA CAGCGCTGTA ATGGATGTGA GGGTATTTCT 2160

GTGTGCAAGG AGCAGAAGGA GAAACAGAAG CAGCACATTT CCTGTTGCAT TCCTCTCAGT 2220

GTATCCGCAT GCAATTGTGG TTATTGCAGA CACAACAAAA AAGAATAAAA ACAATAAAAT 2280

CCGGGGGGGG TTGCCCGGAC AAAACAGTTT TCTGATATTC ATCGGAGTAT ATCGACAACA 2340

TTATTATGAA GAGAACAGGA TAATAAAAAT CAGAAATTAT TGTAAAACAG ATAAAAGCAN 2400

CNATGCAGTA ATAGACT 2417

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGACAAAAAC CAGTTACGGT TATCACGTAC CAGCCCCCGT ATTTCCAATT TATAATCCTG 60

GCCATCAATT ACTGGGATCT CTTCTTCTCC ATAGAAGGCA TTAAAAGGGA ATGGAGTGGT 120

AATGTCCTCT GGAAGATATT CTGGTGCCAC ACTGTTTTTG CTGAACAGAA AACTTTGAAT 180

CCGGTCATTA AATCTGGATA TACGGAACAA TGCTTTTTCA ATATCATCAT TATTGCTTAT 240

ATCACAGCCA GTCAGCATCA TAATTCCCCC AAGCGTCAGT CCCTGTTGGA GTAAACGACG 300

TCTGTCCGGC GCAAGGATTT TTTCTGCATC TTTCACCACG TAATGGGCAT CACTGTCAGA 360

CAAAAAACGT TTTTTCTTCA TTAGTGACCC CGTATCATAG ATAACAATGC ACGCGGAACC 420

AATAACACCA TAACCAGGTG AATAATAATG AACAGTACCA TAATGTTCAT GCACAGAAAG 480

TGGATATAAC GCGCTGTATC ATAACCACCG RATAGTATAG TCAGAAGGGA AAACTGAACG 540

GGTTTCCATA AAACCAGACC AGACAATAGA AGAGCAGCGC CATCTAAAAT AATCAGAATA 600

TAGGCGACTT TTTGCACCAT ATTGTATTCC TGCATATTCG TATGATGCAG CTTTCCATAC 660

AGTGCCTGCG TAAGGGATTT TTTCAGTGAG GTCCATGACA GCGGGAAAAA CTTGCTCCGG 720

AAACGTCCGC TACAAATTCC CAGAGTAAGA TAGATCGTGG CATTAATCAG CAGAATCCAC 780

ATCAGGGCGA AGTGCCACAG TAACGCACCG CCAAGCCAGC CACCGAGAGT TAATGCTGCC 840

GGATAGTTAA AAGAAAACAA AGGAGAAGCA TTATAAATGC GCCATCCACT ACATATCATG 900

CCTGCGACAG TAACAGCATT AATCCAGTGG CAACAGCGTA ACCACAGAGG RTGTATTTGT 960

TTTAACGGTA ATGGCTGCAT TATGTGATCT CTGTCTGTAA ACTAAGTATA TTATGGAAAG 1020

GAATGTTCAT CACATCCTCA CAAGAGTTTA AAAAAAATGT GACAANTCAT CGTCAAATGC 1080

TGGGGTAAAA TTCAGATAAA GAATATGTGG ATAACTTTTG ATGAATAACG TAAAAAAAAT 1140

ACTGCTGATG GAAGATGATT ATGATATTGC AGCTCTGTTG CGGCTTAATC TGCAGGATGA 1200

AGGGTATCAG ATAGTTCATG AAGCGGATGG CGCCAGAGCT CGTTTATTAC TAGACAAGCA 1260

GACCTGGGAT GCCGTAATAC TTGATCTTAT GCTGCCTAAT GTTAATGGGC TGGAGATTTG 1320

CCGTTATATC CGTCAGATGA CCCGTTATCT GCCTGTGATT ATCATCAGTG CCCGTACCAG 1380

CGAAACCCAC CGCGTCCTGG GACTGGAAAT GGGGGCTGAT GACTATCTAC CGAAACCCTT 1440

TTCCATTCCT GAGCTGATTG NCCCGCATCA AAGCGTTGTT TCGTCGTCAG GAAGCCATGG 1500

GGCAAAATAT TCTCCTGGCA GGTGGACTGA TTTGCTGTCA CGGTCTGTGC ATCAATCCAT 1560

TTTCACGTGA AGTTCATTTG CATAATAAAC AGGTTGATCT TACCCCACGC GAGTTTGATC 1620

TGCTGCTCTG GTTTGCACGT CATCCTGGCG AAGTTTTTTC CCGTCTTTCA CTGCTGGATA 1680

ATGTCTGGGG GTATCAGCAT GAAGGATATG AGCATACAGT CAACACGCAT ATCAACCGTC 1740

TTCGTGCCAA AATTGAACAG GATGCAGCAG AGCCAAAGAT GATCCAGACC GTCTGGGGAA 1800

AAGGGTATAG GTTTTCAGTT GACAATGCAG GAATGCGATA AATGAATTGT AGCCTGACAT 1860

TAAGCCAGAG GTTAAGCCTA GTATTTACAG TCGTTTTGCT GTTTTGCGCC GTGGACATGT 1920

GGCGTTCATA TTTACAGCAG TAATCTGTAT GGCAATGCAA TGGTACAGCG TTTATCTGCA 1980

GGCTGGCGCA ACAGATTGTC ATCACGGAGT CTCTGCTGGA TAATCGTGGG CAGGTGAATC 2040

ACCGGACATT AAAGAGTCTG TTTGAGCGTC TGATGACGCT TAATCCCAGT GTGGAGCTGT 2100

ATATTGTCTC GCCGGAAGGT CGGCTGCTTG TGGAGGCCGC CCCTCCAGGT CATATCAAAC 2160

GTCGGTATAT CAATATAGCG CCCTTGAAAA AATTTCTCTC CGGTGCTGTC TGGCCCGTAT 2220

ATGGTGATGA TCCCCGAAGT GTAAATAAGA AAAAAGTTTT CAGTACCGCA CCGCTTTACC 2280

TGAGGGATGA TCTGAAAGGA TATCTGTATA TTATTTTACA GGGAGAGGAA CTTAATGCTC 2340

TTACTGATGC AGCCTGGACA AAGGCACTAT GGAATGCACT GTACTGGTCG CTGTTTCTGG 2400

TAGTGATATG TGGTCTGCTG TCGGGTATGC TGGTCTGGTA CTGGGTAACC CGTCCCATAC 2460

AGCAACTAAC TGAAAATGTC AGCGGGATAG AGCAGGACAG TATTAGTGCC ATTAAACAAC 2520

TGGCAATTCA GCGCCCTGCC ACCCCCCCTA GCAACGAGGT CGAGATATTA CACAATGCCT 2580

TCATTGAACT GGCCCGTAAA ATATCCTGTC AGTGGGATCA ACTTTCAGAA AGTGATCAAC 2640

AGCGCCGTGA ATTTATTGCC AATATCTCCC ATGATTTACG GACGCCATTA ACATCACTTC 2700

TGGGATATCT GGAAACCCTG TCAATGAAGT CGGATTCGCT ATCATCAGAG GACTGTCATA 2760

AATATCTGAC AACAGCTCTC CGGCAGGGAC ACAAGGTGAG GCATCTGTCC TGTCAGCTTT 2820

NSDOCID <WO_ 9822575A2 I_>

TTGAGCTGGC ACGTCTTGAG CATGGTGCTA TAAAACCTCA ACTGGAGCAA TTTTCTGTCT 2880

GTGAACTTAT TCAGGATGTA GCTCAAAAAT TTGAGCTCAG CATAGAAACC CGTCGATTGC 2940

AACTAAGAAT TATGATGTCA CATTCCCTGC CTCTTATCAG GGCAGATATT TCAATGATAG 3000

AGCGTGTGAT AACAAATTTA CTGGATAATG CTGTACGCCA CACACCTCCG GAAGGCTCGA 3060

TCAGGCTGAA AGTCTGGCAG GAAGATAATC GGTTGCACGT CGAAGTGGCT GACAGCGGCC 3120

CTGGACTAAC TGAAGATATG CGAACTCATC TTTTCCGGCG GGCATCAGTG TTATGTCATG 3180

AACCGTCAGA AGAGCCCCGG GGAGGACTGG GATTGCTGAT TGTACGCAGG ATGCTGGTAC 3240

TACACGGTGG TGATATCAGG TTGACTGATT CAACGACTGG AGCCTGCTTT CGTTTTTTTC 3300

TTCCATTATA ACATCAGGCG GCATATTTTG GGGTGGTTAT GTGTATCTGC CTTTGTAAAA 3360

GGGATACAAG TTCTGTAGTG GAGCACAAAA TCAGGACACC GGAATAACCT GTTTCCACTT 3420

TTCTTCATGT AAGCAAGGCG GTAAACCATC GTTGTTCGTG TGAGGTCGAT AAACGTTGTA 3480

ATAACCATTA ATCCACTGGT TTATATCACG TACCGCATGG ATAAAATCAC CATAACCACC 3540

TTTCGGAAGC CATTCATTTT TAAGGCTGCG AAAGACTCTT TCCATCGGCG AATTATCCAG 3600

GCCATTCCCT CTGCAACTCA TACTTTGCAT TACCCCATAA CGCCAGAGTA ACTTTCTGTA 3660

TTTATTGCTT TTATACTGAA CACCTTGATC TGAATGAAAC AGCAGGCGGC CATCACGCGG 3720

TCGAGTTTCC AGTCCGTTAC GCAAAGCCCT ACACACCAAC TCAGCATCAG CGGTTAATGA 3780

GAGGGCTGAA CCGATAATCC GCCGTGAATA TAAATCAACA ACGAGCGCGA GCTAACACCA 3840

TTTGTCCTGC AGGCGAATAA AACTGATGTC GCGCACCAGA CGCAGTTTGG TGCGGCGGGG 3900

TGAAATTGCC GGTTCAGTAA ATTTGGCAAT GGCGGACTTT TGTCTTCGTT TACCCGGTTG 3960

TGATGTTTAA CCGGCTGTCG ACTTGTCAGC CCTCATTCCC GCATCAGTCG TCATGCCAGC 4020

CACCGGCCTG CATCAACGCC ACTCTGGCGC AACATCTGAC TGATTGCCCG GCTACCCGGC 4080

TGCGCCACGA CTGAGAGCAT GGAAAGCCCT CACCCGGCTT CGTAATTCAA TTCTTTGCAC 4140

ATTAACAGGA CGCTTCACCT GCGCGTAATA AACGCTACGG TTAATACCGA ATAAATGACA 4200

AATAACCCAC ACTGGCCACT TTGCTTTCAG CTGTGTGATT AGCGCGACAG CTTCCCGGGG 4260

ATTTCGCTCA TCAGCACGGC AGCCTGCTTT AGTATTTCTT TTTCCATCTC AACGCGCTTT 4320

ATCTGCGCTT TAAGCTGCTG AATTTCGCGT TGTTCAGGGG TAATAGCATT ACCAGCTGGC 4380

TCAATACCCT GAAGTTCCTG CTTATACAAC CGTATCCATT TACGCAAATG GTCAGGGTTG 4440

AGCTCGAGTG CCTGCGCGAC TTCTCTGACA TCACGCTGGT ATTTAACCAC CACCTGCTCG 4500

AAAGCTTCAA GCTTGAACTC CGGGGAAAAG GTACGTTTAG TCCGACGAGT TTTGATCATG 4560

CATCACCTCA TTTTCACTGT TTTAACATTA ACAGGATTTC GAGGTGTCCT GAATTACCGA 4620

TCCACTACAA AGTACGACAG GTACTGTGGA GGTACTCCCG TAAAGACGGC CATCAAGCTC 4680

CCGCTCCGAC ATACCTGCGG GCAGAGGCCA TGAAAAGCCA GCTTTGCGAA AGCGCACGAA 4740

CATACCACAA GCTGTTGATT TTGGTACGCC CAGGCGACGC CCGACCACAA CCTGGGGTAA 4800

ATGTTCTTCA AAGTGAAGAC GTAAAGCTTC AGTGATCCAA GTCCGGTGTT TCATACGATA 4860

GTGTCCATTA AAAATGATGG ACATTATTTT TGTAAAACCG GAGGAAACAG ACCAGACGGT 4920

TTAAATGAGC CGGTTACATG TAATCCATAC TCATCCAAGG TTTAATTCTG ACACAATAAG 4980

AAAATATGGA AAGTCTCGCT CTAGAGATGG GGAGAGGGAT ATTGAAGTGT ATGATATTCC 5040

AAGAACTGCC GGAGATATCC TCGTAAATGG ATTTTCCAGT GCAAACTGAT AACAAATTCG 5100

AAGTCATTAT CTGCAACAAG ATTGATTGAT GTAGGGGATA TGTTAGAGCA TTATAATGCT 5160

CAAGGATTTG GCGTGATGAC ATCTGCGCCA ATTGATGCGA CACTATATGA TAAACTGGAT 5220

GCTATTTGCA GTAAGTGTAA AATAGAACAA ATAAATTTTT CAGTATTAGA GTCAGAACGC 5280

GCACTATATT ATGACGATAT ATTAAGATGC CGTTACTTTG GTAAATAMCA TAAAATTAAT 5340

CAATATGGTA ATATATCAGT TGTAATTGAT CGAAACAAAG CACATAAATG CCATCTTATA 5400

AAGATGGTGT TTKTTAAGCA TATAAAATAT ATTTTCTATA AGATATAGGG CAAACTAAAT 5460

TTCTTGACTT CTATGATGGA CTAACTAGAT ATACATGCCG CCAGTTTTTA TAAAACGACG 5520

GCATATATAA TCATTTATAT ATCTTTTGAT TTTATTCGTA ACCACTCATG TTGATCTAAA 5580

CCTATTCTTG ACAGATTAGC AACAATATCA GTTGTTATTT TTTGCGCGTA CGTTGTTTTT 5640

ATTTCCCCGA TCCATTTCAA TACTTTTGGA GTAGATATTT TTTCAACGAG TAAAGGAACG 5700

AATGAGATAT AGTCAGTATT AACTAGATTG TTCTTTTTCC CTATGATGAC ACCGTTTCCA 5760

TTTTCGACTC CAAATGAAAA TGAAATAATA TTAGAAGCTT TTGCCGGCAT TTTAATTTTA 5820

TAAAAACCGC CATATTCATC TTCGATTAAC AAATTGTAAT TATTATCGTC CAGTGTTCCC 5880

CTGAGGAATA AAAAATCGGC TTTTTCATGC AATCTGACGC TATCACATAA TGGTTGTATG 5940

CATAGATAGA CAAAATTATA TGCATCTAAA AGTAAAGTTC CTTGTTTTAA GGACACATTA 6000

TCTATATGAG AATGATATCT TAAACTCCTG CGCGTGATTT CCAGAGAGCA TAATTGCATT 6060

AACTTTTTAT CTTCTTCACC ATCTTGGCTT AAGTATTCCT TTTTACCTAA AGATGCGTGT 6120

TCAATAGCGT GTTGAATTTC TTCTAAAGAA TCAGCAGAGA GTATATTCCT TAGATGTTCT 6180

ACTGATAAGT CTTTTTGTTT TTTTCCAGTT AATAGAAAAT TCTTACAACC ATTTTTTGCA 6240

TAGTGAAAAA TAGGCCAATG GGATAAGGAG TTTTTGCTTA GAGATTTCTG GGGA 6294

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

NSDOCID: <WO _ 9822575A2 1 >

TATTCCTTTC TCTCCCATGA TAGGGCGAAA GGCTTTATTA CTATCCACTG CTGGTTTATT 60

AATTGCATCA TCGTCGATTA ATTTGCTGGA GGTTCCAATA GTCAACCACC TCTCTTCAAA 120

TTCATCGGTT GTCATACCTA ATCCATCATC TCTCAAGATA AGAAGATTTT CTTTCCTAAA 180

AAAATCAACT TCGACATTAT CAGCATAGGC ATCATGAGCA TTTTTAAATA ACTCACTCAA 240

GGCAGTAGGT ATACCTGCAA TTTGTTGTCT GCCAAGCATG TCCAAAGCTC GAGCCTTTGT 300

TCTTATTTTA GCCATATATC TATGAATCCT TATTAGTACA ATTTTCTATG AGATGTAGCC 360

CAAATAGTCT AGCGAGTTCG CAAGGTACAG CATTGCCGAT TTGCTTTGCC ATTGAATTCA 420

GCGAACCTTT AAAAACATAG CTTAAAGGAA ATGTTTGTAA TCTTGATGCT TCTCTTATGC 480

TAATTGCTCT ATGTTGAGTG GGGTCAGGAT GCCCAAAACG ACCATTGGAG TAACTATTAC 540

ATTTCGTCGT AAGTGTAGGC GCAGGCTTAT CCCAACTCAT TCTTCCATAA GTATCTGTGT 600

GGCCATCATA ATTTTTATGG CATTTATTAA CTAACTCTTC TGGCCAATTT CTTCTATCCC 660

CTCCTTCTGG AGTGTGCATA AKTCTTTTTA GGTTAAGAGG GCTCAGTGTT CCAGCCCTAT 720

GTAAAGGATC TTTGGGGTCG GTTTCTCCTG AACATAACTT TGTGAAGTCC TGGATATAAT 780

CTCGTACAGT TTTGAATGGG ATTTTATTTT TACCATGGGT TATCTCTGGT AGGGTAACTT 840

TACCTACTCG ACTAGCTAAG AGCACGAGTC TTTTTCTTCT TTGGGGAATC CCATAGTTCT 900

CAGCATTGGC TATAAAAGAT ATATAGTTAT ACTCTAACTC TTTAAGTAGC TTAATAAACT 960

CCTGAAATGG GCCTTCTTTT TCTTCATCAA TTTTTTGCAT TCCAGGAACA TTTTCAAGCA 1020

TAATATATTC AGGAAGAAGT TCTCTAATAA AACGATGAGT TTCATTTAGT AGATTTCTCC 1080

TTGAGTCGTC ACTAGTTTTA TTTTTATTCT GTTGCGAAAA TGGTTGACAT GGTGCACATG 1140

CACTCAGTAA CAAAGGCCGT TTAGCTTTAA TATCAATGAT GTCGGAGATA TCTTGAGGTT 1200

CGATTTTCCT AATATCATCT TGGATGAATT TTGCATCAGG GAAATTAGCT TTAAATGTTT 1260

CTGATGCTTG TTGGTCAATA TCTAATCCAA GCTCGATATC AAAGCCAGCC TGACGTAGCC 1320

CTTCACTGGC TCCACCACAG CCACAAAAAA AATCTATAAC TATCAATTTG ATACCTTCTT 1380

TGAACTAAAT AAAACAACTC GAATAAGTTG ATATTTTAAA TAAAAATAAT TGGTATGGAT 1440

ATGAACTTTG GTCACGCTAC CGCCCTGAGK TCATGGCCAT CCCCAGACCT TTTAAAGGGA 1500

TTATGAACAA CACCCAGCCG ACGTTCAACG GTGTTACCCA TACATATCAC AAAGTTAGTT 1560

AATTGGTTGG TCGTAAATTG ACCTAAAATG GATTGAGGGC AATGCAAAAA TCATTGGGAA 1620

ATCCAGGCGA CACAGATGTT CGGAAGAGAC TGAATGTTAA AAATATAGAA TGTATATTCT 1680

CAAAAAAGAG ATATTTCATT ACATTTTATA TGTGTATAGG AAAGTGAGAT TGGCGAATCA 1740

CCTCCCAATC ATCCCGCCAG CGCTCCATTC AGCGCCACGC CAACCCTCAC TCCAGCCCAC 1800

GTCATCGCCC CCAGCCAGAA TGTCGGCAAC ACCAGAAACA TCAACCTCAT CACCAGATTG 1860

ATAATCACGT CATCCTGCGT ATTCTGGATC CCGGCTAAAT TCCAGCTACT GTGGGTATCG 1920

CTGTTGTAGA GCACATCCAG CAGCCAGCTA TCAAGCCACC GTGCCAGTTC CCACCAAAAG 1980

GTGAGGAAAA ATAGTGCAAA CTGCACAAAC GTCAGCGTCA TCACTACTTT CACATCCCAC 2040

GCCGAACAGA GCGTTATCAG CGGAATACAG ATCACCAGCG CTATTTGCAG TGCGCCTGTA 2100

CCATCGGTAG TGCCTAACGC ACGCTGTCGA ATGCCGTACA TGCCGCTATG CTGCCGAGGA 2160

TATTTCTAGC GCCGGATGCC AACCGGGTGG CGGCATTGGC GACGGTGCCA TCAACGTTAC 2220

CGCCATAGCT TGGATAAACG CGCCCATTCT GCGATACCTG CATATTTCGT TCACTGACCC 2280

GCGAGCGCAG CACGGCCTCT TCATACACTA CCTGCGACTG GTCGATTTTT TTAAACGCCG 2340

TCCAGATATC TAGGGCAGGA AGTTGCAGTA GACGGGCTTT CAGCCCAAGC GGTGTCGTCG 2400

GCCCACCGCT GTTTACAAGT GGGATAGCCG CCCGCGCCCG TATCGGCCAG CCCGGCATCG 2460

CGCGATGCAC TGTACGGCCA AGCACTGTGT GGTGAAAGCG CATGGTCGGA AAAGGCCTGT 2520

TCAGCTAACC AAGCACATCC CACCATCACA AGAATCGCCA GAAAACCAAA CTCAGTCAGA 2580

ATAACTCTTC CTGATTCAGG CTTTGCTCCT GCATTATGGC TACCACTATT GTTTGCCTGC 2640

ACGTATCATC TGATAACGGT TAATTAACTG ATTTAGCGCC ATTTCAGCCT GTTTTTGCTG 2700

CTGTTCACTG CCATTCTGGT TACGGACTTC ACCGTAGCGA CGTAACTGCT CTTCCGCCGG 2760

GATATGCCGG TTAAAAGCCT GCATGATGCC AAACACCTCC GTTTTCAGTT CACTGACCGT 2820

CATGTATTTT CCCCGCTGTT CATCCTGACG GTTCAGGCGC TCAGCCAACT GCTGTAAGCG 2880

GATCATGCCT TCGTTCCAGC CCGTCATCGC CTCTTCCGGG AGCGCACGAC TCCTTACACT 2940

CTTCTGCCAG TTATCCACCA TTTCCTGAAC ACGGGGATTG CCGGGGACAA GAACCCTCAG 3000

TTGCTGCAGC AGCTGCGCAC TGCACCGCAG GTTGTATGCT GGAGGTAATT CTGCCAGTCG 3060

CGTTATCTGC TGACCGGAAA GGGTTATCCA GTGCACTCAG GGCAGATACC GGATTCAGGT 3120

TAATTTTTTC AAACAGGGAA GCATATACGC TGTCGCCGGT ATGCGTTTCA GATACCACAC 3180

TCTCTGCGAC GTTCTTTTCT TTCTGTACAG ACATCAGCAT TTTCTGTAAG CGTACAGCGA 3240

GGGCCGTATT GACGGGGATG TGTTATTCAG CTGGCAGTGC TATGCGCCAC GGAAGCAGTT 3300

CGCTGACCCG GTTGACCGGC CAGTCTGCTA TGACGGCAAG CACATGGCGA AGGTAGCTTT 3360

CTGGATCCAC GTCATTCAGT TTGCACGTCC CGATCAGGCT GTACAGTAGC GCTCCCCGCT 3420

CACCACCATG GTCAGAGCCG AAGAACAGGA AGTTTTTACG ACCCAGACTG ACCGCCCGCA 3480

GGNCATNTTT CAGCGATGTT GTTGTCGATT TCCACCCAGC CATCGTTCGC ATAGTACGTC 3540

ATGCCGGCCA CTGGTTAAGT GCGTACGCGA ACGCCTTCGC CACCATCAGG CTGGACAGGG 3600

GACTTTCACC CCCAAGCTGC TGAACATGCC CGGCACACAA AGAAGATCTC GGCTCAGTGG 3660

CCGGGATTAG TTATACAATT ATCTGATTGA TTTTTAATAT ATCTTTTCTT AAATCATCGT 3720

TAATATCTGA CGGTTCTAGC TGGTTTATAA GTTGCCTTAT TTGGGTAAAG GTACTTTTCT 3780

GATCTTTTAG ATCTTCTCCT TTTATCGTTG ATAAAGCTGC AATTAGTTCA CCATCGTAAT 3840

NSDOCID <WO_ 9822575A2 I >

ATTCACCCGC TAACGGCTCT TTAGTTAGAA CTTCCAACAC TCTTGGCATC AACTGATCAA 3900

TACATAAATT TTGTCGGATA GCGCGGCAAA GATCTTCCAC TCTTAACTTT TCAAGAGGCA 3960

CATCTATGAT ACGTTCGAAC CAGAGTTCAA GCGGTGATTG TTGCTCAGGC TCTTTTGTCA 4020

TATTGATGTT TCCAATCAAT TTACGTAAGG TAATCATATT CCATATCCTT TCAAGGCTGA 4080

TTCTATTTTA TTAATAGCAT CTGTTGCTCT GCCATACGCA GCCTGAGCTT CAGGATTGTT 4140

GACGTTTTTC AACGTATCCG CATGATTTCT TAATCCTCTG AGCGTATTTT GCATTTCCTG 4200

CATATGATCC CAATATCCTC CATTCTCTTT AGGAACTGGC TTACCATCCA TATCCTTGAG 4260

AGTTCCAATT AATATCATGA ATCTTTTCAG ANCATTTTTT TAATAGTGGT TAATCGANTC 4320

TTCTTTAANT CGGCAACTTT TCTTGGCCTT CCTGGAATTA AAGGCTTTAA TCCTAACAAG 4380

TTTTTTTCTC AATTTTTGGC TGGCTTTAGG GAATCAATTT TTCCCGGATT GGGTGGGTGG 4440

GTGGTAACCC GGGTTTCCCT TGAAGCCCGG GAAACCCGGC CCCAAGTTCT TACTTTTTTT 4500

CCCGCAATCG GGTCAAGAT 4519

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATTACAGAAT GTGGAAATTA AGTATGATTC GAAAAAAGAT TCTGATGGCT GCCATCCCCC 60

TGTTTGTTAT ATCCGGGGCA GACGCTGCTG TTTCGCTGGA CAGAACCCGC GCGGTGTTTG 120

ACGGGAGTGA GAAGTCAATG ACGCTTGATA TCTCCAATGA TAACAAACAA CTGCCCTATC 180

TTGCTCAGGC ATGGATAGAA AATGAAAATC AGGAAAAAAT TATTACAGGG CCGGTTATTG 240

CCACCCCTCC GGTTCAGCGC CTTGAGCCGG GTGCGAAAAG CATGGTCAGG CTGAGTACCA 300

CACCGGATAT CAGTAAACTT CCTCAGGACA GGGAATCACT GTTTTATTTT AATCTCAGGG 360

AAATACCGCC GAGGAGTGAA AAGGCCAATG TACTGCAGAT AGCCTTACAG ACCAAAATAA 420

AGCTTTTTTA TCGCCCGGCA GCAATTAAAA CCAGACCAAA TGAAGTATGG CAGGACCAGT 480

TAATTCTGAA CAAAGTCAGC GGTGGGTATC GTATTGAAAA CCCAACGCCC TATTATGTCA 540

CTGTTATTGG TCTGGGAGGA AGTGAAAAGC AGGCAGAGGA AGGTGAGTTT GAAACCGTGA 600

TGCTGTCTCC CCGTTCAGAG CAGACAGTAA AATCGGCAAA TTATAATACC CCTTATCTGT 660

CTTATATTAA TGACTATGGT GGTCGCCCGG TACTGTCGTT TATCTGTAAT GGTAGCCGTT 720

GCTCTGTGAA AAAAGAGAAA TAATGTACCG CAATAACGGT TAAATGCGGG TGGGATATTA 780

TGGTTGTGAA TAAAACAACA GCAGTACTGT ATCTTATTGC ACTGTCGCTG AGTGGTTTCA 840

TCCATACTTT CCTGCGGGCT GAAGAGCGGG GTATATACGA TGACGTCTTT ACTGCAGATG 900

AGTTGCGTCA TTACCGGATA AATGAACGGG GGGGACGCAC CGGAAGCCTG ACCGTCAGTG 960

GTGCACTGCT GTCCTCACCC TGCACGCTGG TGAGTAATGA GGTGCCGTTA ARCCTCCGGC 1020

CGGAAAATCA CTCTGCGGCA GCCGGAGCAC CTCTGATGCT GAGGCTGGCA GGATGTGGGG 1080

ACGGTGGTGC ACTTCAGCCC GGAAAACGGG GCGTTGCGAT GACAGTCTCC GGCTCACTGG 1140

TAACCGGTCC CGGAAGCGGA AGTGCTTTAC TTCCTGACCG TAASCTATCC GGCTGTGACA 1200

TCTTGTTATA CAC 1213

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACGCTCTAGT ATTCTCTGTC GTTCTGCCTG GGCCACTGCA GATAGAATAG TGACAACCAT 60

TTTACCCATC TCCCCATCGG TACTGATTCC GTCATCAATA AACCGAATGG ATACACCTTG 120

GGCGTCAAAC TCTTTTATTA ACTGGATCAT GTCAGCAGTA TCGCGCCCAA GGGGTTCAAG 180

TTTCTTCACC AAGATGACGT CACCTTCCTC CACCTTCATC CTCAGCAAGT CCAGCCCTTT 240

CCGATCGCTT GAACTGCCCG ATGCCTTGTC AGTAAAGATG CGATTTGCTT TCACGCCTGC 300

GTCTTTGAGT GCCCGAACCT GAATATCGAG AGATTGCTGG CTGGTTGATA CCCGTGCGTA 360

ACCAAAAAGT CGCATAAAAA TGTATCCYAA ATCAAATATC GGACAAGCAG TGTCTGTTAT 420

AACAAAAAAT CGATTTNAAT TAGACACCNT T 451

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GACAAGGCTT ATAAACTCAC TGACGGGGCT GGCATGTTCC TGCTGGTACA TCCTAATGGT 60

TCCCGTTACT GGCGTCTCCG TTATCGTATT CTGGGTAAGG AGAAGACTCT GGCACTTGGT 120

GTGTATCCAG AAGTTTCTCT CTCCGAAGCT CGTACAAAAC GGGATGAGGC CCGAAAACTG 180

ATTTCGGAGG GGATTGACCC TTGCGAACAG AAAAGAGCTA AAAAAGTAGT CCCTGATTTA 240

CAGCTCTCTT TTGAACATAT TGCACGACGC TGGCATGCCA GTAATAAACA ATGGGCACAA 300

NSDOCID <WO_ 9822575A2 I >

TCACACAGCG ATAAAGTACT CAAAAGCCTC GAAACACACG TTTTCCCCTT TATCGGCAAC 360

CGGGATATCA CAACACTCAA TACCCCGGAT CTGCTTATCC CTGTTCGTGC TGCAGAAGCT 420

AAACAAATTT ATGAAATCGC CAGTCGTCTG CAGCAAAGAA TATCTGCCGT AATGCGTTAT 480

GCCGTACAGT CTGGCATCAT CAGATATAAT CCTGCTCTGG ATATGGCTGG CGCATTGACT 540

ACGGTAAAAC GCCAGCATCG CCCCGCTCTT GATCTTTCAC GTCTGCCTGA ACTTCTGTCG 600

CGTATTAACA GTTATAAAGG NCAGCCTGTC ACCCGGCTTG CGTTGATGCT GAATTTACTG 660

GGTTTTTATT CGTTCCAGTG AACTCAGATA CGCCCGCTGG TTCTGAAAAT TGATATTGGA 720

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

NCNTTAATTT TATATCTCGT AAAATAAAAT GTTTTCTGTA CCGCTCTCCG GAGGGGGGAA 60

TGATTCGTTT ATCATTATTT ATATCGTTGC TTCTGACATC GGTCGCTGTA CTGGCTGATG 120

TGCAGATTAA CATCAGGGGA AATGTTTATA TCCCCCCATG CACCATTAAT AACGGGCAGA 180

ATATTGTTGT TGATTTTGGG AATATTAATC CTGAGCATGT GGACAACTCA CGTGGTGAAG 240

TCACAAAAAC CATAAGCATA TCCTGTCCGT ATAAGAGTGG CTCTCTCTGG ATAAAAGTTA 300

CGGGAAATAC TATGGGAGGA GGTCAGAATA ATGTACTGGC AACAAATATA ACTCATTTTG 360

GTATAGCGCT GTATCAGGGA AAAGGAATGT CAACACCTCT TACATTAGGT AATGGTTCAG 420

GAAATGGTTA CAGAGTTACA GCAGGTCTGG ACACAGCACG TTCAACGTTC ACCTTTACTT 480

CAGTGCCCTT TCGTAATGGC AGCGGGATAC TGAATGGCGG GGATTTCCGG ACCACGGCCA 540

GTATGAGCAT GATTTATAAC TGAGTCATAC CCAAATGAAT AACTGTAATT ACGGAAGTGA 600

TTTCTGATGA AAAAATGGCK CCCTGCTTTT TTATTTTTAT CCCTGTCAGG CTGTAATGAT 660

GCTCTGGCTG CAAACCAGAG TACAATGTTT TACTCGTTTA ATGATAACAT TTATCGTCST 720

CAACTTAGTG TTAAAGTAAC CGATATTGTT CAATTCATAG TGGATATAAA CTCCGCATCA 780

AGTACGGCAA CTTTAAGCTA TGTGGCCTGC AATGGATTTA CCTGGACTCA TGRTCTTTAC 840

TGGTCTGAGT ATTTTGCATG GCTGGTTGTT CCTAAACATG TTTCCTATAA TGGATATAAT 900

ATATATCTTG AACTTCAGTC CAGAGGAAGT TTTTCACTTG ATGCAGAAGA TAATGATAAT 960

TACTATCTTA CCAAGGGATT TGCATGGGAT GAAGCAAACA CATCTGGACA GACATGTTTC 1020

AATATCGGAG AAAAAAGAAG TCTGGCATGG TCATTTGGTG GTGTTACCCT GAACGCCAGA 1080

TTGCCTGTTG ACCTTCCTAA GGGGGATTAT ACGTTTCCAG TTAAGTTCTT ACGTGGCATT 1140

CAGCGTAATA ATTATGATTA TATTGGTGGA CGCTACAAAA TCCCTTCTTC GTTAATGAAA 1200

ACATTTCCTT TTAATGGTAC ATTGAATTTC TCAATTAAAA ATACCGGAGN ATGCCGTCCT 1260

TCTGCACAGT CTCTGGAAAT AAATCATGGT GATCTGTCGA TTAATAGCGC TAATAATCAT 1320

TATGCGGCTC AGACTCTTTC TGTGTCTTGC GATGTGCCTA CAAATATTCG TTTTTTCCTG 1380

TTAAGCAATA CAAATCCGGC ATACAGCCAT GGTCAGCAAT TTTCGGTTGG TCTGGGTCAT 1440

GGCTGGGACT CCATTATTTC GATTAATGGC GTGGACACAG GAGAGACAAC GATGAGATGG 1500

TACAGAGCAG GTACACAAAA CCTGACCATC GCAGTCGCCT CTATGGTGAA TCTTCAAAGA 1560

TACAACCAGG AGTACTATCT GGTTCAGCAA CGCTGCTCAT GATATTGCCA TAAATGGTTT 1620

ATCCGGAGCC GGATAGTGTG TTGTGGATAT CTGGCATGCC CCGGGAAGTC ACCTTTCAGA 1680

CGGGCGGAGG GCTGGTGAAT TATCCGCGAT TACTGAGCAG TATGGATAAT CCTTTTTCAC 1740

AGACTTGTCA GCAGCCAGCA TTTATGTTCT TTTATCTGAG GGAATTTATC TGTACGCTGT 1800

GCCGGGATAT CTCAGTTATA CAGAAATCAG GCAGGAATAA ATTGTAGTGG AAAGTCGATG 1860

TTTACCGGAT GACTGATGCG CGCTTGTACA CAGACAGTGT GTTTCAGTAA TATGGAGAAT 1920

AATGAAATGA ATAACACAGA CACATTAGAA AAAATAATCA GACACCAAAA AAACAAAGAC 1980

CCCGCATATC CTTTCGGGAA CATTTGTTGA TGCAGCTCTG TATTCGCACA AATAAAAGAA 2040

TGCAGGATAA TATATCTGAA TTTCTGGGGG CGTATGGAAT AAATCACTCA GCATATATGG 2100

TCCTCACCAC ATTATTCGCA GCGGAGAACC ATTGTCTGTC ACCTTCAGAG ATAAGCCAGA 2160

AACTTCAGTT TACCAGAACT AATATTACCC GCATTACAGA TTTTTTAGAA AAAGCCGGAT 2220

ATGTAAAAAG GACGGATAGC AGGGAGGATC GCCGTGCTAA AAAAATCAGT CTGACATCTG 2280

AAGGTATGTT TTTTATTCAG AGGCTCACTC TTGCACAAAG CATGTATCTG AAAGAAATCT 2340

GGGATTATCT GACCCATGAT GAACAGGAAC TGTTTGAAGT CATTAATAAA AAATTACTGG 2400

CACATTTTTC TGATGCCAGC TCATAAAGTG CGAAATATCT GAGGATGCCG GATAGCTTCA 2460

GGCAAAATAA TAATGATTCT TGCAGATGTG TTTTTCCGGA TACAAAAACA AATGATAAAA 2520

ATTGCAGCGC CAGGCACCTT TCAAAGCAGG GAGACCTGTA CCGCGTCGAA AATTTCAGCC 2580

AGTTAATATC ATTGTCTGAA CCAGGCACTT TGCCCGGGCA GGAGAAGGAG TTGTGGCGGT 2640

CTCAGCCCGG AACAATTTGA AAACCATAAT CTCGCTTAGG GCCGTGTCCA CATTACGTGG 2700

GTAGGATCAC TCCTGGATTT TCTCTTTTTG GACATTGACG TCTCCATTGG TTTAAACACG 2760

GCAATGGAGA CTGCGGTGAA AAGAGTTAAT TCCCGGAGTG ACTGGCTGGA TGCCAATCAA 2820

TGATCGGAAG CATGCCAAAC TGTGAACGGA GATGGATGCC GCCAAATCAT GATCGATTCA 2880

GATGCCATAT TTGCAATATC GCGTTAATCG TCAGTTCAGC 2920

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

SDOCID: <WO_ 9822575A2_I_>

(A) LENGTH: 1678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGTAAGGAAG TTATATATAT GAGCAACTAT ACATCTTAGA TGTATGATAA AGAAAAAGAT 60

AACAGTTCTT TAGAATATGT ATATTGAAGA GAATGCAATA GCATGGTTTA TATAAATTAC 120

GCATAAAAAT AAGCATATGT AAGCATTTTG GTTTGCTTTT TTTAACCTGC CACCGCAATG 180

AATGCTTTTT TTATGTTAAT GTGCGTTATG AAACTAAATG CAAGAAACAT ATTTAAAGGA 240

TTAATATCGT TCTCTCACAG ACTCCGTTTA CTTATTCAAG AATATAATTT AATTTATAGT 300

GAGCTTATTA TGAATATGAA CAATCCATTA GAGGKTCTTG GGCATGTATC CTGGCTCKGG 360

GGCCAGTTCC CCATTACACA GAAACYGGCC AGTTTCTTTG TTTGCAATAA ATGTATTACC 420

TGCAATACGG GGCTAACCAA TATGCTTTAT TAACCCGGGG ATAATTACCC TGTTGCATAT 480

TGTAGTTGGG GCTAATTTAA GTTTAGAAAA TGAAATTAAA TATCCTAATG ATGTTACCTC 540

ATTAGTCGCA GAAGACTGGA CTTCAGGTGA TCGTAAAKGG TYCATTGACT GGATTGCTCC 600

TTTCGGGGAT AACGGTGCCC TGTACAAATA TATGGGAAAA AAATTCCCTG ATGAACTATT 660

CCGAGCCATC AGGGTGGATY CCAAAACTCA TGTTGGTAAA GTATCAGAAT TTCACGGAGG 720

TAAAATTGAT AAACAGTTAG CGAATAAAAT TTTTAAACAA TATCACCACG AGTTAATAAC 780

TGAAGTAAAA AACAAGACAG ATTTCAATTT TTCATTAACA GGTTAAGAGG TAATTAAATG 840

CCAACAATAA CCACTGCACA AATTAAAAGC ACACTACAGT CTGCAAAGCA ATCCGCTGCA 900

AATAAATTGC ACTCAGCAGG ACAAAGCACG AAAGATGCAT TAAAAAAAGC AGCAGAGCAA 960

ACCCGCAATG GGGGAAAACA GACTCATTTT TACTTATCCC TAAAGATTAT AAAGGACAGG 1020

GTTCAAGCCT TAATGACCTT GTCAGGACGG CAGATGAACT GGGAATTGAA GTCCAGTATG 1080

ATGAAAAGAA TGGCACGGCG ATTACTAAAC AGGTATTCGG CACAGCAGAG AAACTCATTG 1140

GCCTCACCGA ACGGGGAGTG ACTATCTTTG CACCACAATT AGACAAATTA CTGCAAAAGT 1200

ATCAAAAAGC GGGTAATAAA TTAGGCGGCA GTGCTGAAAA TATAGGTGAT AACTTAGGAA 1260

AGGCAGGCAG TGTACTGTCA ACGTTTCAAA ATTTTCTGGG TACTGCACTT TCCTCAATGA 1320

AAATAGACGA ACTGATAAAG AAACAAAAAT CTGGTAGCAA TGTCAGTTCT TCTGAACTGG 1380

CAAAAGCGAG TATTGAGCTA ATCAACCAAC TCGTGGACAC AGCTGCCAGC ATTAATAATA 1440

ATGTTAACTC ATTTTCTCAA CAACTCAATA AGCTGGGAAG TGTATTATCC AATACAAAGC 1500

ACCTGAACGG TGTTGGTAAT AAGTTACAGA ATTTACCTAA CCTTGGATAA TATCGGTGCA 1560

GGGTTAGATA CTGTATCGGG KATTTTATCT GCGRTTTCAG CAAGCTTCAT TCTGAGSCAT 1620

SUBSTITUTE SHEET (RULE 26)
RNSDOCID: <WO 9822575A2 I >

GCAGATGCAG ATACCGGRAC TAAAGCTGCC AGCAGGTGTT GGATTNACCA ACGGAANT 1678

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGGATTACT TTGGAATCTG ACAACAAAGT TACTATGAAA AAGAACTAAC AAAGTTATAT 60

AATGACGCTA AAAATGCTTT GAAAGATGTG CAATCTAAAG CAAATAGGTT AATTTCTGAT 120

AATAAGANAA AACATAAGAG TGAACTAAAA AACATTTCTT ATGAATTCCA ATCAACTAAT 180

CTCAATGGCA AAGATACTGC GTATATATTG GATGTARAAA GAAATCTAGA AAGTAAAATT 240

GAGAATACTT CAAACGAATG AGTGTAATGA AATAAGAAAA CTAACCGACC AGATTGCAAT 300

AATTAGTGAT AGTACCACTT CTGAAAATTT ATCATCGGCT CAAGTAACTG AAGCAATCGA 360

AACTGAACTT GAACATTTAC GAGACCAACA AGCAAATAAC GCAGAGTTAA TACTACTTGG 420

CATGGCTCTT TCTGTAGTAC ATCATGNATT TAATGGTAAT ATTAGGGCAA TTAGAAGTGC 480

GCTAAGGGAA TTAAAAGCAT GGGCTGACAG AAATCCTAAG CTTGATATTA TATACCAAAA 540

AATCAGAACT AGTTTTGATC ACTTAGATGG TTATTTAAAA ACCTTTACAC CATTGACAAG 600

ACGTTTAAGT CGCTCTMAAA CCAATATAAC TGGAACTGCC ATTTTAGAAT TTATCAGAGA 660

TGTATTCGAT GATCGTCTTG AGAAAGAAGG AATTGAATTA TTCACTACCT CAAAGTTTGT 720

TAATCAAGAA ATTGTAACTT ACACATCAAC CATTTACCCT GTCTTTATAA ATCTAATTGA 780

TAACGCAATA TACTGGCTTG GGAAAACAAC TGGAGAAAAA AGACTTATAC TTGATGCKAC 840

TGAAACAGGA TTTGTTATTG GTGATACTGG TCCCGGTGTT TCAACTAGAG ATCGAGATAT 900

AATATTTGAT ATGGGATTTA CACGAAAAAC AGGAGGGCGT GGAATGGGAT TATTCATTTC 960

CAAAGAGTGT TTATCTCGAG ATGGATTTAC TATAAGATTG GATGATTACA CTCCTGAACA 1020

GGGTGCTTTC TTTATTATTG AGCCATCAGA AGAAACAAGT GAATAGCGGA TATAAATAAA 1080

TGACAAGCTC TACTGATTTN CATAAACTTT CTGAAGACTG CGTTCGCCGT TTTTTACATT 1140

CTGTAGTTGC TGTAGATGAC AATATGTCTT TTGGAGCTGG TAGTGATACT TTCCCTACAG 1200

ACGAAGATAT TAATGCTTTA GTTGATCCCG ACGATGATCC TACACCAATA ATAACAGCAT 1260

CAGCATCCCC AAGGATAGAA TCAACTAAAT CAAAAGCAAA GGTAAAAAAC CATCCTTTTG 1320

ATTACCAAGC TCTAGCAGAA GCTTTCGCCA AAGATGGTAT TGCTTGTTGC GGATTATTAG 1380

CTAAGGAAGG TGCGAATAAG CGGGGAAATT CTTCTCGGCT GACTCAGTCA TTTCATTTCT 1440

TCATGTTTGA GCCGATTTTT TCTCCCGTAA ATGCCTTGAA TCAGCCTATT TAGACCGTTT 1500

NSDOCID <WO 9822575A2 I_>

CTTCGCCATT TAAGGCGTTA TCCCCAGTTT TTAGTGAGAT CTCTCCCACT GACGTATCAT 1560

TTGGTCCGCC CGAAACAGGT TGGCCAGCGT GAATAACATC GCCAGTTGGT TATCGTTTTT 1620

CAGCAACCCC TTGTATCTGG CTTTCACGAA GCCGAACTGT CGCTTGATGA TGCGAAATGG 1680

GTGCTCCACC CTGGCCCGGA TGCTGGCTTT CATGTATTCG ATGTTGATGG CCGTTTTGTT 1740

CTTGCGTGGA TGCTGTTTCA AGGTTCTTAC CTTGCCGGGG CGCTCGGCGA TCAGCCAGTC 1800

CACATCCACC TCGGCCAGCT CCTCGCGCTG TGGCGCCCCT TGGTAGCCGG CATCGGCTGA 1860

GACAAATTGC TCCTCTCCAT GCAGCAGATT ACCCAGCTGA TTGAGGTCAT GCTCGTTGGC 1920

CGCGGTGGTG ACCAGGCTGT GGGTCAGGCC ACTCTTGGCA TCGACACCAA TGTGGGCCTT 1980

CATGCCAAAG TGCCACTGAT TGCCTTTCTT GGTCTGATGC ATCTCCGGAT CGCGTTGCTG 2040

CTCTTTGTTC TTGGTCGAGC TGGGTGCCTC AATGATGGTG GCATCGACCA AGGTGCCTTG 2100

AGTCATCATG ACGCCTGCTT CGGCCAGCCA GCGATTGATG GTCTTGAACA ATTGGCGGGC 2160

CAGTTGATGC TGCTCCAGCA GGTGGCGGAA ATTCATGATG GTGGTGCGGT CCGGCAAGGC 2220

GCTATCCAGG GATAACCGGG CAAACAGACG CATGGAGGCG ATTTCGTACA GAGCATCTTC 2280

CATCGCGCCA TCGCTCAGGT TGTACCAATG CTGCATGCAG TGAATGCGTA GCATGGTTTC 2340

CAGCGGATAA GGTCGCCGGC CATTACCAGC CTTGGGGTAA AACGGCTCGA TGACTTCCAC 2400

CATGTTTTGC CATGGCAGAA TCTGCTCCAT GCGGGACAAG AAAATCTCTT TTCTGGTCTG 2460

ACGGCGCTTA CTGCTGAATT CACTGTCGGC GAAGGTAAGT TGATGACTCA TGATGAACCC 2520

TGTTCTATGG CTCCAGATGA CAAACATGAT CTCATATCAG GGACTTGTTC GCACCTTCCC 2580

TAAGAGTTTT AATGTTTGAA GAAAGAGATA TAATTACAGC ATCATCCCAC AAAGCAGATA 2640

TTACAATACC TTGACTGGGN TATTGCCAAG CGGATA 2676

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAATTTGTCC TCCGGNTCTT TTCCCGTGGA TACGGGCATT GAGACCCGAA AGGSCCTGTA 60

TTTGCGACCG GAGAGGCATC CTGGGGGCTC AGTAAACCAG TGGTCGCTGT ATGGCGGGGC 120

TGTGCTTGCC GGTGATTATA ATGNCACTGG SAGCCGGTGC CGGCTGGGAC CTGGGTGTGC 180

CGGGGACCCT TTCCGCTGAT ATCACGCAGT CAGTAGCCCG TATTGAGGGA GAGAGAACGT 240

TTCAGGGAAA ATCCTGGCGT CTGAGCTACT CCAAACGGTT TGATAATGCG GATGCCGACA 300

TTACGTTCGC CGGGTATCGT TTCTCAGAGC GAAACTATAT GACCATGGAG CAGTACCTGA 360

ACGCCCGCTA CCGTAATGAT TACAGCAGTC GGGAAAAAGA GATGTATACC GTTACGCTGA 420

ATAAAAACGT GGCGGACTGG AACACCTCTT TTAACCTGCA GTACAGCCGT CAGACATACT 480

GGGACATACG GAAAACGGAC TATTATACGG TGAGCGTCAA CCGCTACTTT AATGTTTTCG 540

GACTGCAGGG TGTGGCGGTT GGATTGTCAG CCTCAAGGTC TAAATATCTG GGGCGTGATA 600

ACRRTTCTGC TTACCTGCGT ATATCCGTGC CGCTGGGGAC GGGGACAGCG AGCTACAGTG 660

GCAGTATGAG TAATGACCGT TATGTGAATA TGGCCGGCTA CACTGACACG TTCAATGACG 720

GTCTGGACAG CTACAGCCTG AACGCCGGCC TTAACAGTGG CGGTGGACTG ACATCGCAAC 780

GTCAGATTAA TGCCTATTAC AGTCATCGTA GTCCGCTGGC AAATTTGTCC GCGAATATTG 840

CATCCCTGCA GAAAGGATAT ACGTCTTTCG GCGTCAGTGC TTCCGGTGGG GCAACAATTA 900

CCGGAAAAGG TGCGGCGTTA CATGCAGGGG GAATGTCCGG TGGAACACGT CTTCTTGTTG 960

ACACGGATGC TGTGGGAGGT GTACCGGTTG ATGGCGGGCA GGTGGTGACA AATCGCTGGG 1020

GAACGGGCGT GGTGACTGAC ATCAGCAGTT ATTACCGGAA TACAACCTCT GTTGACCTGA 1080

AGCGCTTACC GGATGATGTG GAAGCAACCC GTTCTGTTGT GGAATCGGCG CTGACAGAAG 1140

GTGCCATTGG TTACCGGAAA TTCAGCGTGC TTAAAGGGAA ACGTCTGTTT GCAATACTGC 1200

GTCTTGCTGA TGGCTCTCAG CCCCCGTTTG GTGCCAGTGT AACCAGTGAA AAAGGCCGGG 1260

AACTGGGCAT GGTGGCCGAC GAAGGCCTTG CCTGGCTGAG TGGCGTGACG CCGGGGGAAA 1320

CCCTGTCGGT AAACTGGGAT GGAAAAATAC AGTGTCAGGT AAATGTACCG GAGACAGCAA 1380

TATCTGACCA GCAGTTATTG CTTCCCTGTA CGCCTCAGAA ATAAATGAAA GTCCGGAATA 1440

TTAACGGCTG ATTGAATTGC GGTTTATGCC ATTTTCCCGG ACCAA 1485

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTACCAATTT CATCGTCCGG TACATCCTCC AGAACATCTC GCAATAAACT CTCGTCTGCC 60

TCATTCCATG CCACACCAGC ATTTGGGAAA CGAGGATCGA TCTCTCTTTC CTTCTTCTCC 120

TTCTTACTTT GCTCTTTTCG GGATGATACA GATACGACAG AACGTTCTTT TACCGCTGTA 180

ATTGCCATAA CTGCATTGAG CAGAGATCTG CGCTCCACAT CGTTCAGCAT TTTTCCTTCA 240

CAGATCAAAT CATTCAGGAT GTCAATGACT AGATTCAGAC TTTCTTCTGT TAGCTTCATA 300

TTTCAGACCT TGAAGTATGT AGATAATCAG CACAATTACT AATGTGATAA ATATCAGAAG 360

ATAATTTACA GGTAAACCGG AAAATACATC TGAAGAATAA AGCCCTCAGC TTAACGTTTC 420

AGCCAGTTTG TGAGCTGATT GAGGTACGGC GATGACATTA ACGGGAATTA CTCCCCTATA 480

GCTCTGAGCT TATTTTTCAC CCTGGCAACA TATGGTGGCT ACTGCGCATG GTTTTGGAGT 540

AGATATCTTA CTACTCGTAG AATTGTGCTT ACTGGTCAGG CCAGCGCACA GGCATTCCGT 600

GCAATCAATA GAACACTGGT TTTTTAGTCT TCCGTTACCC ATCAGGATGT TAGTGCAGAT 660

TCCGGTGTAT TCGATCAGTT GTTCGGCGAA TCAGCGATCG ATCACGATGC GATTTCGTAT 720

GTTAGGGATG CTGGTATGAT TACTCGCTGA AAAATAATGT GAAAAGGCAG TTTTTCTTTA 780

GACATTTAGC TCATTCATGC TGTTGTTTTA CGTTTTGCTG TCGTGTGCAG GATTATCTTT 840

TCGTTACGGG ACGATTCATT CCGTTTTAAT CAGGAGCTAT TGGCGTTGCT CATTGGTGGG 900

ATGCCGTAAA GTTTTACCGC GGCGATTAAT GATGTGAAGT CAATCCAAAT CAACGGAGAT 960

CTCTCATCAT GAATCAACCA ATACACAATG ATTACTGGTT ATCCCGTTTT GAAAGTATTC 1020

TCAACAGTGC CCTGGTGCAA CACCGTGCCG TCTCGTTAAT CTGGGTGGAT TTACGTTTCC 1080

CTGAGCATAT GCCTGTCACC ATCATGGATC CCGATCCGGA TTCAGCGGTG ATTTCTCGTT 1140

TTTTCGAATC CCTGAAAGCC AAAATTCAGG CTTACCAGCG GAAAAAACGA CGTACCAACA 1200

AGCGTGTGCG TGCAACCACC CTGCATTATT TCTGGTGTCG GGAGTTTGGC AAGGAAAAAG 1260

GCAGGAAACA TTATCACGTG ATATTACTGC TCAACAAAGA TACCTGGTGC TCGCCAGGGG 1320

ATTTCACCGT TCCTTCTTCG CTGGCGACGC TGATCCAACT GGCATGGTGT AGCGCTCTGC 1380

ATCTTGAGCC CTGGCAGGGT AATGGACTGG TTCATTTTTC CAGGCGGACG CYTTTCCGTA 1440

AACCGGTATC ATCTGATGCT CGCCCTTCTT CCGATGATAC GCCTTTGTCG GGTGGATGTT 1500

CTGAAACCAG GAAGGCTTCA GACAAAAAGC CGGGTGAAGC CGCTGTTCTC TGGATCAAGC 1560

GTGGTGATGT GGAAGCGATG CAGAAAGCCA TGGAGAGAGC CCGTTATCTC GTGAAGTATG 1620

AGACGAAGCA GCATGACGGT TCTGGTCAAC GTAATTATGG TTGCAGCCGT GGAGCGGGGC 1680

GTCTACTGGA TGGCAGGTGA ACCCTGTAAA ACGGCATCCG GTGCCAGAGT ATATGTCACA 1740

GTAAGGGCGT GGTTGATGCC CTTAGCTCGT TTTCTGAAAA AGTCGTCCTG AAGTCATGTG 1800

TCACGAACGG TGCAATAGTG ATCCACACCC AACGCCTGAA ATCAGATCCA GGGGGTAATC 1860

TGCTCTCCTG ATTCAGGAGA GYTTATGGTC ACTTTTGAGA CAGTTATGGA AATTAAAATC 1920

CTGCACAAGC AGGGAATGAG TAGCCGGGCG ATTGCCAGAG AACTGGGGAT CTCCCGCAAT 1980

ACGGTTAAAC GTTATTTGCA GGCAAAATCT GAGCCGCCAA AATATACGCC GCGACCTGCT 2040

GTTGCTTCAC TCCTGGATGA ATACCGGGAT TATATTCGTC AACGCATCGC CGATGCTCAT 2100

CCTTACAAAA TCCCGGCAAC GGTAATCGCT CGAGAGATCA GAGACCAGGG ATATCGTGGC 2160

GGAATGACCA TTCTCAGGGC ATTCATTCGT TCTCTCTCGG TTCCTCAGGA GCAGGAGCCT 2220

GCCGTTCGGT TCGAAACTGA ACCCGGACGA CAGATGCAGG TTGACTGGGG CACTATGCGT 2280

AATGGTCGCT CACCGCTTCA CGTGTTCGTT GCTGTTCTCG GATACAGCCG AATGCTGTAC 2340

NSDOCID: <WO 9822575A2_I_>

ATCGAATTCA CTGACAATAT GCGTTATGAC ACGCTGGAGA CCTGCCATCG TAATGCGTTC 2400

CGCTTCTTTG GTGGTGTGCC GCGCGAAGTG TTGTATGACA ATATGAAAAC TGTGGTTCTG 2460

CAACGTGACG CATATCAGAC CGGTCAGCAC CGGTTCCATC CTTCGTTGTG GCAGTTCGGC 2520

AAGGAGATGG GCTTCTCTCC CCGACTGTGT CGCCCCTTCA GGGCACAGAC TAAAGGTAAG 2580

GTGGAACGGA TGGTGCAGTA CACCCGTAAC AGTTTTTACA TCCCACTAAT GACTCGCCTG 2640

CGACCGATGG GGATCACTGT CGATGTTGAA ACAGCCAGCC GCCACGGTCT GCGCTGGCTG 2700

CACGATGTCG CTAACCAACG AAAGCATGAA ACAATCCAGG CCCGTCCCTG CGATCGCTGG 2760

CTCGAAGAGC AGCAGTCCAT GCTGGCACTG CCTCCGGAGA AAAAAGAGTA TGACGTGCAT 2820

CCTGGTGAAA ATCTGGTGAA CTTCGACAAA CACCCCCTGC ATCATCCACT CTCCATTTAC 2880

GACTCATTCT GCAGAGGAGT GGCGTGATGA TGGAACTGCA ACATCAACGA CTGATGGCGC 2940

TCGCCGGGCA GTTGCAACTG GAAAGCCTTA TAAGCGCAGC GCCTGCGCTG TCACAACAGG 3000

CAGTAGACCA GGAATGGAGT TATATGGACT TCCTGGAGCA TCTGCTTCAT GAAGAAAAAC 3060

TGGCACGTCA TCAACGTAAA CAGGCGATGT ATACCCGAAT GGCAGCCTTC CCGGCGGTGA 3120

AAACGTTCGA AGAGTATGAC TTCACATTCG CCACCGGAGC ACCGCAGAAG CAACTCCAGT 3180

CGTTACGCTC ACTCAGCTTC ATAGAACGTA ATGAAAATAT CGTATTACTG GGACCATCAG 3240

GTGTGGGGAA AACCCATCTG GCAATAGCGA TGGGCTATGA AGCAGTCCGT GCAGGTATCA 3300

AAGTTCGCTT CACAACAGCA GCAGATCTGT TACTTCAGTT ATCTACGGCA CAACGTCAGG 3360

GCCGTTATAA AACGACGCTT CAGCGTGGAG TAATGGCCCC CCGCCTGCTC ATCATTGATG 3420

AAATAGGCTA TCTGCCGTTC AGTCAGGAAG AAGCAAAACT GTTCTTCCAG GTCATTGCTA 3480

AACGTTACGA AAAGAGCGCA ATGATCCTGA CATCCAATCT GCCGTTCGGG CAGTGGGATC 3540

AAACGTTCGC CGGTGATGCA GCCCTGACCT CAGCGATGCT GGACCGTATC TTACACCACT 3600

CACATGTCGT TCAAATCAAA GGAGAAAGCT ATCGACTCAG ACAGAAACGA AAGGCCGGGG 3660

TTATAGCAGA AGCTAATCCT GAGTAAAACG GTGGATCAAT ATTGGGCCGT TGGTGGAGAT 3720

ATAAGTGGAT CACTTTTCAT CCGTCGTTGA CATCATGCAA TCTTTCCTGG TTTTCATGCA 3780

TCCATCATTT GTCGCTGCGA TGCCAGACTT CTGGATGCAC ACATGTTGTT TTACTTTTGT 3840

CAGCATCATA AATGCGCCGG GACTGGTGAA TGGAGATAAG CCATTTTATT ATCGACGTCA 3900

GCGAACATAC TCACCATGCC GGTATGTTCC TGAACTGAAC AATAAGTTTT GCGCTGATTA 3960

CAGTATGTGA AGGAGGTCCG TTACAATGAA TTCCGCTTAT ATGCAATCCT TGCAGACATC 4020

CCACCACTTC CCAGCTGATT TAACCTACAG ATTATTTCCT AGTGAGCTTG CATATCTCAT 4080

TGACGACTTA TATGAAAGTA CCCAACTTCC GCTGGAGCTC ATTTTTAATA CTGTACTGGC 4140

AACGCTCTCA CTCTCCTGTC AGTCACTGGT TGACGTTGTT CATCCTCACA CCAACATGCC 4200

GGAACCCTGC TCACTTTATC TGTTGGCAAT CGCAGAGCCA GGCGCGGGAA AAACAACGAT 4260

AAACAGACTG GTGATGAACC CCTGTTACGA ATTTGCCGAT CGACTCATTC AACAATACGA 4320

AGAGAGAAAC AAAGATTATA AGACTGAACT ACAGATCTGG AATACCCGGC AGAAAGCGCT 4380

TGCTGCCAAT TTAAGAAAGG CTGTTAACCG GGGGTATCCG GGGGAACAGG AAGAAGAGGC 4440

GCTGCGTAAT CACGAAAGAA ATAAACCGAC ACGTCCGGTT CGACCGAATT TTATCTATGA 4500

AGATGTTTCG CTTAAAGCGC TTGTGGAAGG GCTCAATGAA CATCCTGAGG CAGGGGTTAT 4560

TTCTGACGAG GCGGTCACTT TTTTCAGAAG CTATCTGAAA AATTATCCGG GCCTGTTGAA 4620

TAAAGCATGG AGTGGACAAC CGTTTGATTT TGGACGGGCT GACGAGAAAT ACCATATCAC 4680

GCCACGTCTG ACATTTTCGT TAATGTCCCA GCCGGATGTC TTTACGAATT ATATAAATAA 4740

AAATGACGTA CTGGCGTGGG GAAGCGGATT TCTTTCCCGG TTTCTGTTCA GTCAGACCGG 4800

AAGTCCTTCC CGGGTACGGG ATTATACGAG AGGCGAGTTC AGAACAAAAC CAACCCTGGA 4860

GAAGTTTCAT AAAAAGATTA ACGGATTTCT GTTAAGCCAT AACATTAATT CCCCCGGTAT 4920

GAGCACCGAA AGGAAAACAT TAAAACTTGC AAAGAAAGCG TTGGGGGAGT GGCAGGAAAA 4980

CCAGATTAAG ATTGAAAGAA AAGCGCTTGC AGGAGGGGAG TGGGAACACA TCAGAGATAT 5040

TGTTCTGAAA GCAGGTTCTA ATATACTGAG GATAGCTGGA ATATTCACCT GCTATTGCTA 5100

TAAAGATGCT GAGGAAATTG AATCAATTGC GCTTTTTAAA GCTATGCATC TCATGGGCTG 5160

GTATCTGGAG GAGGCGAGCA CAATATTTTA TCCCATGTCT GCACGATGCC AGTTTGAACA 5220

GGATGCCTGT GAACTGTATG CATGGATTAT GACCCGAATA AGGCAGAATA ATTGGCGTGC 5280

TATCAGGAAA ACAGACATTG AAAGATATGG TCCCAATCGT CTGAGAAGAG CAGAAAAACT 5340

TACACCTGTA CTCAATCAGT TAATCGYTCA GAATTATTTC CGTATCATCM AAGATGCGAT 5400

CGCATCAGGC ACTTTATGTT TCTGCTCTTG ATAATAATGG TTACATCCTT CCTTTCGGCG 5460

CAATGTCTTA CGAACCGTTT GATATTGTTC CACCCCAGTA TAACCATAAT GCGAAAACAT 5520

ATTCCGTTGT TATTCCACCG GCATTAATTC AGTCATTTAC ACCTGATTCC TCAGCTTACA 5580

CCTTATTTTA AAACAATTTT GTGAGTAGAA AACGAAAATC ATAATCCTTC GAATGAAGGT 5640

TAATGATAAG GTGTGTTGCA TATCCTGCAC CTGTGCAAAT ATTCACCAAT CATTGGGTGT 5700

GAATGAAAAT TTCTCTGAAA AAATCGCTAT GGTAGCAACA GTAGCAGCAC ATACACTACA 5760

TCTGTGATTT GGTTTTGTTT TCATAATGAC CTGCTGTCAG AGCTGATTGA ATGCTGGGAT 5820

GTGCGCACTG GTGGAAGAGT GGTTTTCGTT TCAGATATAA CGAAAGGTAA TCGAAAGATT 5880

GTTTTAAACA TGGATTAAAG CTAATAATTA ACCATATTGT GTGAGTTTTT ATATATAAGT 5940

TTGTTTGATT CTTGCCGTGA TGAGTGCTGG GGTATATGAC GATGTCGCTC TCTTTCTGAA 6000

TAACAAATTA TTATTCGTCT GTTACTGATA AGGGATGCGA TTCATGTTTT AATAGAGGGT 6060

TGAAGAAAAT TAATTTGATA TTTTTTTGTA AGGGAATGGA ACTGTCCGGA ATATGTTCAG 6120

AACGGCGGAT TTCTCATTTC CATTCATTAA ACATGGATAA TTTTAATTTA GGTTTATTAC 6180

NSDOCID <WO__9822575A2 I_>

TATTATTATA CTCACTCCCT TTTTCATACA ATCTCTATTG TTATTTACTT CCTGTCTTTA 6240

CTCACTCTCT ATCTTTACGA TTATATTCAC TCTATCGTTA CACATTCCAT TAGTATTACT 6300

CTTGTTATCG TATTCATTCC ATCCCTCAAT CATATTTACT GTAACTCATA TGATGTTCAG 6360

GTAAGTTATT CTCTACCATT CTACTGATGA TATCCATCTG TTCTCATTTT CAGTGAAACA 6420

GCAATTGATT TTAATCTTAT CCATCATGAA CTGTATTTGC TTAACAATGA TTGTTTATCT 6480

GAAGTGTTTT AACTATTCTG GTTGGAAACA ATTTCTCTGT CATCACAGAT TAACTGAATG 6540

TTTACTCTTT GATAAGGTAT CCATGATTCC GTCATGTTTA ACAGCGCAGG ATAAACAACA 6600

GAATTAACAG AGTGAATTTC TGATTATATT TGTTGCCGGT TGTATTGTTT AAGGTACTGG 6660

GTGAAAATTA TTCATCCATG GTATGTTGTC TTATGCTATC GTGTGTCGTT AACGTTCATA 6720

TCCTGGAGAA CAGATTGAAT GAGCGCATAT AAGTTTATTG CATTGGCCTT GTACACGGTT 6780

TTTACAACCA CTGAGAGCAA GTTTGTAGTT TATGATGTGA TTGGTCGCAA TATGTTTCTT 6840

AACCTTCTGG TCGTGGTGTT TTATCGCGTA TTTTGCAGTA TTTCGTGATG TTTTATTGAG 6900

TCTGTATTTT CTTTACTCCT CGTTTATCTC ATCTCTTTAG CTAATACCAT CAGATAATCC 6960

ATTTCTTTCT GCATAATGCT GCGTATCGTT AATAACCCGT CGTATCCATT CTGCTACAGC 7020

ATGCCTGATA AATACCATCT GTAAGTTATT ACCGTTTTAG ATCTGATTAT GAGCGAAAGC 7080

ATTAATTCGT TCACAGAGCT TAAAACATCA TTAACTTTCA GGAGTCATCA ACATGCCTAA 7140

ATCTTACACA CCAAACTGGT TTTTTACCGC TTTACTTGAC AATCACATCA ATCAAATGAT 7200

GGCACGCTAT TCCTGCCTGC GGGCCTTACG CATGGATTTC TTCTACAGGA AAGATACGCC 7260

CGATTTCTTA CAACCTGATC ATCGCTGGCT TGAATTGCAG TTGCGTATGA TGCTGGAGCA 7320

GGTGGAACAA TTTGAAAATA TCGTTGGCTT CTTCTGGGTG ATTGAATGGA CGGCTGATCA 7380

TGGTTTTCAT GCGCATGCGG TTTTCTGGAT CGATCGTCAG AGGGTTAAAA AAATATATCC 7440

CTTTGCGGAG CGGATTACGG AATGCTGGCG GTCTATTACG CATAACAGCG GTTCGGCACA 7500

CCGCTGCACA TATCAGCCGC ATTATACATA CAACATCAAC ATTCCTGTGC GCCACAACGA 7560

TCCTGAAAGC ATCGATAATA TTCGCGGTGC CCTGCATTAT CTGGCGAAAG AAGAGCAAAA 7620

AGACGGGCTG TGTGCTTACG GCTGCAATGA AGTTCCTGAA CGTCCTGCTG CAGGGCGTCC 7680

TCGTAAGCCT CACTTCTGAA GCTTAAGGCC TGAGCCTTCG CTCCTGGAAA CACTCCGTCG 7740

GTAAAAACTT ACCGCCTTGA TTAATGATGT GAACTGAAGT CAACGGAGAT CATTCATCCT 7800

GAACCTGCAT CCGGTGTTTT GTTCCTTGTC TTCCCGTTCT GCTTCGGTTC TTCACTTATT 7860

CCATCAATCT CATTCCGCAA GCCATAACAC GTCAGCTCAT TCACGGGCAG GACGCATTGT 7920

GGGCTGCGCA TAACGGAACA TATCTTATGA ATGCTATTCC TTATTTCGAC TATAGCCTGG 7980

CACCCTTCTG GCCATCTTAT CAGAACAAAG TCATCGGCGT CCTTGAGCGT GCGCTGCGTG 8040

AGCAGTCCGG CTCACGGATA CGGCGGATCC TGCTTCGTCT GCCGTGGGAA CATGACAACG 8100

CCTTCAGCAG CAGAAAGATC TGGTTCGGTA TGGACTTTAT CGAAACCGTC AGTGCGCTGA 8160

TGAATGCGAA ACCCGGACGC GACCTTTGCT GGCTCCTGAC CCGTCATCCG GAAAAGCCGG 8220

AATACCACGT GGTGCTGTGC GTCAGACAGG AGTATTTCGA CGGCCCCGAA CTGGATCGGT 8280

TGATACTGGA TGCCTGGAGT AATGTGCTGG GTTTCGCGTC ACCAGGTGAA GCAAAGCCGT 8340

ACCAGAAGCA GATCACCCGG GATGTGGTAC TGGATCGCCG GTCACCGGAC TGCGAAGCCC 8400

TGTTTAAGGA CCTTATCTGG GCGTTCAGTG ATTTCGCCCG CGATCGCCGT GGAGTGTGCG 8460

ATCCGGAAGC CCGTTGCCTT GCCGGCAATC CCGGTTGGCA GTGCTGAAAG CAGCACGCCA 8520

TCCCATCCCC CGTATTACCC CATTCTTCAT AAATCTCACT GAGGACATTC TGACCATGTT 8580

GACCACAACA AGCCACGACA GCGTATTGCT GCGTGCCGAC GATCCCCTGA TCGACATGAA 8640

CTACATCACC AGTTTCACCG GCATGACCGA TAAATGGTTT TACAGGCTGA TCAGTGAAGG 8700

GCATTTTCCT AAACCCATCA AACTGGGGCG CAGCAGCCGC TGGTACAAAA GTGAAGTGGA 8760

GCAGTGGATG CAACAACGAA TTGAGGAATC ACGAGGAGCA GCAGCATGAA ACGTGTTGTG 8820

ATGCCAGTAC GTTGGCAATG TGCAAAATGC CAGCGCTGGT ATTGTGGAAA TCAGCCCTGT 8880

CCCTGGTGCT GGCGACATTC CCGCTTATCT TTCCGCTGAC ACCCTCCGGT CAGCCAACTG 8940

TTAGTCATCA TTTCCTGACT GATTCGTCAT TCCATTCTTA TTGATTATAA CTGGCATTAC 9000

ACCGGTGCTG GCGTGCTTTC CTGCGTGTCT GCACCGGTTT GACAAAATTC AACAGGGTTT 9060

GAAAAGGAAC ATTTCGTGCA AATAACCGAA GCCTTAATTT CAGAGCCGGG AGACATCCGG 9120

CGTTTTATTC AACATGCTGT TGACCACTGG CCGCGTCTGC TGGCAGTCCA CTTCATACTC 9180

CATTCGACAG AAGGAAACAT CTACGGGCAA CAGATTCATG CATTCTGCAC TTCCTTTTAT 9240

CGACAACTGC ATGAACGTAT TACTGAGAGC AATCACACTG CCAGTCCATC ATCGTCGGTG 9300

GTATTACGCT GGTTGCGGGA ACAACATGGA GGAGCAACAA TTCGATGCCT GTTGCTGCTC 9360

AGCCAGACGA GTATTTGTCA CCCGCGAGCC AGTGTCACAG TTGATGAACA ATGTTCGCAA 9420

GTGGTGGATT TACTGCAACA TAGCTGGCAG GTGATAAGTG CTGGCGGACA ATGCCGGGTG 9480

GAAAGGTGTT TTCGGGTTGC CCGGGGTGAT ACATCCGGTC AGTATGTTGC GTTAAAAACA 9540

GTCGCATTGT CTCTGGGGTT ACCGGTTGTG ACCGCCATTA CCCATCGTCC GGTACAGCGC 9600

TGTACATTGA TTACAGCTCA GTGAATCAGC GCTTTCTGGC TTTTCGTCGG TCATTCTGTC 9660

AACGCCACGA TGTTTGACCG TTATGGGGAT GCGGACGATT CCCTGCACAG CGTTGTTTCA 9720

CGGTGGTGGA TGACGCAACA CCGCTGTTAA AAACAGTCGT TCAGTCCTTT GTGTTACCGG 9780

TTGTGACAAC AATCAGTTGG TAATGGACGT GTGAACCATC TGCGCTTCCG TTGATTTTTA 9840

TGGACTGATA AAGTTTTGCC AGCTGAATCT TTATACGGAA TGCTCTTCAG TATGCGTACA 9900

CGAATTGACT ATCTGGCGGA TAAATACTCT TTTACCGAAC GGAATGAATC TCCACGCCTT 9960

CGCCGGCAGT GGCAGGATGT TCTGGAGGAG TGTCGGCTGA CAGAGGCCGG ACCAGAAGAA 10020

CGGCTGCGTA TTGCCCTGCT GAATGTGGAT TACGTCACCA GTTTTGAACT GCCTTTTCGC 10080

TTGTTGCTTA CTCGTACACC ACAACTGATT GCCGCGCTTC GGGAAGAATG GGGCCTCAGC 10140

CAGAAAAATG TGGTGTTCAA CGATAAACGG TTTGGCTGCG TGTACAGCCT GAAGGCCAGT 10200

CTTTCTGGTG TACCGGATAC ATTCCGGTAT CATCTGTCTC ATCGTATTCG CCGGATGGTT 10260

GGGAATGAAA ATACATCATC GCCATATCAG CAGATTGCCC GGGAAGTGAA AGTGCCCCGT 10320

GAACGGCTGA AGTATGCGCT GGAAGCCGGT TTACTGGTGA CTGCACTGGA CGGGCTGTTC 10380

TGGTCTGGTA GTCAGCGCAT TGCGGCTGAT ATCCTGAGAC TGAGAAAGAG CGGAATGCCG 10440

GTGGTGACAA CGTCCGTGGA AGCGAGCGAT AACCTGACGG GAACAACCCG CAAAATACCG 10500

GCATACCATC TCTGACATTG CGATGAAGGG CAGATTTCAC CTTGACAGGG GCAGAGTGCC 10560

GCTTTTTATA CTTTATTCCC GTGTCTGAAA AAAATGTGCA AAGGAAACGG GAATGGCAAG 10620

GTCCGATTAC GATTTTATCA ATCTGTCTCT GGGACATGAA CTGAATGAGT GGCTGGCAGA 10680

GAGAGGTTAT GCCGGACAGG CGGATAACCG GAACCGACTG GCAGAGGTGG TTACCCGCAA 10740

ATTGCGGGAC AGTTTTTATG CGGACGTCTC CTGGGATGCG CTGAATGTGG CATACAGTGA 10800

ACACCCTGAG TGGTTTTCAG AGCTTGCCTC CGGGGATGAG GATTAACAGG CAAATTATGC 10860

TGCTATCGGG CAGAGTGATT ACCTGCAGGG ATTTCCATTT ATAAGAATAC GCCGCTTCGG 10920

GAAAGCTCCG GTTCTCCGGA GAGTTACGAT TATTTTTACT CAAATTCACA ACACCTGAAC 10980

TGGAACTTGC GTTGTGTCCC GGATTGTTAC TCCGCAGAAG CATCCTTTTT ACCATACGGA 11040

TGTTTGTTTT CCATTTCCCC TCCGAAAAAT ACAACTCCGA TCACATTTCT GATATTTTCC 11100

CCGGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTAA ATTTCAGCAC 11160

TGACATTCCG CTTACGTTAA TTTACACTGG ATACCCCACG AGGAGAATAT GCAGCACCGG 11220

CAGGATAACT TACTGGCGAA CAGAAATTTG TTGCCTGGTA TGGTTTCCGG TCAGTACGCA 11280

TTCAGGATCC GTACCTTATC TCAGGTGGTA CGCTATTTTT CCCTCCTCCC CTGCCTTTGC 11340

ATTCTTTCAT TTTCGTCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG TGCAATTCAG 11400

CAGCAACAGC AGCAGTTGTT GGATGAAAAC CAGCGCCAGC GTGATGCGCT GGAGCGCAGT 11460

GCGCCGCTGA CCATCACGCC GTCTCCGGAA ACGTCTGCCG GTACTGAAGG TCCCTGCTTT 11520

ACGGTGTCAC GCATTGTTGT CAGTGGGGCC ACCCGACTGA CGTCTGCAGA AACCGACAGA 11580

CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCACGG GACTGACCGC GGTCACGGAT 11640

GCCGTGACGG ACGGCTATAT ACGCCGGGGA TATATCACCA GCCGGGCCTT TCTGACAGAG 11700

CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT GCAGCAAATC 11760

CGGGCGGAAG GCGCTGACCT TCCTGCCCGC ACCCTGAAGA TGGTTTTCCC GGGAATGGAG 11820

GGGAAGGTTC TGAACTGCGG GATATTGAGC AGGGGATGGA GCAGATTAAT CGTCTGCGTA 11880

CGGAGCCGGT ACAGATTGAA ATATCGCCCG GTGACCGTGA GGGATGGTCG GTGGTGACAC 11940

TGACGGCATT GCCGGAATGG CCTGTCACAG GGAGCGTGGG CATCGACAAC AGCGGGCAGA 12000

AGAATACCGG TACGGGGCAG TTAAATGGTG TCCTTTCCTT TAATAATCCT CTGGGGCTGG 12060

CTGACAACTG GTTTGTCAGC GGGGGACGGA GCAGTGACTT TTCGGTGTCA CATGATGCGA 12120

GGAATTTTGC CGCCGGTGTC AGTCTGCCGT ATGGCTATAC CCTGGTGGAT TACACGTATT 12180

CATGGAGTGA CTACCTCAGC ACCATTGATA ACCGGGGCTG GCGGTGGCGT TCCACGGGAG 12240

ACCTGCAGAC TCACCGGCTG GGACTGTCGC ATGTCCTGTT CCGTAACGGG GACATGAAGA 12300

CAGCACTGAC CGGAGGTCTG CAGCACCGCA TTATTCACAA TTATCTGGAT GATGTTCTGC 12360

TTCAGGGCAG CAGCCGTAAA CTCACTTCAT TTTCTGTCGG GCTGAATCAC ACACACAAGT 12420

TTCTGGGTGG TGTCGGAACA CTGAATCCGG TATTCACACG GGGGATGCCC TGGTTCGGCG 12480

CAGAAAGCGA CCACGGGAAA AGGGGAGACC TGCCCGTAAA TCAGTTCCGG AAATGGTCGG 12540

TGAGTGCCAG TTTTCAGCGC CCCGTCACGG ACAGGGTGTG GTGGCTGACC AGCGCTTATG 12600

CCCAGTGGTC ACCGGACCGT CTTCATGGTG TGGAACAACT GAGCCTCGGG GGTGAGAGTT 12660

CAGTGCGTGG CTTTAAGGAG CAGTATATCT CCGGTAATAA CGGCGGTTAT CTGCGAAATG 12720

AGCTGTCCTG GTCTCTGTTC TCCCTGCCAT ATGTGGGGAC AGTCCGTGCA GTGACTGCAC 12780

TGGACGGCGG CTGGCTGCAC TCTGACAGAG ATGACCCGTA CTCGTCCGGC ACGCTGTGGG 12840

GTGCTGCTGC CGGGCTCAGC ACCACCAGTG GTCATGTTTC CGGTTCGTTC ACTGCCGGAC 12900

TGCCTCTGGT TTACCCGGAC TGGCTTGCCC CTGACCATCT CACGGTTTAC TGGCGCGTTG 12960

CCGTCGCGTT TTAAGGGATT ATTACCATGC ATCAGCCTCC CGTTCGCTTC ACTTACCGCC 13020

TGCTGAGTTA CCTTATCAGT ACGATTATCG CCGGGCAGCC GTTGTTACCG GCTGTGGGGG 13080

CCGTCATCAC CCCACAAAAC GGGGCTGGAA TGGATAAAGC GGCAAATGGT GTGCCGGTCG 13140

TGAACATTGC CACGCCGAAC GGGGCCGGGA TTTCGCATAA CCGGTTTACG GATTACAACG 13200

TCGGGAAGGA AGGGCTGATT CTCAATAATG CCACCGGTAA GCTTAATCCG ACGCAGCTTG 13260

GTGGACTGAT ACAGAATAAC CCGAACCTGA AAGCGGGCGG GGAAGCGAAG GGTATCATCA 13320

ACGAAGTGAC CGGCGGTAAC CGTTCACTGT TGCAGGGCTA TACGGAAGTG GCCGGCAAAG 13380

CGGCGAATGT GATGGTTGCC AACCCGTATG GTATCACCTG TGACGGCTGT GGTTTTATCA 13440

ACACGCCGCA CGCGACGCTC ACCACAGGCA AACCTGTGAT GAATGCCGAC GGCAGCCTGC 13500

AGGCGCTGGA GGTGACTGAA GGCAGTATCA CCATCAATGG CGCGGGCCTG GACGGCACCC 13560

GGAGCGATGC CGTATCCATT ATTGCCCGTG CAACGGAAGT GAATGCCGCG CTTCATGCGA 13620

AGGATTTAAC TGTCACTGCA GGCGCTAACC GGATAACTGC AGATGGTCGC GTCAGTGCCC 13680

TGAAGGGCGA AGGTGATGTG CCGAAAGTTG CCGTTGATAC CGGCGCGCTC GGTGGAATGT 13740

ACGCCAGGCG TATTCATCTG ACCTCCACTG AAAGTGGTGT CGGGGTTAAT CTGGGTAACC 13800

TTTATGCCCG CGAGGGCGAT ATCATACTGA GCAGTGCCGG AAAACTGGTC CTGAAGAACA 13860

GCCTTGCCGG CGGCAATACC ACCGTAACCG GAACGGATGT CTCACTTTCA GGGGATAACA 13920

AAGCCGGAGG AAATCTCAGC GTTACCGGGA CAACGGGACT GACACTGAAT CAGCCCCGTC 13980

TGGTGACGGA TAAAAATCTG GTGCTGTCTT CATCCGGGCA GATTGTACAG AACGGTGGTG 14040

AACTGACTGC CGGACAGAAC GCCATGCTCA GTGCACAGCA CCTGAACCAG ACTTCCGGGA 14100

CCGTGAATGC AGCTGAAAAT GTCACCCTTA CCACCACCAA TGATACCACA CTGAAAGGCC 14160

GCAGCGTTGC CGGGAAAACA CTCACTGTCA GTTCCGGCAG CCTGAACAAC GGTGGGACAC 14220

TGGTTGCCGG GCGCGATGCC ACGGTGAAAA CCGGGACATT CAGTAATACC GGTACCGTCC 14280

AGGGGAATGG CCTGAAAGTT ACCGCCACTG ACCTGACCAG CACCGGCAGT ATTAAAAGTG 14340

GCAGCACACT CGATATCAGC GCCCGCAATG CCACACTGTC CGGTGATGCC GGTGCAAAAG 14400

ACAGTGCCCG CGTTACCGTC AGCGGTACAC TCGAAAACCG CGGCAGACTT GTCAGCGATG 14460

ACGTGCTGAC GCTCAGTGCC ACGCAGATAA ACAACAGCGG TACCCTCTCC GGGGCAAAGG 14520

AACTTGTGGC TTCTGCAGAC ACACTGACCA CCACAGAAAA ATCGGTCACA AACAGTGACG 14580

GTAACCTCAT GCTGGACAGC GCGTCTTCCA CACTGGCGGG TGAAACCAGT GCGGGTGGCA 14640

CGGTGTCTGT AAAAGGCAAC AGTCTGAAGA CCACGACCAC TGCGCAGACG CAGGGCAACA 14700

GTGTCAGCGT GGATGTGCAG AACGCACAGC TTGACGGAAC ACAGGCTGCC AGAGACATCC 14760

TTACCCTGAA CGCCAGTGAA AAGCTCACCC ACAGCGGGAA AAGCAGTGCC CCGTCGCTCA 14820

GCCTCAGTGC GCCGGAACTG ACCAGCAGCG GCGTACTTGT TGGTTCCGCC CTGAATACAC 14880

AGTCACAGAC CCTGACCAAC AGCGGTCTGT TGCAGGGGGA GGCCTCACTC ACCGTTAACA 14940

CACAGAGGCT TGATAATCAG CAGAACGGCA CGCTGTACAG TGCTGCAGAC CTGACGCTGG 15000

ATATACCGGA CATCCGCAAC AGCGGGCTTA TCACCGGTGA TAATGGTTTA ATGTTAAATG 15060

CTGTCTCCCT CAGCAATCCG GGAAAAATCA TCGCTGACAC GCTGAGCGTC AGGGCGACCA 15120

CGCTGGATGG TGACGGCCTG TTGCAGGGCG CCGGTGCACT GGCGCTTGCT GGCGACACCC 15180

TCTCACAGGG TAGTCACGGA CGCTGGCTGA CGGCGGACGA CCTCTCCCTC CGGGGCAAAA 15240

CACTGAATAC CGCAGGACCA CGCAGGGACA GAATATCACC GTGCAGGCGG ACAGATGGGC 15300

GAACAGTGGT TCCGTGCTGG CAACCGGTAA CCTTACTGCT TCGGCAACCG GTCAGTTGAC 15360

CAGTACCGGC GATATCATGA GCCAGGGTGA CACCACGCTG AAAGCAGCCA CCACGGACAA 15420

CCGGGGCAGT CTGCTTTCGG CCGGCACGCT CTCCCTTGAT GGAAACTCAC TGGATAACAG 15480

CGGCACTGTC CAGGGTGACC ATGTCACGAT TCGCCAGAAC AGTGTCACCA ACAGTGGCAC 15540

GCTCACCGGG ATCGCCGCGC TGACGCTTGC CGCCCGTATG GTATCCCCTC AACCTGCGCT 15600

GATGAATAAC GGAGGTTCAT TGCTGACCAG CGGCGATCTG ACAATCACCG CAGGCAGTCT 15660

GGTAAACAGC GGGGCGATCC AGGCGGCTGA CAGCCTGACT GCACGTCTGA CGGGTGAGCT 15720

CGTCAGCACA GCGGGCAGCA AAGTCACCTC GAACGGTGAA ATGGCGCTCA GTGCACTGAA 15780

NSDOCID <WO 9822575A2_I >

TTTAAGCAAC AGCGGACAAT GGATTGCAAA AAATCTGACC CTGAAGGCGA ACTCACTGAC 15840

CAGTGCGGGT GACATCACCG GTGTGGATAC TCTCACGCTC ACGGTGAATC AGACGCTGAA 15900

CAATCAGGCG AACGGAAAAC TGCTCAGTGC AGGTGTGCTG ACGCTGAAGG CAGACAGTGT 15960

CACAAACGAC GGGCAATTAC AGGGAAATGC CACCACCATC ACGGCAGGAC AACTCACAAA 16020

CGGCGGGCAT CTGCAGGGCG AAACGCTGAC GCTGGCCGCC TCCGGTGGCG TGAACAACCG 16080

TTCCGGTGGT GTTCTGATGA GCCGGAATGC ACTGAATGTC AGTACTGCGA CCCTGAGTAA 16140

CCAGGGCACG ATACAGGGTG GTGGCGGGGT TTCCCTGAAC GCCACTGACC GTCTGCAGAA 16200

CGACGGCAAA ATCCTCTCCG GCAGTAACCT CACGCTGACG GCGCAGGTGC TGGCGAACAC 16260

CGGCAGCGGA CTGGTACAGG CTGCCACCCT GCTGCTGGAT GTGGTGAATA CTGTCAACGG 16320

CGGACGCGTA CTTGCCACCG GCAGTGCCGA CGTTAAAGGA ACCACGCTGA ATAATACCGG 16380

TACGCTTCAG GGTGCGGACC TGCTGGTGAA TTACCACACA TTCAGCAACA GCGGTACCCT 16440

GCTGGGAACC TCCGGGCTTG GCGTCAAGGG CAGTTCACTG CTGCAAAATG GTACAGGGCG 16500

GCTGTACAGT GCAGGCAACC TGCTGCTTGA CGCTCAGGAC TTCAGTGGTC AGGGGCAGGT 16560

GGTGGCCACC GGTGATGTCA CACTGAAACT GATTGCTGCC CTCACGAATT ACGGTACCCT 16620

GGCCGCAGGG AAAACCCTTT CCGTCACGTC GCAAAATGCC ATCACCAACG GCGGTGTCAT 16680

GCAGGGTGAT GCCATGGTGC TCGGTGCCGG AGAGGCATTC ACCAACAATG GAACGCTGAC 16740

TGCCGGTAAA GGCAACAGTG TTTTCAGCGC ACAGCGTCTT TTCCTTAACG CACCGGGTTC 16800

ACTTCAGGCC GGTGGCGATG TGAGTCTGAA CAGCCGGAGT GATATCACCA TCAGTGGTTT 16860

TACCGGCACG GCAGGCAGTC TGACAATGAA TGTGGCCGGT ACCCTGCTGA ACAGTGCGCT 16920

GATTTATGCG GGGAATAACC TGAAGCTGTT TACAGACCGT CTGCATAACC AGCATGGTGA 16980

TATCCTGGCC GGCAACAGTC TGTGGGTACA GAAGGATGCT TCCGGCGGTG CAAACACAGA 17040

GATTATCAAT ACTTCCGGGA ATATTGAGAC GCATCAGGGC GATATTGTTG TAAGAACCGG 17100

GCATCTTCTG AACCAGCGGG AGGGATTTTC TGCCACAACA ACAACCCGGA CTAACCCCTC 17160

ATCCATTCAG GGAATGGGAA ATGCTCTGGT TGATATTCCC CTTTCCCTTC TTCCTGACGG 17220

CAGCTATGGC TATTTCACCC GTGAAGTTGA AAATCAGCAC GGTACGCCCT GCAACGGGCA 17280

CGGGGCATGC AATATCACAA TGGATACGCT TTATTATTAC GCTCCGTTTG CTGACAGTGC 17340

CACACAGCGC TTTCTCAGCA GCCAGAACAT CACAACAGTA ACCGGTGCTG ATAATCCGGC 17400

AGGCCGCATT GCGTCAGGGC GTAATCTTTC TGCTGAGGCT GAACGACTGG AAAACCGGGC 17460

GTCATTTATC CTGGCGAATG GGGATATCGC ACTCTCGGGC AGAGAGTTAA GCAATCAGAG 17520

CTGGCAGACG GGGACAGAGA ATGAATATCT GGTATACCGC TACGACCCGA AAACGTTTTA 17580

CGGTAGCTAT GCAACAGGCT CTCTGGATAA ACTGCCCCTG CTGTCACCGG AATTTGAAAA 17640

CAATACCATC AGATTTTCAC TGGATGGCCG GGAAAAAGAT TACACGCCCG GTAAGACGTA 17700

TTATTCCGTT ATTCAGGCGG GCGGGGATGT TAAGACCCGT TTTACCAGCA GTATCAATAA 17760

CGGAACAACC ACTGCACATG CAGGTAGTGT CAGTCCGGTG GTCTCTGCAC CTGTACTGAA 17820

TACGTTAAGT CAGCAGACCG GCGGAGACAG TCTGACACAG ACAGCGCTGC AGCAGTATGA 17880

GCCGGTGGTG GTTGGCTCTC CGCAATGGCA CGATGAACTG GCAGGTGCCC TGAAAAATAT 17940

TGCCGGAGGT TCGCCACTGA CCGGTCAGAC CGGTATCAGT GATGACTGGC CACTGCCTTC 18000

CGGCAACAAT GGATACCTGG TTCCGTCCAC GGACCCGGAC AGTCCGTATC TGATTACGGT 18060

GAACCCGAAA CTGGATGGTC TCGGACAGGT GGACAGCCAT TTGTTTGCCG GACTGTATGA 18120

GCTTCTTGGA GCGAAACCGG GTCAGGCGCC ACGTGAAACG GCTCCGTCGT ATACCGATGA 18180

AAAACAGTTT CTGGGCTCAT CGTATTTTCT TGACCGCCTC GGGCTGAAAC CGGAAAAAGA 18240

TTATCGTTTC CTGGGGGATG CGGTCTTTGA TACCCGGTAT GTCAGTAACG CGGTGCTGAG 18300

CCGGACGGGT TCACGTTATC TCAACGGACT GGGTTCAGAC ACGGAACAGA TGCGGTATCT 18360

GATGGATAAC GCGGCCAGAC AACAGAAAGG ACTGGGATTA GAGTTTGGTG TGGCGCTGAC 18420

AGCTGAACAG ATTGCTCAGC TTGACGGCAG CATGCTGTGG TGGGAGTCAG TCACCATCAA 18480

CGGACAGACA GTCATGGTCC CGAAACTGTA TCTGTCGCCG GAAGATATCA CCCTGCATAA 18540

CGGCAGCGTT ATCAGCGGGA ACAACGTGCA GCTTGCGGAC GGCAATATCA CCAACAGCGG 18600

CGGCAGCATC AACGCACAGA ACGACCTTTC GCTCGACAGT ACCGGCTATA TCGACAACCT 18660

GAATGCAGGG CTGATAAGCG CGGGCGGTAG CCTGGACCTG AGCGCCATCG GGGATATCAG 18720

CAATATCAGC TCAGTCATCA GCGGTAAAAC CGTACAACTG GAAAGCGTGA GTGGCAACAT 18780

CAGCAATATC ACCCGGCGTC AGCAATGGAA TGCGGGCAGT GACAGCCGAT ATGGTGGTGT 18840

GCATCTCAGC GGTACGGACA CCGGTCCGGT TGCGACCATT AAAGGCACTG ATTCACTTTC 18900

ACTGGATGCA GGGAAAAACA TTGATATTAC CGGGGCAACG GTCTCGTCCG GTGGAGACCT 18960

TGGAATGTCT GCGGGTAATG ACATCAACAT TGCCGTAAAC CTGATAAGCG GGAGCAAAAG 19020

TCAGTCCGGT TTCTGGCACA CTGATGACAA CAGTTCATCA TCCACCACCT CACAGGGCAG 19080

CAGCATCAGC GCCGGCGGTA ACCTGGCGAT GGCTGCAGGC CATAATCTGG ATGTCACAGC 19140

ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTTCTGCA GGTAACGACC TGAGTCTGAA 19200

TGCAGTCAGG GAAAGCAAAA ACAGTCGCAA CGGCAGGTCA GAAAGTCATG AAAGCCACGC 19260

AGCTGTGTCC ACGGTGACGG CGGGCGATAA CCTCCTCCTT GTTGCCGGTC GTGATATTGC 19320

CAGTCAGGCT GCCGGTATGG CTGCGGAAAA TAACGTGGTC ATCCGGGGCG GACGTGATGT 19380

GAACCTGGTG GCAGAGTCTG CCGGCGCAGG CGACAGCTAT ACGTCGAAGA AAAAGAAAGA 19440

GATTAACGAG ACAGTCCGTC AGCAGGGAAC GGAAATCGCC AGCGGTGGTG ACACCACCGT 19500

CACCGCAGGA CGGGATATCA CCGCTGTTGC GTCATCCGTT ACCGCAACCG GCAATATCAG 19560

CGTGAATGCC GGTCGTGATG TTGCCCTGAC CACGGCGACA GAAAGTGACT ATCACTATCT 19620

NSDOCID <WO 9822575A2 I >

GGAAACGAAG AAAAAAAGCG GAGGTTTTCT CAGTAAGAAA ACCACCCACA CCATCAGTGA 19680

GGACAGTGCC TCCCGTGAAG CAGGTTCCCT GCTGTCGGGG AACCGCGTGA CCGTTAACGC 19740

CGGTGATAAN CTGACGGTAG AGGGTTCGGA TGTGGTGGCT GACCGGGATG TGTCACTGGC 19800

GGCGGGTAAC CATGTTGATG TTCTTGCTGC CACCAGTACA GATACGTCCT GGCGCTTTAA 19860

GGAAACGAAG AAATCCGGTC TGATGGGTAC CGGCGGTATT GGTTTCACCA TTGGCAGCAG 19920

TAAGACAACG CACGACCGCC GCGAGGCSGG GACAACGCAG AGTCAGAGTG CCAGTACCAT 19980

CGGCTCCACT GCCGGTAATG TCAGTATTAC CGCGGGCAAA CAGGCTCATA TCAGCGGTTC 20040

GGATGTGATT GCGAACCGGG ATATCAGCAT TACCGGTGAC AGTGTGGTGG TTGACCCGGG 20100

GCATGATCGT CGTACTGTGG ACGAAAAATT TGAGCAGAAG AAAAGCGGGC TGACGGTTGC 20160

CCTTTCCGGC ACGNTGGGCA GTGCCATCAA TAATGCGGTC ACCAGTGCAC AGGAGACGAA 20220

GGAGAGCAGT GACAGCCGTC TGAAAGCCCT GCAGGCCACA AAGACAGCGC TGTCTGGTGT 20280

GCAGGCCGGA CAGGCTGCGG CAATGGCCAC CGCAACCGGT GACCCGAATG CGACGGGAGT 20340

CAGCCTGTCG CTTACCACCC AGAAATCGAA ATCACAACAA CATTCTGAAA GTGACACAGT 20400

ATCCGGCAGT ACGCTGAATG CCGGGAATAA TCTGTCTGTT GTCGCAACCG GCAAAAACAG 20460

GGGAGATAAC CGCGGAGATA TTGTGATTGC AGGAAGCCAG CTTAAGGCCG GTGGTAACAC 20520

AAGCCTGGAT GCCGCGAATG ATGTTCTGTT GAGTGGCGCT GCAAACACAC AAAAAACAAC 20580

GGGCAGGAAC AGCAGCAGTG GCGGTGGCGT GGGTGTCAGT ATCGGTGCCG GTGGTAACGG 20640

TGCCGGTATC AGCGTCTTTG CCAGCGTTAA TGCGGCAAAA GGCAGCGAGA AAGGTAACGG 20700

TACTGAGTGG ACTGAAACCA CAACAGACAG CGGTAAAACC GTCACCATCA ACAGTGGTCG 20760

GGATACGGTA CTGAACGGTG CTCAGGTCAA CGGCAACAGG ATTATCGCCG ATGTGGGCCA 20820

CGACCTGCTG ATAAGCAGCC AGCAGGACAC CAGTAAGTAC GACAGTAAAC AGACCAGCGT 20880

GGCTGCCGGC GGCAGTTTTA CCTTTGGCTC CATGACCGGC TCAGGTTACA TCGCTGCCTC 20940

CCGGGATAAG ATGAAGAGCC GCTTTGACTC CGTTGCTGAA CAAACCGGGA TGTTTTCCGG 21000

AGATGGCGGC TTCGATATCA CGGTCGGCAA CCACACCCAG CTCGATGGTG CGGTTATCGC 21060

TTCCACGGCG ACGGCAGATA AAAACAGCCT CGATACCGGG ACGCTCGGCT TCAGCGATAT 21120

TCACAACGAA GCGGATTATA AAGTCAGTCA CAGTGGAATC AGTCTGAGCG GTGGTGGCAG 21180

CTTCGGGGAT AAATTTCAGG GTAACATGCC GGGTGGCATG ATATCCGCCG GAGGTCACAG 21240

CGGACATGCG GAAGGAACGA CTCAGGCCGC AGTGGCAGAT GGCACAATCA CCATCCGGGA 21300

CAGGGACAAT CAGAAGCAGA ATCTGGCGAA CCTGAGCCGT GACCCTGCGC ACGCTAATGA 21360

CAGTATCAGC CCGATATTTG ACAAGGAGAA AGAGCAGAGG CGTCTGCAGA CAGTGGGGCT 21420

TATCAGTGAC ATTGGCAGTC AGGTGGCGGA TATCGCGCGG ACGCAGGGGG AACTGAATGC 21480

GTTGAAGCTG CGCAGGATAA ATATGGGCCT GTTCCGGCGG ATGCGACGGA AGAACAGCGG 21540

CAGGCATATC TGGCAAAACT GCGTGATACG CCGGAATACA AAAAGGAACA GGAAAAGTAT 21600

GGTACCGGCA GCGATATGCA GCGCGGTATC CAGGCTGCAA CGGCTGCACT TCAGGGCCTG 21660

GTGGGCGGCA ATATGGCAGG CGCGCTGGCA GGTGCTTCAG CGCCGGAGCT GGCGAACATC 21720

ATCGGTCATC ACGCGGGTAT TGATGACAAT ACAGCGGCAA AAGCCATTGC CCATGCCATT 21780

CTCGGTGGTG TGACAGCAGC CCTTCAGGGC AACAGTGCGG CAGCAGGCGC AATTGGTGCG 21840

GGTACTGGTG AAGTGATCGC GTCAGCCATT GCGAAAAGCC TCTACCCGGG CGTAGATCCG 21900

TCGAAACTGA CAGAAGATCA GAAGCAAACT GTAAGCACGC TGGCAACGCT GTCAGCGGGT 21960

ATGGCCGGCG GCATTGCCAG TGGCGATGTG GCTGGCGCGG CTGCTGGAGC TGGTGCCGGG 22020

AAGAACGTTG TTGAGAATAA TGCGCTGAGT CTGGTTGCCA GAGGCTGTGC GGTCGCAGCA 22080

CCTTGCAGGA CTAAAGTTGC AGAGCAGTTG CTAGAAATCG GGGCGAAAGC GGGCATGGCC 22140

GGGCTTGCCG GGGCGGCAGT CAAGGATATG GCCGACAGGA TGACCTCCGA TGAACTGGAG 22200

CATCTGATTA CCCTGCAAAT GATGGGTAAT GATGAGATCA CTACTAAGTA TCTCAGTTCG 22260

TTGCATGATA AGTACGGTTC CGGGGCTGCC TCGAATCCGA ATATCGGTAA AGATCTGACC 22320

GATGCGGAAA AAGTAGAACT GGGCGGTTCC GGCTCAGGAA CCGGTACACC ACCACCATCG 22380

GAAAATGATC CTAAGCAGCA AAATGAAAAA ACTGTAGATA AGCTTAATCA GAAGCAAGAA 22440

AGTGCGATTA AGAAGATCGA TAACACTATA AAAAATGCTC TGAAAGATCA TGATATTATT 22500

GGAACTCTCA AGGATATGGA TGGTAAGCCA GTTCCTAAAG AGAATGGAGG ATATTGGGAT 22560

CATATGCAGG AAATGCAAAA TACGCTCAGA GGATTAAGAA ATCATGCGGA TACGTTGAAA 22620

AACGTCAACA ATCCTGAAGC TCAGGCTGCG TATGGCAGAG CAACAGATGC T 22671

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT 60

ATCAGGGTTA TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGGCA ACTGAAACCC 120

GCTGACGGAT NANGTGTACA GTGGCATCAG TGGACGGMTT ACAGCATAAG TGCTTAAGGC 180

GCGTGACCAT ACAGMTACGG TCGCTGCAGA GAACAGGGAG AATATCATCC GGAACACGGT 240

GGCCATAAAC CGTAACAGCA GGGGGCTGCT TTCCCCGGGA GAGGTGCTGG AGATGCATGC 300

GGACGTCTGA ACAGTCAGCA GGGCTGATTA ATGAGAATCA CGAGGAAATG AAGCGGGAGC 360

CGTACAGTGA GGATAAATTT AACGCCATAG CGGCTGTGGG CGGGTATAGT GCCAAGCAGA 420

NSDOCID <WO 9822575A2 I >

CTGCTTAAAG GCAGGTACTA CTTTCAGTGG CGGCTATGTT TCCTGGAATG TGGGTGTCAA 480

CTGGTAGTTC TGAACCCGGG CCTGAGTCAC CGGGGAGGCA GTTTTCGGTA TGAAGTAATG 540

ATTCGCTGCC TGTTTTTCTC CCCGATGGCA TAACTGACTG TTCCCGGGTA TTCCTGAAGA 600

TCTGAGAGGA AGAGTGTATA TGCTGAACTA TCGCATAAGG TCAGTGCAGC TATTTATTGT 660

AAACGGTCGG GCTGACAGGG CGCAGGTGCG TCTGGAATGC GACGATGAAG CCGTTTTTGA 720

ATGTTATCTT CTTGCTGAAG GGGAAGGGGA ACTGAAAGAA CTGAGCCTGT CAGAGCTGGA 780

AGAGCGGGCG CTGATGTATG CGGCAGACAG TTTCCGTTAT GAATGATAAG TCAGTTATAC 840

CGGTAATGGT AAACGGAGCC GGTATCCGGG ATACAAGGGG CAGAGAGTAT GCTGATTATT 900

ATTATGACCC GGGACAGATA TCTGGAATAT GGCCTGATGC GTATACTGAG CGGATATCAG 960

GTCACGACAG GCAGAGAGCT GTTTAATGCC GGAAAGCAAC GTCAGTCACT TCCCGAAGAC 1020

AGTTATGTGA TTCTCTGTGA CCGTAATCTG GAAAGGCTTA CATACTCTAT GTTCTGTGGG 1080

CGTCGGTTTC TTGTCATTCC TGTTTCCTCT GTGAGATGCC TGACAGATAT CAGGCAAACC 1140

ATCCGCCGTG GAGCGTGGCT GTTCGGACAT ACGGCAAGGC CACTGACCCG GACAGAGATG 1200

GTGGTGGTCT TCGGGGTTGT TTTCCATGAC TACGGGTTTA CCTTTCTGGC AGACCGGCTG 1260

GGGATAACCA TGAAGACGGT ATGTGCGCAT CTTTACAATG CGATGGAGAA AAATGGTATG 1320

CGCGGCGTCA GTATTAAATA TCTCTGCAAC ACCATAGACC GGTAAAAAGA TGGTTTTCTG 1380

ATAAAGGCTG TTGCGACGGG GATTTCTGTG CATGCTGTGT CACGGGCATC CCAGCTCTCC 1440

GGATAATTAA TGTTATGTAG TCAGGCGTGA TAAATTTCAT ATGGAACAGG TATGCGTTTT 1500

ATTTGTGATA ACAGTTAATG AGGTGTTTCC ATACACACTG AAGTTACCTG TAATATTAGC 1560

GGGGGATTTG AATGATGTTG CGTGTCTGCG ACCACTCGTT TATTCATGCA AATAAGTGGA 1620

CTGCTGGATC CACGGTAAGA GTACAGCGAG GGCCGTATTG ACGGGGATGT GTTATTCAGC 1680

GGGCAGTGCT ATGCGCCACG GAAGCAGTTC GCTGACACGG TTGACCGGCC AGTCAGCTAT 1740

GACGCCAAAC ACATGGCGAA GGTAGTTTTC TGGATCCTCG TCGTTCAGTT TGCACGTCCC 1800

GATCAGGCTG TACAGTAGCA CTCCCCGCTC ACCACCATGC TCAGAGCTGC GTATTACCGT 1860

GAAGGAGATC GGTGAGTAAC CCTCTGTGTC GGCACATTAT AGCCGTCACA TCGGATAACT 1920

GTTATCCTTC TGTTCTGATG TATTCTGGGA GGTGATGTTT CACTCCTGAT AAGAGCATTA 1980

CTAATTACAG CTGCTTTTCG GATAACATTC GGGCAGTTTT CTTTAATTCT GAAGTCTGAA 2040

AGAGATATCA GTAATTGTAT TGCTTTTAAA CATTGTCAGT ATTTATTTGT CCAAATCGTT 2100

CACGTTTCTC ATAATCTTCC CGACAGTCAC CATCACAAAA CAATCCAGTC TTAACAGGTT 2160

CTCCGCAGTT ATAGCAGAAT CCTGTTTCAG GGAGTCTATT CCGGATACGA TTTTTTAGTC 2220

TGATGCTCAT GCTGAATTGT TCATTTTCAT AAGCAATATC TGCACTATCT GCCATAAACG 2280

ATCCTCTGAG GAGACCACAT CTTTATAACC CACCACCGAA ATATTACAAA GTAATACTCA 2340

TTGTATAATC TTTAACCRGG GGCAGGATAA TTGTATCCTG CCCCT 2385

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 746 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CTTTCAGACC AGCGTTTCCT GTCAGGAGAT GAGGAAGAAA CATCAAAGTA TAAAGGCGGC 60

GATGACCATG ATACGGTATT CAGTGGCGGT ATTGCGGCCG GTTATGATTT TTATCCGCAG 120

TTCAGTATTC CGGTTCGTAC AGAACTGGAG TTTTACGCTC GTGGAAAAGC TGATTCGAAG 180

TATAACGTAG ATAAAGACAG CTGGTCAGGT GGTTACTGGC GTGATGACCT GAAGAATGAG 240

GTGTCAGTCA ACACACTAAT GCTGAATGCG TACTATGACT TCCGGAATGA CAGCGCATTC 300

ACACCATGGG TATCCGCAGG ATTGGCTACG CAGAATTCAC CAGAAAACAA CCGGTATCAG 360

TACCTGGGAT TATGAGTACG GAAGCAGTGG TCGCGAATCG TTGTCACGTT CAGGCTCTGC 420

TGACAACTTC GCATGGAGCC TTGGCGCGGG TGTCCGCTAT GACGTAACCC CGGATATCGC 480

TCTGGACCTC AGCTATCGCT ATCTTGATGC AGGTGACAGC AGTGTGAGTT ACAAGGACGA 540

GTGGGGCGAT AAATATAAGT CAGAAGTTGA TGTTAAAAGT CATGACATCA TGCTTGGTAT 600

GACTTATAAC TTCTGACGAC ACTGCTCCTG AACGATAATT GCGTATATTC TGTAATTAAG 660

ATAATTGCAT ATCKTCTGCA ATTAARCAGA AATACCCTGC AGTCTATTAC TGCAGGGNTG 720

TCTTTTATCT GTTTTACAGA NAATTT 746

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TCTGTTTGTC GTTTTTTCCC CGTTGTAGCG GYTCTGCTCC TGGCTTCCCT GATAGTCAGC 60

CCGCAGGCGC CAGGGCCCCA GATTCCCCCC CACAGTCCCG TTATAACTGA ACTGATGAGA 120

GTCTCCTCCC TGATAATTAC GGGAAACCGT CCCGTTGAGG TTATAATCCA GCATCAGTCC 180

GGGAATGCCG TCGTCCCAGC GTGAGGGAGG CAGCCAGGTG GCATCAGAAT ACTCAAGCCC 240

AGCTGCGGCA TATTGATGGG TAATACGCCC GCTCCGGTAT CAGGACGAAT ATCCACTCCC 300

GGCAACCCAT GAAAATCCGC ACACTGACCA TCATGCCAGT AAACAACTTT ATCCAGAGAT 360

TCTGCTGTTA ACCCCATCAG TCTGACCATA TCTGATGTCA GACAGGCCTG C 411

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 977 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TATTATCGCG CGCGCGCTGC ACAGGGGTTA TCTACATCTG CTGCTGCTGC CGGTTTAATT 60

GCTTCTGTAG TGACATTAGC AATTAGTCCC CTCTCATTCC TGTCCATTGC CGATAAGTTT 120

AAACGTGCAA ATAAAATAGA GGAGTATTCA CAACGATTCA AAAAACTTGG ATACGATGGT 180

GACAGTTTAC TTGCTGCTTT CCACAAAGAA ACAGGAGCTA TTGATGCATC ATTAACAACG 240

ATAAGCACTG TACTGGCTTC AGTATCTTCA GGTATTAGTG CTGCKGCAAC GACATCTCTT 300

GTTGGTGCAC CGGTAAGCGC ACTGGTAGGT GCTGTTACGG GGATAATTTC AGGTATCCTT 360

GAGGCTTCAA AGCAGGCAAT GTTTGAACAT GTTGCCAGTA AAATGGCTGA TGTTATTGCT 420

GAATGGGAGA AAAAACACGG TAAAAATTAC TTTGAAAATG GATATGATGC CCGCCATGCT 480

GCATTTTTAG AAGATAACTT TAAAATATTA TCTCAGTATA ATAAAGAGTA TTCTGTTGAA 540

AGATCAGTCC TCATTACTCA ACAACATTGG GATATGCTGA TAGGTGAGTT AGCTAGTGTC 600

ACCAGAAATG GAGACAAGAC ACTCAGTGGT AAAAGTTATA TTGACTATTA TGAAGAGGGA 660

AAGCGGCTGG AAAGAAGGCC AAAAGAGTTC CAGCAACAAA TCTTTGATCC ATTAAAAGGA 720

AATATTGACC TTTCTGACAG CAAATCTTCT ACGTTATTGA AATTTGTTAC GCCATTGTTA 780

ACTCCCGGTG AGGAAATTCG TGAAAGGAGG CAGTCCGGAA AATATGAATA TATTACCGAG 840

TTATTAGTCA AGGGTGTTGA TAAATGGACG GTGAAGGGGG TTCAGGACAA GGGGTCTGTA 900

TATGATTACT CTAACCTGAT TCAGCATGCA TCAGTCGGTA ATAACCAGTA TCGGGNAATT 960

CGTATTGAGT CACACCT 977

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCTTAAGT CCGGCATTGC CACGCGTAAC CCCCACTTCA ACCGCATGAT TGAGCAGATC 60

GAAAAAGTGG CGATCAAATC CCGCGCGCCG ATTCTGCTTA ACGGTCCAAC CGGCGCGGGC 120

3NSDOCID <WO__ 9822575A2 I_>

AAGTCATTTC TGGCGCGACG CATCTTAGAG TTAAAACAGG CGCGGCATCA GTTTAGCGGC 180

GCKTTTGTGG AAGTGAACTG CGCCACCCTG CGCGGCGATA CCGCCATGTC GACGCTGTTT 240

GGTCATGTAA AAGGCGCGTT TACCGGGGCG CGGGAATCTC GTGAAGGTTT ATTACGCAGC 300

GCCAACGGGG AAATGTTGTT TCTTGATGAG ATTGGCGAAC TGGGCGCGAC GAACAGGCAA 360

TGCTGCTGAA ACCCATTGAA GRGGAAAACC TTTTACCCGT 400

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GTATGCGTTT TCATTAAGAT ATTCTCTGCT GTAGAGAAAC TTATAGCAAT ATAATCTGAT 60

AATATCTTTT ATGTAAAATT TAAATAGTTC ACCTGTGACA GATATATGTT TTCTGCTCAG 120

TAACTCCTGT GTATTAAGCC ATTCCCGTGA CCGAAGCACA CCCTTGTGAA AACTTTTTCT 180

TACTTGCTTT GAGGCACGGC ATTGATGTAA TATTTTTGCG TCCTCAATAA TTCTCTTTCC 240

CGTTTTATTT TTTGCAGCAT CTCTTACTCC ATAAAATATC TCCCGGTCCA GACTTTTGTC 300

ATATTTACTG ATTATACGAC AAATATTCCT GACCCGACGA TTCTCTTTAT TTCGCTTCCA 360

TAGCTTATAA TGATCATCGC ATAACCTTAA GGCATTTGCC TCATCAAATT CTGAAACAGG 420

ATTACTGCAT TTTTTATTCC GACAAATACC TTTGTTTTTA GCCATACTCT TCTTCCCGTC 480

AATGGAAAAA TTTTCACACC CATATTACCT GAATGATAAA CCGGATTAGT GTGATCCGGT 540

TCAGTGAAAT CAACAGGATA CCGGTATGCC ATTCAGCAAT TCTTCCCTCT CCGCGCAAGT 600

GAAATCATAT CTGACGTTTC TTCCTGAAGA AATACGCCAG AAAATCCTTG AACATCTCCA 660

CGGTGTTATT CATTACGAGC CCGTGATTGG CATTATGGGT AAATCCGGCA CCGGCAAGAG 720

CAGCCTGTGT AATGCCATTT TTCAGTCCCG TATCTGCGCC ACGCATCCCC TGAACGGCTG 780

CACCCGCCAG GCTCATCGTC TTACCCTGCA GCTCGGTGAA CGCAGAATGA CGCTGGTCGA 840

TCTGCCCGGC ATTGGTGAAA CACCGCAGCA TGATCAGGAA TACCGAGCGC TTTATCGTCA 900

GTTACTGCCG GAACTGGATC TGATTATCTG GATCCTGCGG AGTGATGAAC GTGCGTATGC 960

TGCCGATATT GCCATGCATC AGTTTTTACT GAATGAGGGC GCAGATCCCT CGCGCTTTCT 1020

GTTTGTTCTC AGCCATGCCG ATCGCATGTT TCCTGCTGAA GAATGGAATG CCACAGAAAA 1080

ATGCCCGTCC CGTCACCAGG AACTCTCACT GGCGACAGTA ATAGCCCGGG TGGCCACCCT 1140

GTTCCCTTCA TCATTTCCGG TACTCCCTGT AGCCGCACCT GCAGGCTGGA ACCTTCCAGC 1200

GCTGGTGTCA CTGATGATCC ACGCGCTGCC ACCACAGGCA ACCAGCGCAG TTTATTCACA 1260

TATCAGGGGG GAAAACCGCT CTGAACAGGC CCGGAAACAC GCACAACAGA CTTTTGGTGA 1320

TGCCATCGGG AAAAGTTTTG ACGACGCCGT TGCCCGGTTC AGTTTTCCGG CCTGGATGTT 1380

ACAGCTTCTG CGTAAAGCCC GGGACCGCAT TATCCACCTG CTGATCACAC TGTGGGAGCG 1440

TCTGTTCTGA CACACTCACG CCGACAGATG TGTCGCTGGA TTAACGAGCA TTCTTCTTTT 1500

TATGAAATCA TGCTTAAAAA TCAGATAATT ARAAGAATAT TTTTTCTGCT GCATTTTATT 1560

CCTGATTATC CGGATGCGAC ACATCCTTTC AACATCATGA TGCATAATAA CATCATGAAA 1620

TAAAAGATGT TTTCTTACGG AGTGCACATC TATGTCTGAT AATCGTTCCC GGCATGATCG 1680

CCTGGCGGTT CGCTTATCAC TCATTATCAG CCGACTGATG GCCGGAGAAT CTCTGTCACT 1740

AAAAACACTG TCAGATGAAT TTGGCGTTAC AGAACGTACT TTACAGCGCG ATTTTCATCA 1800

GCGTCTGGTT CACCTAGATT TAGAGTACAG AAATGGCAGG TACAGCCTCA GACGACAGAG 1860

CAGCCCAGGT GCGATCCCTG AAATGCTTTC TTTTATACAG AATACCGGGA TCGCACGGAT 1920

ACTTCCGCTC CGGAACGGAC GACTGATAAC CTGTCTTACC GACAACCAGG AGCCCTCTCC 1980

CTGCCTTATC TGGCTACCGG CGCCGGATAT CACTGCAACG TTCCCCGAGT GTTTCTCGCA 2040

ACTCATCCTG GCAATAAGAC AGTGTATCCA CATCTCTCTG ATGACTGAGC GATGGTATCC 2100

GTCACTGGAG CCCTGCCGGC TCATTTATTA CAGCGGTAGC TGGTATCTGA TCGCGTTACA 2160

GAAGGGAAAA CTGCAGGTCT TTCCTCTGGC AGATATCAAA TCAGTCAGCC TGACATCAGA 2220

ACGGTTTGAA CGGAGAGGCC ACATCCACAG TCTGGTCGCT GAAGAGCGTT TTATCTCCGC 2280

CCTGCCACAT TTCTCTTTCA TCCATAAACT TATCAACACC TTTAACCTGT GATCGCCGGC 2340

CTGCCAAAGC CGTCCCGACA GGTATGGAGA CAATATGTTG AACAGAAAAC TAAATATACG 2400

GCTACGTCAT TCCCTGAACA GTCACTGCAT ACCTTCCATC ATTATCAATA ACACCGTACG 2460

TTCATTTCAG AGGTCAGTCA TGAATACCAG AGCTCTTTTT CCCCTGCTGT TCACTGTGGC 2520

ATCATTCTCC GCCTCCGCCG GCAACTGGGC TGTCAAAAAC GGCTGGTGTC AGACCATGAC 2580

GGAAGATGGT CAGGCGCTGG TAATGCTGAA AAATGGCACG ATTGGTATTA CCGGCCTGAT 2640

GCAGGGATGC CCGAATGGTG TACAGACGCT CCTGGGCAGC CGTATCAGTA TTAACGGTAA 2700

CCTGATCCCC ACATCACAAA TGTGTAATCA GCAGACGGGA TTCAGGGCTG TTGAGGTGGA 2760

AATCGGACAG GCGCCGGAAA TGGTCAAAAA AGCCGTTCAC TCCATAGCAG AGCGTGATGT 2820

GTCCGTTTTA CAGGCATTTG GTGTACGAAT GGAATTCACC CGCGGTGATA TGCTGAAGGT 2880

CTGTCCGAAA TTTGTCACAT CACTTGCCGG TTTTTCCCCG AAACAGACGA CCACTATTAA 2940

TAAAGATTCC GTCCTGCAGG CTGCCCGGCA GGCATACGCC CGGGAATATG ACGAGGAAAC 3000

AACAGAAACC GCTGATTTTG GCTCTTACGA AGTAAAAGGC AATAAGGTTG AGTTTGAAGT 3060

ATTCAATCCT GAAGACCGTG CGTACGACAA AGTGACCGTC ACGGTTGGTG CTGACGGTAA 3120

TGCCACCGGC GCCAGCGTTG AATTTATCGG AAAATAGCCG GTATGTCGGA CTGCCACCCT 3180

3NSDOCID <WO__ 9822575A2 I_>

GTTTTATTGC CCGAAGGCCC TTTCTCACGC GAACAGGCGA TGGCTGTCAC AACAGCTTAC 3240

CGCAATGTGC TTATTGAAGA TGACCAGGGA ACGCATTTCC GGCTGGTTAT CCGCAATGCC 3300

GAAGGGCAGC TACGCTGGCG GTGCTGGAAT TTTGAACCTG ATGCCGGAAA ACAGCTAAAT 3360

TCGTATCTCG CCAGTGAGGG AATTCTCAGG CAATAAACGT CTTCATTTCA TCCATCAGGC 3420

CGCGTCTTCT CCGGGAGACG CGGCCTTTTC GTTTATACCG CTAATTCATT CATAAGGAGC 3480

AAAGTATGCA ATTAGCCAGT CGTTTTGGTC ATGTAAATCA GATCCGTCGG GAGCGCCCAC 3540

TGACACGCGA AGAACTGATG TACCACGTCC CGAGTATTTT TGGAGAAGAC CGGCACACCT 3600

CCCGCAGTGA ACGGTATGCG TACATTCCCA CCATCACCGT CCTGGAAAAT CTGCAGCGGG 3660

AAGGCTTTCA GCCGTKCTTC GCCTGCCAGA CCCGTGTGCG CGACCAGAGC CGCCGGGAAT 3720

ATACCAAACA TATGCTGCGT CTGCGGCGGG CCGGACAGAT AACCGGTCAG CATGTGCCTG 3780

AAATTATTCT GCTCAACTCC CATGACGGTT CATCCAGCTA CCAGATGTTA CCCGGATATT 3840

TTCGTGCCAT TTGTACCAAT GGCCTGGTCT GCGGTCAGTC GCTGGGAGAA GTCCGGGTGC 3900

CACACCGGGG AAACGTGGTG GACAGGGTCA TAGAAGGTGC TTACGAAGTG GTGGGCGTGT 3960

TTGACCTGAT TGAGGAAAAG CGTGATGCCA TGCAGTCGCT GGTCCTGCCG CCACCGGCAC 4020

GCCAGGCGCT GGCACAGGCG GCGCTGACTT ACCGTTATGG TGATGAACAT CAGCCCGTCA 4080

CCACTACCGA CATTCTGACG CCACGACGCC GGGAGGATTA CGGTAAGGAC CTGTGGAGTG 4140

CTTATCAGAC CATCCAGGAG AATATGCTGA AAGGCGGGAT TTCCGGTCGC AGTGCCAGAG 4200

GAAAACGTAT CCATACCCGG GCCATTCACA GCATCGATAC CGACATTAAG CTCAACCGGG 4260

CGTTGTGGGT GATGGCAGAA ACGCTGCTGG AGAGCCTGCG CTGATACCGT TTCCCTGAAA 4320

GCGCAGTCCT GTTCACGGCT GTCCCTTCCC CCAGACATTC CACCATTCAT TTACTTTTTA 4380

TAAGGAATAA TCTCATGACA ACCTCTTCGC ATAATTCCAC CACACCTTCT GTTTCCGTGG 4440

CCGCTGCATC AGGGAATAAC CAGTCTCAGT TGGTTGCCAC TCCCGTCCCT GATGAACAGC 4500

GCATCAGCTT CTGGCCGCAG CATTTTGGCC TCATTCCACA GTGGGTCACC CTGGAGCCCC 4560

GTGTCTTCGG CTGGATGGAC CGTCTGTGCG AAAACTACTG CGGGGGTATC TGGAATCTGT 4620

ACACCCTGAA CAACGGTGGC GCATTTATAG CACCTGAACC GGATGAAGAT GATGGAGAAA 4680

CCTGGATACT GTTCAATGCC ATGAACGGTA ACCGCGCTGA AATGAGCCCG GAAGCTGCCG 4740

GCATTGCCGC CTGTCTGATG ACGTACAGCC ATCATGCCTG TCGTACGGAG AATTATGCCA 4800

TGACGGTCCA TTATTACCGG TTGCGGGATT ACGCCCTGCA GCATCCGGAA TGCAGCGCCA 4860

TTATGCGCAT CATTGACTGA AAGGGGCCGG AATAATGCAA CAGATTTCCT TTCTGCCCGG 4920

AGAAATGACG CCCGGCGAGC GCAGTCACAT TCTGCGGGCC CTGAAAACCC TGGACCGCCA 4980

TCTTCATGAA CCCGGTGTGG CCTTCACCTC CACCCGTGCG GCACGGGAAT GGCTGATTCT 5040

GAACATGGCG GGACTGGAGC GTGAAGAGTT CCGGGTGCTG TATCTGAATA ACCAGAATCA 5100

GCTGATTGCC GGTGAAACCC TCTTCACCGG CACCATCAAC CGCACGGAAG TCCATCCCCG 5160

GGAAGTGATT AAACGCGCCC TGTACCACAA TGCCGCTGCC GTGGTGCTGG CGCACAATCA 5220

CCCGTCCGGT GAAGTCACAC CCAGTAAGGC AGACCGGCTT ATCACCGAAC GTCTGGTACA 5280

GGCACTGGGC CTGGTGGATA TCCGGGTGCC GGACCATCTG ATAGTCGGTG GCAGCCAGGT 5340

TTTCTCCTTT GCGGAACACG GTCTGCTTTA ACCCGTCACC GTCACAATCA CCTTCATATC 5400

ACTTCAGTTT CTCTTTCTCA GCTGTTTCTT ACTTTCACAT TCAGGAGGAC TATTCTCATG 5460

AAAATCATCA CCCGTGGTGA AGCCATGCGT ATTCACCGTC AGCATCCTGC ATCCCGTCTT 5520

TTTCCGTTCT GTACCGGTAA ATACCGCTGG CACGGTAGCA CGGATACATA TACCGGCCGT 5580

GAAGTACAGG ATATTCCCGG TGTGCTGGCT GTGTTTGCTG AACGCCGTAA GGACAGTTTT 5640

GGCCCGTATG TCCGGCTGAT GAGCGTCACC CTGAACTGAA TCAGGACGGG CATTCAGAAG 5700

AGCAGAATTA TCGCCACCAC CGGACCATTC TTAACCAATT TTCTGTGAGG ATTTTATCGT 5760

GTCAGACACT CTCCCCGGGA CAACGCATCC CGACGATAAC AACGACCGCC CCTGGTGGGG 5820

GCTACCCTGC ACCGTGACGC CCTGTTTTGG GGCACGTCTG GTGCAGGAGG GTAACCGGTT 5880

GCATTACCTT GCAGACCGCG CCGGTATCAG AGGCCGGTTC AGCGACGCGG ATGCGTACCA 5940

TCTGGACCAG GCCTTTCCGC TGCTGATGAA ACAACTGGAA CTCATGCTCA CCAGCGGTRA 6000

ACTGAATCCC CGCCATCAGC ATACCGTCAC GCTGTATGCA AAAAGGCTGA CCTGCGAANC 6060

GACACCCTCG GCAGTTGTGG CTACGTTTAT ATGGCTGTTT ATCCGACGCC CGAAACGAAA 6120

AAGTAACTCT CCAGAATAAC CTTCTGCCCC GGCCTGGTGC TTTCACCACG CCACTTTTCC 6180

ATTTTTCATC TCTGCATATC AGGAAAATCT TCAGTATGAA CACATTACCC GATACACACA 6240

TACGGGAGGC ATCGCATTGC CAGTCTCCCG TCACCATCTG GCAGACACTG CTCACCCGAC 6300

TGCTGGACCA GCATTACGGC CTCACACTGA ATGACACACC GTTCGCTGAT GAACGTGTGA 6360

TTGAGCAGCA TATTGAGGCA GGCATTTCAC TGTGTGATGC GGTGAACTTT CTCGTTGAAA 6420

AATACGCACT GGTGCGTACC GACCAGCCGG GATTCAGCGC CTGTACTCGT TCTCAGTTAA 6480

TAAACAGTAT TGATATCCTC CGGGCCCGCC GGGCAACCGG CCTGATGGCC CGCGACAATT 6540

ACAGAACGGT AAATAACATT ACCCTGGGTA AGCATCCGGA GAAACGATGA AACTTTCCCT 6600

GATGCTGGAA GCCGACAGAA TTAATGTGCA GGCACTGAAC ATGGGGCGAA TTGTCGTTGA 6660

CGTCGATGGT GTTAATCTCA CTGAACTGAT TAACAAGGTC GCTGAAAACG GTTATTCACT 6720

CCGCGTGGTG GAGGAATCCG ACCAACAGTC AACCTGCACA CTACCACCGT TTGCAACCCT 6780

TGCCGGCATA CGCTGCAGTA CCGCACATAT CACGGAAAAG GATAACGCCT GGCTGTACTC 6840

GCTGTCACAC CAGACCAGTG ACTTCGGTGA ATCAGAATGG ATTCATTTCA CAGGTAGCGG 6900

ATATCTGTTA CGTACCGATG CGTGGTCATA TCCGGTTCTG CGGCTTAAAC GCCTGGGGCT 6960

GTCAAAAACG TTCCGTCGTC TGGTTATCAC ACTTACCCGA CGTTATGGCG TCAGTCTCAT 7020

NSDOCID: <WO_ 9822575A2 I_ >

TCATCTGGAT GCCAGCGCTG AATGCCTGCC GGGTTTACCC ACTTTCAACT GGTAACCAGG 7080

AACAACATGA AATCATTAAC CACGGAAACC GCACTGGATA TTCTGATTGC GTGGCTGCAG 7140

GACAATATCG ACTGCGAATC GGGAATTATC TTTGACAACA ATGAGGATAA AACGGATTCA 7200

GCAGCACTGT TGCCCTGTAT CGAACAGGCC AGAGAGGATA TCCGTACCCT GCGCCAACTG 7260

CAGCTTCAGC ACCAGAACCG GTGAGTCTCA CTCATCATCT CACTCACCAG ACTTCATTCC 7320

ACTSACGCCA GCCTGAACAC GGCTGGCGTT TTCATTTATC TGCAAAAAGG AATATCGATT 7380

ATGTCTGAAA TCACAGTCTC CCGTCCGGAA GTGGTCAACG AGAATACGGA CGTTATCTGC 7440

TCCACCTCAG TCAGGTACAG GTCACTGGAA TATGATAATT TTCCGGAAAT CAGCGAAGCG 7500

AACATTCTGA GCACATTTGA ACAACTGCAC CAGAACAAAG ATGAAGTGTT TGAACGGGGA 7560

GTGATCAACG TCTTCAAAGG GCTGAGCTGG GATTACAAAA CCAACTCACC CTGTAAATTT 7620

GGCAGTAAAA TTATCGTCAA CAATCTGGTG AGATGGGACC AGTGGGGATT TCATCTTATC 7680

AGTGGAATGC AGGCAGATCG CCTGGCTGAC CTGGAAAGAA TGTTGCATCT GCTCAGCGGT 7740

AAACCGATCC CCGACAACCG AGGGAATATC ACCATTAATC TGGATGACCA CATACAGTCC 7800

GTTCAGGGTA AAGGACGCTA TGAAGATGAG ATGTTCATCA TTAAATACTT TAAGAAGGGA 7860

TCTGCACACA TCACTTTCAA AAGGCTGGAG CTGATTGACA GAATTAACGA TATAATAGCC 7920

AGGCACTTTC CTTCTGTGCT CTCAGCCTGA CCCCGAGTTT GATTCCCTTT CGATATCAAA 7980

AGGGACTGCG GGTACAAAAG AGGGTACATC TTTCACCAAA CCAAACAAAA TAAACTAATA 8040

TCAACATGAT AGAAGCATTC TTCGATTCCG AGTCCGGCAC CAAATTCATA TAAACGGACC 8100

TCCACGGAGG TCCGTTTTTC GTTTCAGGAC GCCACGATTT AAGCGTCCTG CCGCCAAATC 8160

AATTCTACCG AACTCAACCA GATTCTCCCC ACATCACCAG CAATTTGCGG GCATATCCCA 8220

ATTCGGGAAA ATTTGTTTCT GAGCTATAGC GCTGACTGAC GTGAAATGTC GTGCGGCCCC 8280

GTGATGCTGT TGAAMGTCAA ATGACGTCAT CAGGAGCGTA ACGCACCCAT AAAGCACAAC 8340

ATCGGGCAGA ACGCCAACTG ATGAGATTTT CTGAATGAGA ACAAAGAGAA ATGTATCAGT 8400

CCGTTTGCTC ATGCAAAGAC TAACAATCCA TTAAAATAGT AAGCGCTCCG GACAATTTTC 8460

CATGGATTAT TTTCTGAACA TTTTTCTTTG GCAAAGATGA TGAATTTTGA TGGTAAGGAA 8520

AATTACTTCT GGTTCTCAGT AAAATCCTTT CGTAATACTA TGTAATCAAG AAGTTTATGG 8580

CTAGTAAAAA TAACGTCTTG CATTCACCAA TAATATGTAA ATAAACCCAT CTATAGATGG 8640

AAAAAATAGG TTATGGAATT ATCATTGCAT CATTCCCTTT TCGAATGAGT TTCTATTATG 8700

CAACAACCTG TAGTTCGCGT TGGCGAATGG CTTGTTACTC CGTCCATAAA CCAAATTAGC 8760

CGCAATGGGC GTCAACTTAC CCTTGAGCCG AGATTAATCG ATCTTCTGGT TTTCTTTGCT 8820

CAACACAGTG GCGAAGTACT TAGCAGGGAT GAACTTATCG ATAATGTCTG GAAGAGAAGT 8880

ATTGTCACCA ATCACGTTGT GACGCAGAGT ATCTCAGAAC TACGTAAGTC ATTAAAAGAT 8940

INSDOCID <WO_ 9822575A2 1_>

AATGATGAAG ATAGTCCTGT CTATATCGCT ACTGTACCAA AGCGCGGCTA TAAATTAATG 9000

GTGCCGGTTA TCTGGTACAG CGAAGAAGAG GGAGAGGAAA TAATGCTATC TTCGCCTCCC 9060

CCTATACCAG AGGCGGTTCC TGCCACAGAT TCTCCCTCCC ACAGTCTTAA CATTCAAAAC 9120

ACCACAACGC CACCTGAACA ATCCCCAGTT AAAAGCAAAC GATTCACTAC CTTTTGGGTA 9180

TGGTTTTTTT TCCTGTTGTC GTTAGGTATC TGTGTAGCAC TGGTAGCGTT TTCAAGTCTT 9240

GAAACACGTC TTCCTATGAG TAAATCGCGC ATTTTGCTCA ATCCACGCGA TATTGACATT 9300

AATATGGTTA ATAAGAGTTG TAACAGCTGG AGTTCTCCGT ATCAGCTCTC TTACGCGATA 9360

GGCGTGGGTG ATTTGGTGGC GACATCACTT AACACCTTCT CCACCTTTAT GGTGCATGAC 9420

AAAATCAACT ACAACATTGA TGAACCGAGC AGTTCCGGTA AAACATTATC TATTGCGTTT 9480

GTTAATCAGC GCCAATACCG TGCTCAACAA TGCTTTATGT CGGTAAAATT GGTAGACAAT 9540

GCAGATGGTT CAACCATGCT GGATAAACGT TATGTCATCA CTAACGGTAA TCAGCTGGCG 9600

ATTCAAAATG ATTTGCTCCA GAGTTTATCA AAAGCGTTAA ACCAACCGTG GCCACAACGA 9660

ATGCAGGAGA TGCTCCAGCA AATTTTGCCG CATCGTGGTG CGTTATTAAC TAATTTTTAT 9720

CAGGCACATG ATTATTTACT GCATGGTGAT GATAAATCAT TGGATCGTGC CAGTGAATTA 9780

TTAGGTGAGA TTGTTCAATC ATCCCCAGAA TTTACCTACG CGAGAGCAGA AAARGCATTR 9840

GTTGRTATCG TGCGCCATTC TCAACATCCT TTAGACGRAA AACAATTAGC CAGCACTGAA 9900

CACAGAAATA GATAACATTG TTACACTGCC GGAATTGAAC AACCTGTCCA TTATATATCA 9960

AATAAAAGCG GTCAGTGCCC TGGTAAAAGG TAAAACAGAT GAGTCTTATC AGGCGATAAA 10020

TACCGGCATT GATCTTGAAA TGTCCTGGCT AAATTATGTG TTGCTTGGCA AGGTTTATGA 10080

AATGAAGGGG ATGAACCGGG AAGCAGCTGA TGCATATCTC ACCGCCTTTA ATTTACGCCC 10140

AGGGGCAAAC ACCCTTTACT GGATTGAAAA TGGTATATTC CAGACTTCTG TTCCTTATGT 10200

TGTACCTTAT CTCGACAAAT TTCKCGCTTC AGAATAAGTA ACTCCCGGGT TGATTCATGC 10260

TCGGGAATAT TTGTTGTTGA GTTTTTGTAT GTTCCCGTTG GTATAATATG GTTCGGCAAT 10320

TTATTTGCCG CATAATTTTT ATTACATAAA TTTAACCAGA GAATGTCACG CAATGCATTG 10380

TAAACATTGA ATGTTTATCT TTTCATGATA TCAACTTGCG ATCCTGATGT GTTAATAAAA 10440

AACCTCAAGT TCTCACTTAC AGAAACTTTT GTGTTATTTC ACCTAATCTT TAGGATTAAT 10500

CCTTTTTTCG TGAGTAATCT TAGCGCCAGT TTGGTCTGGT CAGGAAATAG TTATACATCA 10560

TGACCCGGAC TCCAAATTCA AAAATGAAAT TAGGAGAAGA GCATGAGTTC TGCCAAGAAG 10620

ATCGGGCTAT TTGNCCTGTA CCGGTGTTGT TGCCGGTAAT ATGATGGGGA GCGGTATTGC 10680

ATTATTACCT GCGAACCTAG CAAGTATCGG TGGTATTGCT ATCTGGGGTT GGATTATCTC 10740

TATTATTGGT GCAATGTCGC TGGCATATGT ATATGCCCGA CTGGCAACAA AAAACCCGCA 10800

ACAAGGTGGC CCAATTGCGT ATGCCGGAGA AATTTCCCCT GCATTTGGTT TTCAGACAGG 10860

TGTTCTTTAT TACCATGCTA ACTGGATTGG TAACCTGGCA ATTGGTATTA CCGCTGTATC 10920

TTATCTTTCC ACCTTCTTCC CAGTATTAAA TGATCCTGTT CCGGCGGGTA TCGCTGTTAT 10980

TGCTATCGTC TGGGTATTTA CCTTTGTGAA TATGCTCGGC GGTACCTGGG TAAGCCGTTT 11040

AACCACGATT GGTCTGGTGC TGGTTCTTRK TCCTGTGGTG ATGACTGCTA TTGTTGGCTG 11100

GCATTGGTTT GATGCAGCAA CTTATGCAGC TAACTGGAAT ACTGCGGATA CCACTGATGG 11160

TCATGCGATC ATTAAAAGTA TTCTGCTCTG CCTGTGGGCC TTCGTGGGTG TTGAATCCGC 11220

AGCAGTAAGT ACTGGTATGG TTAAAAACCC GAAACGTACC GTTCCGCTGG CAACCATGCT 11280

GGGTACTGGT TTAGCAGGTA TTGTTTACAT CGCTGCGACT CAGGTGCTTT CCGGTATGTA 11340

TCCGTCTTCT GTAATGGCGG CTTCCGGTGC TCCGTTTGCA ATCAGTGCTT CAACTATCCT 11400

CGGTAACTGG GCTGCACCAC TGGTTTCTGC ATTCACCGCC TTTGCGTGTC TGACTTCTCT 11460

GGGCTCCTGG ATGATGTTGG TAGGCCAGGC AGGTGTACGT GCCGCTAACG ACGGTAACTT 11520

CCCGAAAGTT TATGGTGAAG TCGACAGCAA CGGTATTCCG AAAAAAGGTC TGCTGCTGGC 11580

TGCAGTGAAA ATGACTGCCC TGATGATCCT CATCACTCTG ATGAACTCTG CCGGTGGTAA 11640

AGCCTCTGAC CTGTTCGGTG AACTGACCGG TATCGCAGTA CTGCTGACTA TGCTGCCGTA 11700

CTTCTACTCT TGCGTTGACC TGATTCGTTT TGAAGGCGTT AACATCCGCA ACTTTGTCAG 11760

CCTGATCTGT TCTGTACTGG GTTGCGTGTT CTGCTTCATC GCGCTGATGG GCGCAAGCTC 11820

CTTCGAGCTG GCAGGTACCT TCATCGTCAG CCTGATTATC CTGATGTTCT ATGCTCGCAA 11880

AATGCACGAG CGCCAGAGCC ACTCAATGGA TAACCACACA GCGTCTAACG CACATTAATT 11940

AAAAGTATTT TCCGAGGCTC CTCCTTTCAT TTTGTCCCAT GTGTTGGGAG GGGCCTTTTT 12000

TACCTGGAGA TATGACTATG AACGTTATTG CAATATTGAA TCACATGGGG GTTTATTTTA 12060

AAGAAGAACC CATCCGTGAA CTTCATCGCG CGCTTGAACG TCTGAACTTC CAGATTGTTT 12120

ACCCGAACGA CCGTGACGAC TTATTAAAAC TGATCGAAAA CAATGCGCGT CTGTGCGGCG 12180

TTATTTTTGA CTGGGATAAA TATAATCTCG AGCTGTGCGA AGAAATTAGC AAAATGAACG 12240

AGAACCTGCC GTTGTACGCG TTCGCTAATA CGTATTCCAC TCTCGATGTA AGCCTGAATG 12300

ACTGCGTTTA CAGATTAGCT TCTTTGAATA TGCGCTGGGT GCTGCTGATG ATATTGCTAA 12360

CAAGATCC 12368

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

NSDOCID <WO 9822575A2 I_>

GCACGGCACT CTGATGTANC TTTTATCTGT TCCCAGTGGA AGCATGCCCC ACAACTGAGT 60

CATTAAGTGT GGAAGAACAG TTTTGTCCCC GCCTGCAATC TCTCCCTTTC NAAAAACCAG 120

TATGTCGCCA TGCCTCGCCT TAATGGAGAG CGCTGAACCA TACCTTCTTT TTCCCAGTAA 180

TAACAGGTAA TAGCGTGCCT GGTAATCCGT TACCGCCAGC GCCTCCGCAA TTTCTGCGGT 240

TTTCCCTCCA TTATGCCTGT TCAGAAATYC CAGTATTTCA TTCTTCATAT ATTCACTCAT 300

CTCACTGTAA CAAAGTTYCT YCGAATAATA AAAATCATGC TTTCTGTTAT CAACGGAAAG 360

GTATTTTTAT TCTCTGTGTT TGCTTTATTT GTGAAATTTA GTGAATTTGC TTTTTGTTGG 420

CTTTATTTGN ATGTGTGTCA CATTTTGTGT GTTATTTTTC TGTGAAAAGA AAGTCCGTAA 480

AAATGCATTT AGACGATCTT TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA 540

GTGCATTCTT TTTGTTGGTG TTTTATTCTA GTTTGATTTT GTTTTGTGGG TTAAAAGATC 600

GTTTAAATCA ATATTTACAA CATAAAAAAC TAAATTTAAC TTATTGCGTG AAGAGTATTT 660

CCGGGCCGGA AGCATATATC CAGGGGCCCG ACAGAAGGGG GAAACATGGC GCATCATGAA 720

GTCATCAGTC GGTCAGGAAA TGCGTTTTTG CTGAATATAC GCGAGAGCGT AYTGTTGCCC 780

GGCTMTATGT CTGAAATGCA TTTTTTTTTA CTGATAGGTA TTTCTTCTCA TTC 833

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2916 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TGCACCATCA CTGATACCAC CGGGACCCCG GATTTTATCC GGTCCCCGCG GACTGACAGG 60

GTTTGTGACA CCTGAGTCAT ATCCGATGTA AACTTCATTT TCACGGGTTG TACAGGAAAA 120

CTCCCCTGTG CCATTGAGTT CTGATGTGTG CCCTTCGCCA CAACTCCCAC CGTCACGGCA 180

CCAGTTGCAT CTGACGCCGA CCAACTGCTG AGAGCCATGC CGTTTCCGGC TTTGTCGACA 240

ACGCATGCTG CAGTTCCCAG CGATGCGAAC TGGTCTGGCA TGCATTCACG AACCAACAGC 300

AGTGGTGCTA CGTCCGGATG CAATTCGCAT GAGCTCCAAC CGCGGTTGTA AGTTCAGCAG 360

CCCGGGCCTC TGCCCCCGGC ACAGTCGCAT AAGTATTCGA TACCGTGCGA CACCATTACC 420

TTCAGGATAC GCCACGGACC CGTCACCCTA CGAAAACGCC GGAGCACCGG CAATCAGCAA 480

AGGCAGCAGT GATAAAAGAC TGATATATTT CCTGTCATTA TTTTTCATAT TAATTTAACT 540

CCTGATTAAC CGGTTTTTAT TGATATGAGA AAGTAATAGT TGCAATAGCC TTCACACTTC 600

CAGGTGTAGT TGCATCAGCA ATTTTTATAT AATTGGCTCT TAAATTGATA TGTGGATTTA 660

CCTCTCCCCT GTAATCGGAG AAGTGCCATT GACTGCCATT TCCTTTCACA GGGGAGTCTT 720

NSDOCID <WO__9822575A2 I >

CACCATAGCT GATGGCAGTT ACATCACTGT CTTTATATAG CCTGATGCCA AATCCTTTTG 780

CAGTGGATTC ACTGCTTAAG GTCAATATAT CTGTTCTGTT CACTGGCTGT GATGCATCTG 840

TCAATGTAGC ATAAACATCA ATTCCATCCG GGCATTGTAG GTGTATGTCA ATTTTACCTC 900

CCTGTATTTC TTTATACAAA GATGTGAACT GTGATTGATA TACGGTATTT AATGGCACCA 960

CATAGTTTTT TTGCCCCATG GTACATGTCT GACTCTGTAC CTGAATGCGC CCACCATTTA 1020

ACATAACAGG TGCTGTCAGT CCTTTATTAT TTAAACTTGT ACGTTTTGCT TCCAACAAAA 1080

TAGTACCAAG CTGCCTGGTG GGTATTGTTA TATATCCATT GGGTAATCTT CCCGTTGCGA 1140

CAAAAGCAAC AAACAAACGA GCTCCGAAGC TTGCTGTCGC ACCGTTATAA GTATTGGGGT 1200

TTGTATTGGC ACCTACAGGG TCAATATATA TACCTGAGCT ATTTATGGGG ACCAGAGGCG 1260

TTGCGGGCCA ATAGCCCGCC ATGCCAATAA TAATACCCAG TCCGGATACA CCAATATCAT 1320

AGATATCAAA ATCAGATGAA TCACGGCTGT TTCCTTGATG GAAAGTATAC GTAATACTTC 1380

CAATTTTAGG CAGTGCGGGT GTAAACTTTC CACGCATCAG AGCGATGGCA CCGCCATTAA 1440

AAACATACTG GTTACTTGTT CCCGCCAGCT CTCCTATCAC CCGGGGATAG GTATGGGCAT 1500

CAGCAGGACC AATCACAACA CCTGGCAATG TGGATGTATT AACCGCTATC TGCGAAGGCA 1560

CATAATCATC CGGACCCGCT ACCGCCAGCT TAGGGAGTAA AATTAAAAAC AATGGTATGA 1620

AAAAGATTCT TTTCATGTTT TTTCCTGATT AGGGTGCTGT ATACACAGAA CAGGAACGAG 1680

CTGAGATTGC ATATCATCTT TATTGTGTGC AACATGATAT ACAAATGAAC ATCTGTCTTT 1740

ATTATCTGGT CCCCATACAA CGCTGAGATG ACCTTTTTCA GGGAGTCCCC TGGTAAATAC 1800

CTTCCCGGCC TGAGCGACAT ATCCGGCCAA CTGTCCATGT TCATCCAGAA CTTCAGAAGC 1860

CATTGGAGGG GGATTGCCAG TAGACATACG AATATCAAAT AACAGACTTC TTCCTGTTTT 1920

AGTGTCAAAT TTYACTAACG TGGCGCTATT AGCACGAGGA ATGATTTCCT GCTCCGTCGC 1980

CGATAATTCA ACATTCAAAT CTAAATTGGA GGGATCGATG CTAATTTGAT TTTTCTCATA 2040

GGGTGTAACA TAAGGAACAA TACCATTTCC CCAAAAATCC AGACGACTAC CAGAGGCATT 2100

ATTGATGGCA GCCCCCTGAG CTCCTTCAGC ATGGATAATG GCAAAAGTAT CACTCAGGTC 2160

ATTACTCAAT GTCACTCCAT AGGGGTGTGC GACCACCGCT CCCGACGCAC CAAATGACCT 2220

TTGATTATTA TTCTGAGTAT CATGCCCGAC TGTTGTGGTT ATATTTACAT AAGGTGAACG 2280

ATAACCCCCA TTCATTGCAT AACCGGAAGG CCCGTTTTCC TGGCTGTTTC CTGAAAGACC 2340

ATAAGAGAAC TGATTATCCT CCCCGCCAGT ACCACTAATT GATGTCTGAA TACTATTTTT 2400

CTCTTCTTTG CTATAATTTA AAACAGTGGA AAACACCGGG CTTTGAACAC TTNCCTCCCA 2460

GAGGGAGAGT AAAATTAATA TAAAATCTGT CATCACGGCG TTGTTGCTCA TTATCTCTTG 2520

ACTGAGACAA TCCAATTTGA TAGCCGAGTT GTTTCCAGAA GTTGCTGTAC CCCATCTGGT 2580

ATTCATTACG ACTTCCTTTA TGTCCCCAGT AATTATAGGT TGTTCCTGTT AAATACATCC 2640

\SDOCID <WO__ 9822575A2_I_>

CACCCCATTT TTCACCTAAT TCCTGGTTGA TTGAAATCTG GAATTGATTC CTGGGACGAT 2700

AAAACGCTGT ACTTTTTACA GAAACATCAT CAATAAACGC GTTGTGATTA GCTGATAGCG 2760

CATCCTTCAG ATGATAAAAA TCTTTTGATG AATAACGATA AGCCGCCAGA GTTATATTTG 2820

TGTTTTGAGG GCTGGGAATA TTGGATGGCT AATAACTTGG AGTNGCAGGA CTAATAAACC 2880

TTTTACGGCG GTTACACCGG GAATACCNGG AAATGC 2916

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACCGCATCGC CAATCTCAGC GGCAGTGGTT TACATGTCTT CCGTGATGGA AGGTCATGGC 60

ATCAGCTACC TCCATCTGCT CTCCGTGGTC ATCCCGTCCA CCCTGCTGGC GGTTCTGGTG 120

ATGTCCTTCC TGGTCACTAT GCTGTTCAAC TCCAAACTCT CTGACGATCC GATTTATCGC 180

AAGCGTCTGG AAGAGGGCCT GGTTGAACTG CGCGGTGAAA AGCAGATTGA AATCAAATCC 240

GGTGCAAAAA CGTCCGTCTG GCTGTTCCTG CTGGGCGTAG TTGGCGTGGT TATCTATGCA 300

ATCATCAACA GCCCAAGCAT GGGTCTGGTT GAAAAACCAC TGATGAACAC CACCAACGCA 360

ATCCTGRTCA TCATGCTCAG CGTTGCAACT CTGACCACCG TTATCTGTRA ARTCGATACC 420

GACAACATTC TCAAYTCCAG CACCTTCAAA GCAGGTATGA GCGCCTGTAT TTGTATCCTG 480

GGTGTTGCGT GGCTGGGCGA TACTTTCGTT TCCAACAACA TCGACTGGAT CAAAGATACC 540

GCTGGTGAAG TGATTCAGGG TCATCCGTGG CTGCTGGCCG TCATCTTCTT CTTTGCTTCT 600

GCTCTGCTGT ACTCTCAGGC TGCAACCGCA AAAGCAYTGA TGCCGATGGC TCTGGCACTG 660

AACGTTTCTC CGCTGACCGC TGTTGCTTCT TTTGCTGCGG TGTCTGGTCT GTTCATTCTG 720

CCGACCTACC CGACACTGGT TGCTGCGGTA CAGATGGATG ACACGGGTAC TACCCGTATC 780

GGTAAATTCG TCTTCAACCA TCCGTTCTTC ATCCCGGGTA CTCTGGGTGT TGCCCTGGCC 840

GTTTGCTTCG GCTTCGTGCT GGGTAGCTTC ATGCTGTAAT GACCCATYGC GGGGCGTTCA 900

CGCCCCGCTT TCTTTCCCGC CGACTAACAT CCTTTCCCCG TCCGTTGTAT AGTGACCTCT 960

CTCTTGCGGT TCCATCTGTT CTTGCGAGGT GTTTATGCTT GATGAAAAAA GTTCGAATAC 1020

CACGTCTGTC GTGGTGCTAT GTACGGCACC GGATGAAGCG ACAGCCCAGG ATTTAGCCGC 1080

CAAAGTGCTG GCGGAAAAAC TGGCGGCCTG CGCGACCTTG ATCCCCGGCG CTACCTCTCT 1140

CTATTACTGG GAAGGTAAGC TGGAGCAAGA ATACGAATGC AGATGATTTT AAAAACTACC 1200

GTATCTCACC AGCAGGCACT GMTGAATGCC TGAAGTCTCA TCATCCATAT CAAACCCCGG 1260

INSDOCID <WO 9822575A2 I_>

AACTTCTGGT TTTACCTGTT ACACACGGAG ACACAGATTA CCTCTCATGG CTCAACGCAT 1320

CTTTACGCTG ATCCTGCTAC TTTGCAGCAC TTCCGTTTTT GCCGGATTAT TCGACGCGCC 1380

GGGACGTTCA CAATTTGTCC CCGCGGATCA AGCCTTTGCT TTTGATTTTC AGCAAAACCA 1440

ACATGACCTG AATCTGACCT GGCAGATCAA AGACGGTTAC TACCTCTACC GTAAACAGAT 1500

CCGCATTACG CCGGAACACG CGAAAATTGC CGACGTGCAG CTGCCGCAAG GCGTCTGGCA 1560

TGAAGATGAG TTTTACGGCA AAAGCGAGAT TTACCGCGAT CGGCTGACGC TTCCCGTAAC 1620

CATCAACCAG GCGAGTGCGG GAGCAACGTT AACTGTCACC TACCAGGGCT GTGCTGATGC 1680

CGGTTTCTGT TATCCGCCAG AAACCAAAAC CGTTCCGTTA AGCGAAGTGG TCGCCAACAA 1740

CGAAGCGTCA CAGCCTGTGT CTGTTCCGCA GCAAGAGCAG CCCACCGCGC AATTGCCCTT 1800

TTCCGCGCTC TGGGCGTTGT TGATCGGTAT TGGTATCGCC TTTACGCCAT GCGTGCTGCC 1860

AATGTACCCA CTGATTTCTG GCATCGTGCT GGGCGGTAAA CAGCGGCTTT CCACTGCCAG 1920

AGCATTGTTG CTGACCTTTA TTTATGTGCA GGGGATGGCG CTGACTTACA CGGCGCTGGG 1980

TCTGGTGGTT GCCGCCGCAG GKTTACAGTT CCAGGCGGCG CTACAGMACC CATACGTGCT 2040

CATTGGCCTC GCCATCGTCT TTACYTTGCT GGCGATGTCA ATGTTTGGCT TKTTTACTCT 2100

GCAACTCCCC TCTTCGCTGC AAACACGTCT CACGCTGATG AGCAATCGCC AACAGGGCGG 2160

CTCACCTGGC GGTGTGTTTA TTATGGGGGC GATTGCCGGA CTGATCTGTT CACCYTGCAC 2220

CACCGCACCG CTTAGCGCGA TTCTGCTGTA TATCGCCCAA AGCGGGAACA TGTGGCTGGG 2280

CAGCGGCACG CTTTATCTTT ATGCGCTGGG CATGGGCCTG CCGCTGATGC TAATTACCGT 2340

CTTTGGTAAC CGCTTGCTGC CGAAAAGCGG CCCGTGGATG GAACAAGTCA AAACCGCGTT 2400

TGGTTTTGTG ATCCTCGCAC TGCCGGTCTT CCTGCTGGAG CGAGTGATTG GTGATATATG 2460

GGGATTACGC TTGTGGTCGG CGCTTGGTGT CGCATTCTTT GGCTGGGCCT TTATCACCAG 2520

CNTACAGGCC AAACGCGGCT GGATGCCGCT GGTGCAAATA ATCCTGCTGG CAGCGGCATT 2580

GGTTAGCGTG CGCCCACTTC AGGATTGGGC ATTTGGTGCA ACACATACCG CGCAAACTCA 2640

GACGCATCTC AACTTTACAC AAATCAAAAC AGTAGAT 2677

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATCCTGATGA CGCCGTAAAT GTGCATTTGC CAGGATTGCC GCATAGAGGG CACGAAGAAA 60

AGGTCGGTTG TCAGGATGTA TCCAGATGAT TCTGCCACTG AAACCTTCAG GGATAAGACG 120

ATTGCCAACT GCCAGTCCTT TAAGGGCAGC ATTCAGCGCC TTACGCGGGG CATTCTGCTC 180

CAGAAATACG TATGCCAAGT GAGCGTGTAC ATCAATAAAG TCATTCTCCT GTCGGGCAAG 240

GCGCCTGAGT TTGTTGATGT AACTTGTTTC GCTGATTTCA TCCGCATCGT ATGCATCAAT 300

CAGTTCTTCA AACTCATCCA GCAACGAGCC AAACCAGGTT TCCGGAAATA TGAAACAGCC 360

CTGGTTATCG TTCACTTCAA AGCGTAATTT GCCAGTCATA TTCTGAACCT GTAAAAAAGG 420

ATAGACCATA ATCTGCAGGC TATAAAAATT GTGGATGCCT GGCATCGGGT GTCCTTTTAT 480

TGTCCGGGAT TAACGTTGCC CATGATAATA CAGTGAATCC NGTTCTGTGG TAAGACG 537

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CGCTCGAGCA CCAGATTCAC TGACATGCGC AAACTCATGT GTAAATCCTG TCTGGGCATC 60

TATCTCAAGT AACAGTTCCG TTAAATCTAC CGGTGGGAGT AGCTGTTTGA TCCGATTATT 120

TAGACGAAGC AATGATGGTG GCTCTTCCTG TTTCTCCAGA CAACTGATAG TCAGGGATGG 180

ATATTTACCT TCATTACAGA TATGAACTTC CGCATTCTTT TCAAATCGTG ATGCCAGGCT 240

TTCCAGGTCT CATCCAGCTG AATAGCCAGT TGTTGCACAC CTTTACGTCC ATCGACAGGA 300

TGTCCCAGTG CCCGACAGAC AGGAATACGC TGAGTCTGCC ACTCTTCACC TTGCAACAAC 360

TTCTCGCGAG GATCTCCCCA GCGATCACTG TTTTCAAGCC CAGATGTCCC CGGCGGCGCA 420

RTGCATCCTG AAGGCGTTCC AGCAAACATA GTGAATAACC TGCACGCTGT ATCCCGTCCC 480

TCCGCATCGT ATACGAGGCG TTTCCAGGGA CCGGTGATAA TATGTTCAGC GCATCATCAA 540

GGATGCGCTT TTTCGAACCA TTCAGTTCTG CCAGATAATG AATCGCAGCC AGTACATGTC 600

ACCTGCCGGT GCCGCACGGA AATGCAGGTC CCGCAACACC GCCGGAAGAA AACGTTTAAC 660

CCGACCGTAC TGCTCAACCA TTTCGTCATG GAAATTATTG TTCTGTGGAC GAGCAAGTTC 720

ATTAACCTTG CTTACAGATT CTGCCAGTCT GTTTTTGGGT ACGCACTTGA AGATAACCTG 780

CCTGAGATCT GGGACATCTG TATTATCATC CAGCAACAAT GCACATGCCC GCGCCAGTAA 840

CAATGCGGCC TGATCAAGAT CTTTCAGTGT CCTGAGTCTT TTTTTTTGCC CGGTTTTCTT 900

TGCTTCGCGG ATAATGTCCA GAATTAGCAT ATCAAGCACA TCAACGGCAT CGTCTAATGC 960

CGTTATTTCC TGTGCTTTAA CGAATGCAGT AAGTACAGCA AGCTTTCTCT GCTGTGGCAT 1020

TCGAGCGATA TATTTTACCG ACGCCATGCC AGCATGAACG AGCCAGATTA CGCNTTGGNA 1080

ATGGTCAGGC AGACCGGGAA AAGTTCCAGT CGGGNAAAAC TCCAAGAA 1128

3NSDOCID <WO 9822575A2 I >

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGNTGATAAA AATCYTTTGA TGAATAACGA TAAGCCGCCC AGAGTTATAT TTGTGTTTGA 60

GGCTGGAATA TTGATGCTAT AACTTGAGTG CAGACTATAA CCTTTACGCG TTACACCGGA 120

ATACCTGAAT GCTGTTCTGG ACAATGTAAT GTCAGATGCT ATAGCACCCA GATGGGTATT 180

AAAGGCCAGG CCAGCTAACC CCGCTGTATA TCCTGAAGCT GTGGTAAGAC CACTGTTTAA 240

AGTAATATCA TTCGTCAGGC CGTATTGATA GGTGCCTTGT GCTATTAAAT CATTATATGT 300

TTTATTCGCA TAACGATACT TTCCCACTGA CATTTGCCAG CGACTAAATC CGGGACGAAT 360

GAGTTGAGCA ACGGCCGCAA AAGGAACCGT GAACATTCGT GTCTGGCCAT TAGACTCTGT 420

TATCTTAACG AGAAGGTCAC CAGCATATCC ACTGGGATAT AAATCATTGA TGACAAATGG 480

TCCGGCTGGC ACCGTCGTTT CATAGAGGAT ATGAGCATTT TGATAAATGG TTACTTTAGC 540

ATTACTGTTA GCTATTCCCC GGACAGCAGG RGCATAGCCA CGTAAAGAAC CGGGTAACAT 600

TCGTTCATCC GATGCTAACC TGACTCCCCG CAAACTGAGG CTATCCATTA GCTCACCATT 660

CGTATAAAAA TCCCCTAATG TGAATTGTGC TCTCAATGGG GCAAGGTCAT GCATTATACT 720

TGTTTCTATA TTCTGATATC CGGCAGGATA GCTATTATTC CAGCTCTCAC TGCCACGGTG 780

GCGCAAAGCC ATCCCCACAA ATTGAATCCA GCTTTTAATC CCAGATAAGT CTGTTCGTTA 840

CTCGTCCCGG AAGAGCTATA CTGGTAATAG TTAGCATCAT AGTTTATAAA TGCTGCAGGA 900

ACACCACTTT GCCACTGAGA AGGGGAAATA TATCCTCTTG GACGTGTATT CAGCAGTGCT 960

GCGGGATTTC GATATTCAAC CTTAAAGTCG ATAAGTCAAA ATTAATTCTG GCTGAAGAAA 1020

GCCCTGTTGA CGCCGGAAAG CAGGAGGTGT TTCCCGACAT AGTATCTTTG ACTAAATCAA 1080

TCAATGAAAG CAGCTCAGGC GTCAGGCATA ACGTCGGAGC ACCGGTATTG GCAGTACGTA 1140

AATACTGCAA ATCAGCCTTC CCCTTCCATA CATTATTAAC ATAAATATCA GAATAATACC 1200

TGCCCTCAGG CACAGGGTTA CCATGACTAA AGCGGCGGAT ATCAATAGCA TTTATCCCTT 1260

TATCCAAATG CAAAAACTCA GAATCAAACT CAGCCTCTTC AGCAGCAAAT GAATGGTTTG 1320

TTACTGTTAA CCCTAATGCA GCAAAAAGCA GAAGAGAACA ACGACAGTAA ATCAGGCATG 1380

ACAGATTATT AGCGTTCATT ATTACCTTAC TCCAGAACAG ATTCTCCTTG CTGATATCCT 1440

CCGTAATCAT TAACAATAAC CCAGGAAACT TTGCTGGTGG CGCAGTTCTG CCTTTAAGTG 1500

CAAATACTGT TGAAGAGAAA GGGGGAATCA TTCCACCATG TTCAACAGGC GTTAAGTGCT 1560

NSDOCID <WO_ 9822575A2 I >

TATTCTGGTC AACTGCAATT TTGTTGTAGG TTATGTAATA AGGTGTTGGA TTAACTGCTT 1620

TAATTCGGCC TTCCTCCTGG TGCCAGGTAA CTTTCAGATA AGCATCATTT GGTGTTAACT 1680

TCAGGTGAGC AGGACGAAAG AAAAATTTTA TGCGACTACG AACAGCTAGT TGCAAATAAT 1740

TATTATTCCG CTGCTCTGAG TTATCGGAGT CTTTTTTTGC CCTGGGCTTT GCTGGAATAT 1800

CCAGAACATT TAGATAGAAA AGAGATTCTC GGTCTTTCGG TAGTGACTCG CCTGTATATA 1860

CAATTCTGAC TGTTTGTCCT GATTTAGAGT CCATACGAAA TATTGGCGGA GTAATGATAA 1920

AAGGACGTGG ACTGACTCAG GGGGAGCTGC TGCATCTCCA TCGYCAACCA GGACTGGACT 1980

AATGCCGAGA TTTCATTGTC ATTATTTNAA CGTATGCTAA TACTCTTTTG AGTCGCCGGA 2040

TAAACAACAC GGGTTCCCAT GATAACTACA CTACCCTGAA CAACTGCAGA TACAGATAGA 2100

GTAAAAAAAA ACAGCACAAA CCTTAGCATG GTATCTCCAG AAGAAAGCAG GGCAGTATTT 2160

CCTGCCCCAA AATACAAAAC CGTTTGTTAT TCGTAGGCGA TGGTATAATT GACTGTTGTT 2220

TTTACATTGC CTGGAGTTGA TGTCCCGGTC GCATAATATT GAGCCATATA ACGTAATGTG 2280

GCATTACCAT CCCCACCAAT AGTTTCAGAA T 2311

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TATTACCTGT GATTTTTCCG GGCGTAAATG GAGTCCCTAA AGTTATCGCA GTCCCAATAT 60

TTCCTGCATT ACTGTTATAA AGATAAACGA GTAACCCATC AGAAGATGTG TTTGATGTAT 120

TCTGAACTAA AATAGCATTG TNATAAGTGT TTGTTGCCGT TATCGTAACC TTCATTGTTC 180

CCAGATTATA GGGACACCGC ATATTCACAG TAAACTCTTT TTCGTGANTT CCATTTTGAC 240

TCAGGGTCTG AATCTCTACA NCCTGCCAGT CAACAGTTGT GTTGCTTACA GTACAGGCAG 300

GAATAATCAG TTTTCCTCTG AAGGTCAGAT TATCAACTGC ATGTACATGC TGAGACATTA 360

ACACTGCCCC CAGCATTACC GGAAGACACA AACCTCTTAT CTTTTTCATC TGAAATATCC 420

TGTACAAAAA TTTTGCTAAC GATATGTCAA TTCAAACGTG GCTGTTGCTT CATAATCACC 480

GGGTACCACA CTCTTCGTCC GCAGGGCTTC CGGCGTTGCC ACAACATACG CGCCGAAAGG 540

AAGCTCAAGA CTGTTTCCGG TAACCTTTTC CCCCTGGCCT TTGTTATGGG AGGTGCCGGG 600

TTTCAGCAGA CTGCTGCCAT CGGTGTCCAG CAGTGCAATG CCTAACCGGC CAGCATTCAC 660

TCCGGTTACC TTCAGATGGC CCGGGAGRCG CYNTCTTCCG TCCCCTTAAA GGTCAGGGTC 720

ACAATTTTGC CAACTGCTGT TGCATGGCAG TTTTCCAGCC TGATGACAAA CGACTCTGTC 780

NSDOCID <WO_ 9822575A2 I >

GGCGAACGTC CGGGCGGATA CCAGAAATCC CTGGACGCCC GGGTTTTGAA GACGACATGT 840

TTATTCAGAC TGTCACCGGA CACATGGCAG GGTCTGTCAA GCAGATTACC CCTGAATGCC 900

ACATCTGAGG CTATTGCCTG TCCGGCAGAC AGTGCGGCAA ACAGTAAAAG AGCGCCTGTG 960

CTTTTTATCA TCACATTCCC TTACTCATAT TTTATGCTCA GACGCAGCAT GGCCGGATTG 1020

CTCCTGGCAT CAGAATACTC AACCTCCTGT GGCGGCCTTT TCCTCCAGGC GGGCAAGCAT 1080

CTCCTCCTGG CGGCGGGTAA GGCGGGGACA GTAAAAAA 1118

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTCGTGGGTG AAATCGTAGG CCGCGCTTTT TTGCTGATCG GCCAGTTGAT GAATAGGGTG 60

GCCAKGATCG GGATAAAACG TACAGGCAGC GATAAACAGA CAGCCCGGAT AGCGGTTGTT 120

TTTAACGCAC TCCGATAACG CCTGATAACG TGCCAGCAAC TTTTGTTCGG CGGTTTGCGT 180

TTCGTCCAGC ATCAGCTGAC GACGCCAGAC ATCTATCTGT TGGCTAAGAT AACGCAGCGC 240

ATCGTAGAGG ATTGCCTCTT TGTCTGGCCA GAAGCGGCGT ACTCGTCCAG TGGATAATCC 300

ACACGTTCAG CAACCATCTC CAGCGTGGTG TTGGCAATCC CTTGTAATTC TAATAATTTC 360

AGGGCTTCTC CCAGTACATC TTCACGTTGC ACGCTATTTT CCTCCGKCTT TCCCACTGCA 420

ATGTTCGKTC ACGGTTGGCG ATCGCGCAAA TGTGCGCTGG AAGGTTTCAG CATCCATAAA 480

GCCCGTGACG CGTGCTTGTG GATGCTCCTG GCCTTGGTCC GGTCAAAAAA GAGAATTTGT 540

CCGGTAGGGC CAAGGATATT AA 562

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCATCGCTTT ACCCCAGAAA AGTTAAGCCA TATAATGTGA GGGATATAAG TCGTCGTATC 60

CGGTAAGTAC AGATAACCAC AACATAAGCT CATTCAGTAA ATTTTATCTC TGAACAAACG 120

ACTATGGCAT GCTCATTTAT ACTATTCATA AGAAAGTGTG ATTATCTGTA AGCATTAACC 180

ATCAAATCAT ATAACCATAC TAAACTGGCG GATCATCAGC ACCATTAGCA GGTAACTTAT 240

NSDOCID <WO_ 9822575A2 I >

TGAAATTTTA TTATGTGTTT TTTGTTGATA ATTAATATGC AATATGAATT TGCTATTTTA 300

GAATCATGAA CACCATTTAA AATTACCATC ATTAACATCA TATAAAAATA TATTTTTACT 360

AAAACATGAA TTGTATATAT TTATTAGCTC AGGAAAATTA TCAGGGTTCA CCTTCAAATT 420

AACCTGAATG TTATGCTTAA TTTCACCCAG TAGTTCTTCA TGTGTAGATT TTATTATCCC 480

ATTATTATAA TCGATAAATG CACACATGTT TTTTATGAAT TCAAAACCTT TTCCTGTATA 540

CAGTTTAATG AATGCCACCA GAGCAAACAT TTCAAGATGT AGCCATAATG CTACGTTAGT 600

TTTTTGCAAA GTATAAAAAA TTGAATTCGC CACTTTTTTA CTTATTGCTC TTTTATACTG 660

TGATCGAGCA AGATTCAGTA GCGGAAGTCC TCGTTCAATA AATGAATGTG AAAAGACTGG 720

ATAAATTGAT GTCGGAAACC TTTCA 745

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCGTTNATGC ATTTCGASAT TTTCCACTTC GTTCTGACGT TGCACTGCTT TGGCGTCATC 60

ATTACGTAAC GTATCGAGGA AATCGAGGTA GCCCTGATCA ACATCTTTGG TGACGTAGAC 120

GCCGTTGAAC ACCGAGCATT CAAACTGCTG GATATCCGGA TTTTCAGCGC GAACGGCGTC 180

GATCAGATCG TTCAGATCCT GGAAAATCAA CCCGTCAGCA CCGATGATCT GGCGAATTTC 240

ATCAACTTCG CGACCGTGAG CGATCAGTTC CGTGGCGCTC GGCATATCAA TACCATAAAA 300

CGTTCGGGAA AGCGAATTTC CGGTGCCGCA GAAGCGAGGT ACACTTTCTT CGCTCCGGCT 360

TCGCGTGCCA TCTCGATAAT CTGTCAGAAG TGGTGCCACG 400

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGTCGACGAT GAGGCAGCCA GAGCATTAGA GCCGAAAAGA AGGGATGATG CCATGACTGC 60

TGTTGCTATA AAATGTTTCA TATATTCTCC ATCAGTTCTT CTGGGGATCT GTGGGCAGCA 120

TATAGCGCTC ATACTAGGGG TTTGAGGGCC AATGGAACGA AAACGTACGT TAAGGAGATA 180

ATTCGTTGTT TATATTTAAA TTTAGAGCTC TCAGTTCCCC TTTTAAAATA TCCTCTGGCA 240

ACGTGAATGT ATAATGGCCC AACATATTGA TATGCCCGTG CATCAGGGGA GATAGCCGAG 300

CGATATCTTC ATCTATAATT TCTTCGCCAT TACGGCGCAT CCAGCTCAAC GCTTCCTCCA 360

TATAGAGCGT GTTCCACAGA ACCACTGCAT TAGTAACCAG GCCCAGCGCC CCCAGTTGAT 420

CTTCCTGCCC TTCACGATAA CGCTTTCTGA TCTCTCCGCG TTGTCCGTAA CAAATCGCAC 480

GAGCCACAGC GTGCGKTCCT TCTCCTCGAT TAAGCTGCGT CAGGATCCGC CGACGATAAT 540

CTTCATCATC AATATAATTG AGGAGATATA GCGTTTTGTT TACACGCCCT ACTTCCATAA 600

TTGCCTGTGC CAGTCCTGAT GGGCGCGAGC TTTTCAGTAA AGAGCGAATG AGTTCTGACG 660

CATGAATTGT ACCCAACTTC AGGAACCAGC GGTTCGCATC ATCTCATCCC ACTGACTCTC 720

CGCTTTTGAC AGATCTGCAT ATCCTCGGGC CAACTTATCC AGTACTCCGT AGTTTGCCGA 780

TTTATTCACC CGCCAGAACA CCGCCTCACC TGCATCGGCA AGCC 824

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACAAATCAGA CCAGTTAACC AGTCAGTCGG TTTTATGATT TCACTCACTA TACTTTGTTT 60

CATAAGGATT TCAGGATCTG CCAGACTGCG CAGAAATGAT GCTTACGAAT ACACAGTAAA 120

GGCAATGTCA TTTCCGATAC AGAGCCTGAC ATTGCCATAA TGAGCTATTT ATCTGAAAAA 180

CGACAGAATA TGATGTTTTA TCGTAACGTA ATTTTAAGTT CTCAACTTAT TGAGACATAT 240

TGTCTTTTTT ACCCATGTGG TCATTTTTCA TCCCATCCGT TTTGCTCATG TGTTCTTTCT 300

CCATTTTCTC TTTATCCATT GCATTTTTGC ACATACCATC CTTGCACATT TTATCATGCG 360

CGCTGGACAT GCTGCCTTTT ACTTCATGTG TTTTATCCAT TGTGTCTGCT GCCTGAGCAT 420

TGAACATGAA CAGCGCGGAT AGTACAGTTG CAGAAATAAT ATTTTTCATG GTTCTTCCTC 480

ATTTTTAACA ATTGTATCAA CAACCACCAA ACCAGTTATA ACCCTGGTCT TCCCAGTACC 540

CCCCCGGAAA ATGATTAGTG ACCTCTATAA CCTGAACATG CTTGGGGTTT TTATATCCCA 600

GCTTAGTAGG GATACGTATC TTTATGGGAT AGCCATATTC TTTTGGCAAT ACCCTGTTAT 660

TCCATGTCAA TGTCAGCAAT GTTTGTGAAT GTAGTGCTGT CGCCATATCA ATACTGGTGT 720

AGTAACCATC GACGCAACGA AAACTGACGT ATTTTGCCCG CATATCGGCA CCAATCAGCG 780

TCAGGAAATG CCGGAATGGT ATCCCTCCCC ATTTTCCTAT TGCACTCCAT CCTTCAACAC 840

NGATATGACG GGTTATCTGA CTCACATGCT GCATGTTATA CAATTCAGAC CAAAAACCAG 900

TTACGGGTTA T 911

NSDOCID <WO 9822575A2 I >

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

NGGGGCAGGA TAATTGTATC CTGCCCNGTA TATAATTCTC AGCACAGGTG TTGACTAAAG 60

AGCGTGAAAC TTTGCTATTA TGTCTTCGTA AGATTCACGG ACGGTTATAC TTGAGCCTGA 120

TTCTGTGAAG TAAACAACAG CAGAAGCATC GTTGCCTTTT TCAATGTATG AAACATTCCA 180

GTCATGGATA GCCACTGCGG GCTGACCATT ATCCCGACGG TGCGTCTTAA TGAATCGCGG 240

AAGTAATTCT GCAATATCGT TAAAAACACC ATTTACGGTA TGAGTGATAC CACCAACGCA 300

ATGTAGATGA GTTGACTCCG GGGTATCATT GTCTGCTTCT GCAAAGAGTA TAGCTGTCTT 360

GCTAATTGTA ACAGGCGCCT GTGARCGGGA TAATTCGAGA GAAATAAACC CGGATTCTGC 420

CATAAAAACT CCAGTTTGTG ATGTTATATC ATTTCATATG TTT 463

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTCTAACCTC TGACCAAAAA CAGAATTACG GTTGTTATGC TGCAGAACCT AATGACGTGC 60

AACTGGCGCG CTATTTTCAT CTTGATGAAC GGGATCTGGC CTTCATTAAC CAACGACGGG 120

GCAAACATAA TAGGCTGGGC ATTGCGCTTC AGCTCACCAC AGCCCGTTTT CTGGGAACAT 180

TTCTGACGGA TTTAACTCAG GTTCTGCCTG GTGTTCAACA TTTTGTCGCG GTACAGCTTA 240

ATATCCACCG TCCAGAAGTT CTCTCCCGCT ATGCTGAACG GGACACTACC CTTAGAGAAC 300

ATACTGCATT AATTAAGGAA TATTACGGCT ATCATGAATT TGGTGATTTT CCATGGTCTT 360

TCCGCCTGAA GCGTCTGCTA TATACCCGGG CGTGGCTCAG TAATGACGAC CGGGTCTGAT 420

GTTTGATTTT GCCACTGCAT GGTTGCTTCA AAATAAGGTA TTACTGCCCG GAGCAACCAC 480

ACTAGTACGT CTCATCAGTG AAATTCGTGA AAGGGCAAAT CAGCGGCTGT GGAAAAAGCT 540

GGCCGCACTG CCGAACAAAT GGCAG 565

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGATGGCGTC CGGGGTGAAC GCCGGATAAG TTTAATTTAT CCGGTCAGGC AAAAGGCATT 60

AATCTGCAGA TAGCTGATGT CAGGGGAAAT ATTGCCCGGG CAGGAAAAGT AATGCCTGCA 120

ATACCATTGA CGGGTAATGA AGAAGCGCTG GATTACACCC TCAGAATTGT GAGAAACGGA 180

AAAAAACTTG AAGCCGGAAA TTATTTTGCT GTGCTGGGAT TCCGGGTCGA TTATGAGTGA 240

GTCACTCCGG TGAGATGTCC GGTTATTTAT CTTTTTTGTG AATCTGGTGA TGCGTGGAAT 300

GAAAGACAGA ATACCTTTTG CAGTCAACAA TATTACCTGT GTGATATTGT TGTCTCTGTT 360

TTGTAACGCA GCCAGTGCCG TTGAGTTTAA TACAGATGTA CTTGACGCAG CGGACAAGAA 420

AAATATTGAC TTCACCCGTT TTTCAGAAGC CGGCTATGTT CTGCCGGGGG CAATATCTTC 480

TGGGATGTGG AATTGTTAAC GGGGCCAAAG TA 512

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGCCGGTGC GGTTANTAGT GGCAGTGGTG TCTTTTGGTG TAAATGCTGC TCCAACTATT 60

CCACAGGGGC AGGGTAAAGT AACTTTTAAC GGAACTGTTG TTGATGCTCC ATGCAGCATT 120

TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC TTTCAAAAAG CTTCCTTGAG 180

GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT TGGTTAATTG TGATATTACT 240

GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA AGCTGGCTTT TACTGGCCCG 300

ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG GTACGGGCAC AGCTATCGTA 360

NTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG AAGTGATGCT AATACCCTGA 420

AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTTAA GAAGTCGTCA GCCGTTGGTG 480

CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT CAACCTGACT TATCAGTAAT 540

ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATTCCGCTG TTTATTTCTC AGGGTATTTA 600

TCATGAGACT GCGATTCTCT GTTCCACTTT TCTTTTTTGG CTGTGTGTTT GTTCATGGTG 660

TTTTTGCCGG TCCGTTTCCT CCGCCCGGCA TGTCCCTTCC TGAATACTGG GGAGAAGAGC 720

ACGTATGGTG GGACGGCAGG GCTCCTTTTC ATGGTGAGGT TGTCAGACCT GCCTGTACTC 780

TGGCGATGGA AGACGCCTGG CAGATTATTG ATATGGGGGA ATACCCC 827

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CCAGGGGCCC AAAATCCGTG TATCCACCTT TAAAGAAGGC AAAGTTTTCC TCAATATTGG 60

GGATAAATTC CTGCTCGACG CCAACCTGGG TAAAGGTGAA GGCGACAAAG AAAAAGTCGG 120

TATCGACTAC AAAGGCCTGC CTGCTGACGT CGTGCCTGGT GACATCCTGC TGCTGGACGA 180

TGGTCGCGTC CAGTTAAAAG TACTGGAAGT TCAGGGCATG AAAGTGTTCA CCGAAGTNAC 240

CGTCGGTGGT CCCCTCTCCA ACAATAAAGG TATCAACAAA CTTGGCGGCG GTTTGTCGGC 300

TGAAGCGCTG ACCGAAAAAG ACAAAGCAGA CATTAAGACT GCGGCGTTGA TTGGCGTAGA 360

TTANCTGGCT GTCTCCTTCC CACNCTGTGG CGAAGATNTG 400

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 578 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CCGATTTTTT GCGAAACGTT CCGCCTGGCA TCAGGATAGT TTGTTCGTTA TCCAGTTCGG 60

ATAGCGCATT GACGATATGC AGGCTGTTGG TCATCACCGT GATGTNATTA AAGCGCGAGA 120

GCAGGGGAAC CATCTGCAAA ACGGTACTGC CAGCATCAAG AATGATCGAA TCGCCATCAT 180

GGATAAAACT AACGGCAGCT TCTGCAATCA GCTCTTTCTT GTGGGTGTTG ATGAGTGTTT 240

TATGATCGAT AGGCGGATCG GATTCCTCTT TATTCAACAC CACTCCGCCA TAAGTACGAA 300

TGACGGTTCC GGCATGTTCC AGAATGACCA GATCTTTGCG AATGGKTGTG CCTGTGGTGT 360

CAAATATTGC GCCATTCTTC AACCGAGCAT TTACCCTGCT TTGCAGATAC TCCAGAATGG 420

CGGCCTGACG CTGACGAGTT TCATGGGCGT GATACCTGAT TTAGGTTCAA ATGATAACTC 480

GCAAGCAGTA ACATCACACG NAATATCCAC GTTCAGTTAA GCGCCATGAT AGAGCATCCG 540

TGATAGGGNC AGGGGNAGTC ACACGGCGTA ATCACCGC 578

(2) INFORMATION FOR SEQ ID NO: 39:

NSDOCID <WO 9822575A2 I_>

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TGTTAGGTCA GGGCCCACAG TCAAGCTTAG GTTTTACTGA ATATACCTCA AATGTTAACA 60

GTGCASATGC AGCAAGCAGA CGACACTTTC TGGTAGTTAT AAAAGTGCRC GTAAAATATA 120

TCACCAATAA TAATGTTTCA TATGTTAATC ATTGGGCAAT TCCTGATGAA GCCCCGGTTG 180

AAGTACTGGC TGTGGTTGAC AGGMGATTTA ATTTTCCTGA GCCATCAACG CCTCCTGATA 240

TATCAACCAT ACGTAAATTG TTATCTCTAC GATATTTTAA AGAAAGTATC GAAAGCACCT 300

CCAAATCTAA CTTTCAGAAA TTAAGTCGCG GTAAATATTG GATGTGCTTA AAGGACGGGG 360

AAGATTTCAT CGACACGTCN GCGTGCAATC TATCCGTAT 399

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CAGCCTCCGT TACCGGACAG CAAGGAGGCT GAATGGAGTT TACAGGATTT GCTTTTTTAT 60

AATGTCTGGC CATGCAGTMA AACCGGACAG GTTTTATTAT CATGTGAGGT ATTCTGACAT 120

AAAATGCTGG ATTTTTATTT TGTGACGAAT GCTGCAAAAT TGCATCTGCA CTCTGATGTA 180

GCTTTTATCT GTTTCAGTGA AGCATGCCCA CAAACTGAGT TATTAAGTTG TGGAAGAACA 240

GTTTTGTCCC GCCTGCATAT CTCCTTTCAA AAACCAGTAT GTCGCCATGC CTCGCCTTAA 300

TGGAGAGCGC TGAACCATAC CTTCTTT 327

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGAGATGGGC ATGGAACTCA CTTCATAATA ATGCCTACCG AAGAAATATT AATAGATGAC 60

ATTTCCACGA GNGATAGCAA TAAAACATCA GAGCAGTCTT CTCGCTTAGA AAAAGCTTTA 120

TTAGGTTTTA CAAACACAAT GTACAGTGAT TCAAACCCTC CTATTATAGC TCGTTTTAGA 180

GACTATCTGG AAGATGGTGA GTGCATTGAC AGAATTAGCG AATCAATTTT TTTTACACCG 240

CAAGAATTCA ATCTTGCAGA TCACCACATT GAAGGATGGT TCAATGAATT TGGTCAATTC 300

AGTGGAACTG TTTC 314

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TCCCAAGATC TTTTTGGCCG CAAATCCACA AAACCCGTCG TTANTGTCGC GCAGCCANTT 60

GCAGGCCGAA TTTGCACCGT TTTAGAAAGC GGCGTTTTGT AGAGCAGCAC GCAGTGAGAA 120

GCCACCGCGC CACGACCTAC GNGCNCGCGC AGCTGGTGTA ATTGCGCCAG ACCCAGACGC 180

TCCGGGTTTT CGATAATCAT CAGACTGGCG TTAGGCACAT CAACGCCGAC TTCAATAACG 240

GTTGTGGCAA CCAGCAGGTG TAGCTCACCT TGTTTAAACG ACGCCATCAC CGCCTGTTTC 300

TCGGCAGGTT TCATCCGCCC GTGTACCAGG CCAACGTTCA ACTCTGGTAG CGCCAGTTTC 360

AACTCTTCCC AGGTAGTTCC GMCGCCTGCG CTTCCAGCAA TTCCGACTCT TCAATCAACG 420

TACAAACCCA GTATGCCTGA CGACCTTCAG TTATGCAGGC GTGGTGCACC GGGTGCAATG 480

GATGTCGGTA NNGCGGGTAT CAGGAATAGC GACCGTAGTC ACTGGGCGTG CGGCCTGGGC 540

GGCACTCCAT CTATCACCGA GGGTATCGAG ATCGGGCATA CGCNTGCATT 590

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT 60

CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT 120

TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGGATA AATGCTTCAA 180

TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCCTTT 240

TTTGCGGCAT TTTGCCTTGC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA 300

TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGGATCTG CAACAGCGGT 360

AAGATCCTTG AGAGTTTTTC GCCCCGAAGG AACGTTTTTC 400

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATTCGGAAAG ATGCTTCTAN TTTTTTTAAG CACGTATAAA CTGTTAATTC AGGTTCAATG 60

CTACGAAATG CACTAGTTAT AACCTGTATT GAAGGAAAGA TCTTCTGATA CTCTTTCCAG 120

AGATCTTCAA GTCTGGCCAT GGAAATTGAC TTGGCTGCAT ATTCTAGGTC AGTGTTTATG 180

ATAGTTTCTC TATTCTCTCT GAATGCGGAA AAAAAAGCTT CATTCAACAA TGATAGTAAA 240

TCCCTGGGCC GGTAAAGGGT AAATTGCAAA CATCGCTTAA AACCATTCCT CCCTTTAAGA 300

TCATCCGCTG TGCATCTATC CCAAACTCGT TGATCTTTCT CAATATCTAG CTTAAATGCT 360

ACTTTCATTC TTTTAGCTGA CAGCATTAGG AGTTGTGCCC 400

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TAATGTTGAA GACAGAGATA TAATNTACAG CATCATCCCA CAAGGCAGAT ATAACAATAC 60

TTGACTGGGA TATGCAAAGC GATAGTGGGC AATTTGCTAT TGAAATAATA AAATCGATAA 120

TCGTTTCAGA TATAAATTCT GGAGGACGTT TACGTCTTCT TTCTATTTAT ACTGGTGNAC 180

ATGTTACTGC TGTTATAACT AAGTTGAACA ATGAGTTAAA GAAAACATAC CGTAGCGTAA 240

TAAAAAATGA TGATAGTATT TTTATTGAAG ATAACTATGC ACTCGAACAA TGGTGTATAG 300

TTGTTATTAG TAAAGACGTT TATGAAAAAG ATCTTCCAAA TGTGTTAATA AAAAAATTCA 360

CTAACCTTAC AGCTGGGTTG CTATCCAACG CCGCACTCTC TTGCATTTCT GAAATAAGAG 420

AWAAAACCCA TGGGATATTA ACAAAATATA ATAATAAATT AGACACTGCA TATGTTTCCC 480

ACATCTTAAA TTTAATAAAA TCCAAGGRGT CAAGGGCATA TGCTTATGAA AATGCTCATG 540

ATTATGCAGT AGATTTAATT TCTGAAGAAA TAAGATCAAT ATTGC 585

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ANTCATCCAA CTGGCCGATC AGCAAAAAAG CGCGGCCTAC GATTTCACCC ACGAACTGTT 60

AACCACGCTG GAAGTTGACG ATCCGGCGAT GGTAGCAAAG CAGATGGAAC TGGTGCTGGA 120

AGGCTGTTTA AGCCGAATGC TGGTGAATCG TAGCCAGGCG GATGTCGACA CCGCACATCG 180

GCTGGCGGAA GATANTCNTT GCGTTCGCCC GCTGCCGTCA GGGTGGTGCA CTGACCTGAC 240

AGAAACACAG AAAAGAAGCG ATTTGCCGCA ATCTTAAGCA GTTGAATCGC TTTTACTGAA 300

ATTAGGTTGA CGAGATGTGC AGATTACGGT TTAATGCGCC CCGTTGCCCG GATAGCTCAG 360

TCGTAGAGCA GGGGATTGAA AATCCGTTGT 390

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGATGCCAGT GTCAGCGACT GGTTAAAGTG GTCGATATCG ATGAGCAAAT TTACGCGCGC 60

CTGCGCAATA ACAGTCGGGA AAAATTAGTC GGTGTAAGAA AGACGCCGCG TATTCCTGCC 120

GTTCCGCTCA CGGAACTTAA CCGCGAGCAG AAGTGGCAGA TGATGTTGTC AAAGAGTATG 180

CGTCGTTAAT TTTATCTCGT TGATACCGGG CGTCCTGCTT GCCAGATGCG ATGTTGTAGC 240

ATCTTATCCA GCAACCAGGT CGCATCCGGC AAGATCACCG TTTAGGCGTC ACATCCGTCG 300

TCCCCTGGCA AACGGGGGCG ATTTTCCTCC ATTTGCCTCA GTGGCTGGCG TTTCATGTAA 360

CGATACATGA CAGCGCCCGA CAAGATCCTG ATACTCTTTG GGTATTCAAC CGTTTCCAGT 420

GTAATTCGTC GTTCACNAAC ATTGGCGTTA CAGGCGGGGC TGGCNGTNAC CCA 473

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

3NSDOCID <WO 9822575A2 I >

GAAGTGACGG ATGGCTGTGG TTTCTCCATC GGTCACCAGC AGCAGTTNGC ATCATGGATT 60

GCCTATAAAG TCGCGCCGTT CCTCGGNAAA AAAGAGGAGA GCGTTGAAGA CCTCAAATTG 120

CCGGGCTGGC TGAACATTTT CCACGACAAC ATCGTCTCCA CGCGATTGTG ATGACCATCT 180

TCTTTGGTGC CATTCTGCTC TCTTCCGTAT CGACACCGTG CAGCGATGGC AGGCAAAGTG 240

CACTGGACGG TGTACATCCT GCAAACTGGT TCTCCTTTGC GGTGGCGATC TTCATCATCA 300

CGCAGGGTGT GCGCATGTTT GTGGCGGAAC TCTCTGAAGC ATTTAACGGC ATTTCCCAGC 360

GCCTGATCCC AGGTGCGGTT CTGGCGATTG ACTGTGCAGC TATCTATAGT TCGCGCCGAA 420

CGCCGTGGTC TGGGGCTTTA TGTGGGGCAC CATCGGTCAG CTGATTGCGG TTGGCATCCT 480

AG 482

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GACGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA 60

AAACCCTGGC GTTACCCAAC TTAATCGSCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG 120

TAATAGCGAA GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCANCT GAATGGCGAA 180

TGGCG 185

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAACGCTTCA ATACGCGCGA CCAGCTGGCG GCGCTCATAC GGCGTAATTT TGGCGTCGGC 60

GAGCAAAATC CCTTGTTTAA AGGTATTTTG CCAGCTGCCG TCGTCATATT GGCGAGCTTG 120

CTGACGCGAC TGCGCAGGCA TTAAACGATC AGCACAATCC ATCGCCCGCA GCCAGTAAAG 180

CGGATTGGTT TCGGTTGATT TACCTTGCAG CGCCCAGATG TCGCTACATT CAGTAGAAAG 240

ATAGTCAGCC AGTTGATAAA CCGGAATTTT TTCTTCTGCT GGCGTATCAA TGGCTGGCTT 300

ATTGTGATTC TGCACGCAAC CCAGCAATGC CAGACATGGA GACCCTGCCA GCCACAGCCG 360

TCGGGGCAAT AATCGTTGAA AAATGTGTCG CATATTCACC AGACTTAAAG CCTATCCCAG 420

TGGGCGTAAT TGTTGCAGAC AGTCTGGACA TGGACAGCGC GGAGAAACCG GNAGCGTACA 480

TATCGTACGT G 491

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACTTGAACGG CAATTATTAT TTATCCATGC AACTTCAAGT TGCAGTATCG GAACATTAAC 60

TTTTCTGGGG TGAATATCAC TCTGATATCG TTTTTTGTAT GCGTNT 106

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TTTATGTGCG GTATTGATGG CTGAAGCCTG TAATATCGGA CTGGAACCGC TGATAAAGCA 60

CAATATACCA GCACTGACCC GCCATCGGCT CAGTTGGGTG AAACAGAATT ACCTTCGTGC 120

AGAAACGCTG GTCAGCGCCA ATGCCCGCCT GGTTGATTTT CAGTCCACAC TGGAGCTTGC 180

TGGTCGTTGG GGAGGTGGAG AAGTGGCATC AGCTGACGGC ATGCGCTTTG TCACACCAGT 240

GAAGACCATC AACTCAGGAT CTAACAGAAA ATATTTTGGT TCTGGGACGA GGCATCACCT 300

GGTATAACTT CGTATCTGGA TCAGTACTCT GGGTTCCATG GCATTGTGGT ACCCGGTACA 360

TTACGGGRCT CGATTTTGTA CTGGAAGGAC TTCTTGAGCA GCAGACAGGG CTGAATCCAG 420

TTGAAATCAT GACAGACANT GCGGGTAGCA GCGATATTAT TTTCGGTCTG TTCTGGCTAC 480

T 481

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGGNCCGTAA TTCCCAACCA TTTGCCGAGG TCCAGNTTTT TCACCATGTT ACTCGGGATA 60

GCCAAAACNG ATACCGATGT TGCCGCCGTC CCGGTGCGAG GATCGCGGTG TTGATACCGA 120

TCAGTTCGCC GTTCAGGTTA ACCAGCGCAC CACCGGAGTT ACCACGGTTG ATCGCTGCAT 180

CGGTCTGGAT GAAGTTTTCG TAGTTTTCGG CATTCAGGCC GTACGCCCCA GCGCAGAGAC 240

AATCCCGGAA GTTACCGTCT CGCCCAGACC AAACGGGTTA CCAATCGCTA CGGTGTAATC 300

ACCCACGCGC AGTGCATCAG AATCCGCCAT CTTAATTGCG GTCAGGTTTT TCGGGTTCTG 360

GATTTGGATC AGCGCGATAT CAGAGCGCGG ATCTTTGCCA ACCATCTTCG CGTCGAACTT 420

ACGGCCATCG CTCAGTTGAA CTTTAATGAC CGTCGNGTTA TNAACAACGT GGTTGTTGGT 480

GACGACATAG CCTTTATCGG CATCAATGAT GACGCCGGAA CCCAGCGCCA TGAATTCTGT 540

TGCTGGCCGC CACCATTA 558

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CACCTGCGTG ACGTGACCGA CCTTTTCTCC TCGCTGNTTG TTTCCCCTAT CGTCGGCCTG 60

GTCATTGCGG GAGGCCTGAT ATTCCTGCTG CGACGCTACT GGCGCGGGAC GAAAAAAGCG 120

TGACCGTATT CGCCGCATTC CGGAAGATCG CAAAAAGAAA AAACGGCAAA CGTCAACCGN 180

CATTCTGGAC GCGTATTGCG CTGATTGTTT CCGCTGCGGG CGTGGCGTTT TCGCACGGCG 240

CGAACGACGG ACCAAAAGGG ATC 263

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTAACGCGTC TGGAAGATGG CCTGCCAGTG GGCGTCGTCG ATGTGGTCGA GGGGCTGGAC 60

GGTTGCCATT CCGCCAATAT CTCACCGGAC AACCGTACGC TGTGGGTTCC GGCATTAAAG 120

CAGGATCGCA TTTGCCTGTT TACGGTCAGC GATGATGGTC ATCTCGTGGC GCAGGACCCT 180

GCGGAAGTGA CCACCGTTGA AGGGGCCGGC CCGCGTCATA TGGTATTCCA TCCAAACGAA 240

CAATATGCGT ATTGCGTCAA TGAGTTAAAC AGCTCAGTGG ATGTCTGGGA ACTGAAAGAT 300

CCGCACGGTA ATAATCGAAT GTGTCCAGAC GCTGGATATG ATGCCGGAAA ATTCTCCGAC 360

NSDOCID <WO 9822575A2 I >

ACCCGTTGGG CGGCKGATAT TCATATCAGC CCGGATGGTC GCCATTTATA CGCCTGCGAC 420

CGTACCGCCA GCCTGATTAC CGTTTTCAGC GTTTCGGAAG ATGGCAGCGT GTTGAGTAAA 480

GAAGGCTTCC AGCCAACGGA AACCCAGCCG CGCGGCNTCA ATGTTGATCA CAGCGGCAAG 540

TATCTGATTG CGGCCGGGCA AAAATCTCAC CACATCTCGG TATACGAAAT TGTTGGCGAN 600

CAGGGGCTAC TGCATGAAAA AGGCCGCTAT GCGGTCGGGC AGGGACCAAT GTGGGTGGTG 660

GTTAACGCAC ACTAACCGCT GAT 683

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGATGCAGG GAAAAACATT GATATTACCG GGGCAACGTG CTCGTCCGGT GGAGACCTTG 60

GAATGTCTGC GGGTAATRAC ATCAACATTG CCGTAAACCT GATAAGCGGG ACAAAAGTCA 120

GTCCGGTTTC TGGCACACTG ATGACAACAG TTCATCATCC ACCACCTCAC AGGGCAGCAG 180

CATCAGCGCC GGCGATAACC TGGGCGATGG CTGCAGGCAG AGATKCTGGG NTGTCACAGC 240

ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTTCTGCA GT 282

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATGAACGGCC CCCCCCACAG CCCGTTAACA AACGGNTGCC CCGGCGATAA TCGTACTGAT 60

AAGTTAACTC CAGCAGGCGG TTAATTGAAA GCGAACGGGA GGCTGATGCA TGGTAATAAT 120

CCCTTAAAAC GCGACGGCAA CGCGCCAGTA AACCGTGAGA TGGTCAGGGG CAAGCCAGTC 180

CGGGTAAACC AGAGGCAGTC CGGCAGTGAA CGAACCGGAA ACATGACCAC TGGTGGTGCT 240

GAGCCCGGCA GCAGCACCCC ACAGCGTGCC GGACGAGTAC GGGTCATCTC TGTCAGAGTG 300

CAGCCAGCCG CCGTCCAGTG CAGTCACTGC ACGGACTGTC CCCACATATG GCAGGGAGAA 360

CAGAGACCAG GACAGCTCAT TTCGCAGATA ACCGCCGTTA TTACCGGAGA TATACTGCTC 420

CTTAAAGCCA CGCACTGAAC TCTCACCCCC GAGGCTCAGT TGTTCCACAC CATGAAGACG 480

GTCCGGTGAC CACTGGGCAT AAGCGCTGGT CAGCCACCAC ACCCTGTCCG TGACGGGGCG 540

CTGAAAACTG GCACTCACCG ACCATTTCCG GAACTGATTT ACGGGCAGGT CTCCCCTTTT 600

CCCGTGGTCG CTTTCTGCGC CGAACCAGGG CATCCCCCGT GTGAATACCG GATTCAGTGT 660

TCCGACACCA CCCAGAAACT TGTGTGTGTG ATTCANC 697

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TTCGACTGAG CACCACAAAT ACTGGGTATC TCCCCAGATA GTTCATTGCG GTACAAGCAA 60

TATAGGTGCA GAAAGTCAAC CTGCTGCACC CTATTGGATA ATTATATATG GCCTTCAATA 120

AAGTTTGCGG TTGTCGACGT TGGCTATATC AGCCATTTCC AATGCATAGT TCTTTGGTTT 180

AGCACCATCA AGTTATAGAT TTGGGAATAG TTTCAACTGG TATTGATTGA ATTGGGTTTC 240

ATCGTCGATG ATTAATACTA TTTGTAAAGA CTTTATTGTT GATTTCTTAT TATACCACAA 300

ACCCAAACTG GTCTAGGTCA TCATTTGGTG TTGATAACGG GCTCTGATAA TTTCTGCTCT 360

TCTGCTATAC TGGGGATTAT GAAGAATATT AAGGCTGAGT GTATTGAGGT AGTGTTCTTT 420

GAACCGACCA TTCATGACAA TATATTCTTC AATTCGTGAG TGATCCAGCA ACTGGTTGAA 480

TTTAAAACAC TGAGTGATGT TATCCTCTGT AATCGTATGG TTGCTGAACT AGTTGATGTA 540

GCCGATAAGG TTTATACCAG ATATCTTTTG GGGGGATTAG ATAACGTAGC CGCGGATAGC 600

AAACGAGATA GTTGAATTTT ATTACCGTAA TTTCTTCCAT TGAGAAAAGC TTATTTTTCT 660

TGGTGGTATT CGCAGTTATG TATCTTCCAT AAAGACTTGG GAATATCTTG CTTGAAARGC 720

TATCTGGAGA TAGCCTTAGT TATTTGATAA ATATTTCAAA TAGGAGGAGC CGTATGGCTG 780

TCATTTATAC CCTCACTAAA TCGTCACTTG TCAAGTCTGG TGGTCAATTA CATTGGAATA 840

TTGATTCGCC ATCAGAACAA CAGCCACAAA AGATCGTCAA TGGTCGGGTT GCGCTTCGGG 900

GATGGTTACT GGCAGATGTG GAAAAAGATC TCCGTGTTGC GGTTAAAATT GAACATTTGA 960

CATACAGTTT TCCCTTCAAT ATAAAGCGCC CTGATGTTAT TTCAGCTATA CTGAAACAGC 1020

CACCTGAAAA ACATCAAAGA CTTCATTGTG GATTTGATAT CAATGTCCCA TTTTCTACTA 1080

AAATAATTAT TGGCCTTGAG TCTGATGGGT TGATTACCTG GTTGGAAGAG TTATTATTTC 1140

TCCTGCCTGA TAATTGAATT AAGTATCTAT ACCGATAGTA TCGCGATAGA TATATTTTTT 1200

TACAGGATGA TAATTTGAGA ATCTATATAG CCGCTATTAT CAAGGATGAG TATTCAAGTT 1260

TACTTGAATG GATTGCCTAC CATCGAGTAT TAGGTGTTGA TGGGTTTAKT ATTGCAGATA 1320

ATGGCAGTCG TGAWGGTAGC CGAGAATTAC TATTTTCCCT CGCTCGCCTA GGTATTGTGA 1380

CGATGTTCGA ACAACCGACT TTGGTGAATC AAAAGCCACA ATTACCTGCA TATGAACATA 1440

TTTTACGTAG CTGTCCCAGA GACATAGACC TGCTTGCATT TATAGATGCT GATGAATTTT 1500

TATTGCCACT TGAATCGGAT ACCAATTTGT CAGATTTTTT TTCTGAAAAG TTTCAGGATG 1560

AGAGTGTCAG CGCTATTGCA TTGAATTGGG CAAATTTTGG TTCTAGTGGT GAATGGTTTG 1620

CTGAAGAGGG GTTGGTTATT GAACGTTTTA CCTATCGTGC CCCGCAATCC TTTAACGTTC 1680

ATCATAACTT CAAAAGCGTG GTCAAACCCG AACGAGTTAA CCGCTTTCAT AATCCGCATT 1740

ATGCTGATTT GCGTTATGGT CGATATATCG ATGCATTGGG TCGTGATTTG ATTCTGCACC 1800

CGAGGCATGG TAATGGGGTT AGTGCTGAAG TGACTTGGAG CGGTGTCAGG GTAAATCACT 1860

ATGCAGTTAA ATCACTTGAG GAATTCTTGT TGGGCAAGCA TCTGCGTGGT AGTGCTGCCA 1920

CTGCTAATCG AGTAAAGCAT AAAGATTATT TCAAGGCACA TGATCGTAAT GATGAAGAGT 1980

GCCTTCTCGC TGCCGCATTC TCAGAACAAG TAAAAGCTGA AATGGAACGA TTAAGTGTGA 2040

AGTTGACTGA GTTACCAGCA GTTGAACCTA TTCCTACTGG TTCTTGGTTC AAAAAAAAAA 2100

TGAAGAAATG GATGGTTTGA ATATATTGAG CAAGCACTTT GGTATTTATT TCTGCTCTTA 2160

TCTACAGGTC TGCTAATAAG GATCTGTATC CCCCAGGTGT TACCTTGGAC TGTAAGTTAT 2220

ATTATGTGTA GCTATTGCGA TTGGCAGCCT CTGACATTGC CAGACTCGTT TTCTCTTCAT 2280

TCTGGTTGGC TTCTGATTCG GGGGCGCGTG TTGACGACTC AAACTCGAGG TGAAACTCGT 2340

CTGCGCTGGC AATGCGGACA AGGAATATGG CATGAACAGA AGTTGCCGGT CACTCGTCGA 2400

GGCACGTTGC TGGAGCTGGT TTATCTACCY TCGGGAGCTA GTCATTKGTC TTTGCTGGCA 2460

AGTAATAAGG GCGCTGAGTG TAATGTTGAA ATTACTCAGC TTTGTTGTGT ATCCCGTGCC 2520

GAGAGTCTCT GGCGTCGATT GCGCCGGGTT GTACCTTTTT ACCGACGCTT AACGAAGTCC 2580

AGACGCAAAA GGTTAGGCCT TTCATGGCAT TTGTGGCTCA CGGACTTGCA GCAAGCTTAC 2640

CAACTTGTCA GCAGAGTTCG CGATGATAAA CCACTCAATA GCTATGATGA GTGGCTAGCA 2700

GACTTCGACA CCCTTGAACC CGCCGAATAC AAGCTGATTA AGCGCCAGCT GGCTCGCTGG 2760

GGCACATTAC CACGTTTCTG TTTGCATCTT GTTGGCGTTG GGGATGAACA GAGCCGCCAC 2820

AAGACCCTGG AGAGTATTCA GGCACTCTGT TATCCGGCAA GCAATATAAA CCTGCAGGAG 2880

CATGGTGCAT ATCCAGAAAT CTCCAGTCAG TCAAGCGGCG AATGGCAGTG GGTGTTGCCT 2940

GTAGGGGCAG TGGTTTCGCC AAGCGCCTTA TTTTGGGTTG CCCACCAGTT ACGCCAGAAT 3000

CCTGATTGTT TATGGATATA CGGTGATCAC GATCTGCTTG ACGAGAGAGG TGAACGTCAC 3060

TCTCCCAACT TCAAACCTGA TTGGAATGAA ACGCTGCTAC AGAGCCAAAA CTATATTAGT 3120

TGGTGTGGTT TGTGGCGTGA ACAAGGTGCT GGCCGTGTTC CCTTTGATGC GGCGACATGC 3180

CATCAGTGGT GGCTACAGTT GGCAAAGATG TGTGAACCGA AACAGATAGT CCATATTCCA 3240

TCATTGATGA TGCATTTGCC TGCAAGAGCG TTGATTTCGG ATGATTTTGA GTCGCTGAAA 3300

NSDOCID <WO 9822575A2 I >

GATAAAGAAG ATTTACTGCC ATCAGGAGTG AGCATTGAGG CAGCACCTCA TGGTGTATGT 3360

CGTTGGCGCT GGCCGTTGCC AGCGCAATTG CCATTGGTTT CAGTGATTAT CCCTACTAGA 3420

AATGGTATTG CTCATTTACG CCCTTGTATC GAAAGCCTGA TACAAAAGAC GCAATATGCC 3480

AATATGGAAG TCATAGTGAT GGATAATCAG AGCGATGAGG AGGAGACGCT TGCTTATCTT 3540

GCTCATATCG AACAGGTTTA TGGCGTTAGG GTGATTTCTT ATGATCAACC GTTTAACTAT 3600

TCAGCCATCA ACAATCTGGC AGTGAGAAAC GCACATGGAG ATATGATATG TTTGCTGAAT 3660

AATGATACTC AGGTAATCAG TATTGACTGG CTGGATGAAA TGGTTTCTCA TTTATTACGC 3720

CCCGGCGTGG GTGTGGTAGG AGCAAAGCTG TATTACGGAA ATGGCTTGAT TCAGCATGCA 3780

GGCGATGCTG TCGGCCCTGG CGGTTGTGCA GATCATTTTC ATAATGGTTT GTCAGCTAAC 3840

GATCCTGGAT ATCAGCGTAG GGCTGTTAGT GCCCAAGAGC TGTCAGCTGT GACTGCAGCT 3900

TGTTTATTGA CTCATAAAGA GTTATATCTG GCGCTCGGAG GACTTGATGA AACGAATTTG 3960

CCGATAGCTT TTAATGACGT RGATTATTGT CTCAGAGTTC GAGATGCTGG CTGGAGAGTA 4020

ATCTGGACTC CCTTCGCTGA ATTGTATCAT CATGAGTCTA TTTCCCGTGG TAAAGATGTA 4080

TCAAAACAAC AGCAGATACG AGCGAAATCT GAGTTGCGCT ATATGAAAAA ACGATGGGCA 4140

TGTGCACTTA AACACGATCC AGCCTACAAC CAAAATTTGA GTTATGAACG TCCTGATTTC 4200

TCTTTAAGTA GAGCTCCTAA TATAGTATTG CCATGGATGA ATTAATTCGC AGGAAACTAT 4260

TTAAGCCTTA TCGTAAATTA AATAAACAGA GTTATAGAAG TCCGCAAAGC TCTGAGATTA 4320

ACTTTGAACG ATTGTTTATA TTACATGAGG GAAAATCACC TACATTAGCC TATTTTGAAT 4380

CGGCTATTAT AAGTCGGTTT CCTGATGCAG AATGTCATTT TATCGACACA TTAGCATCCA 4440

CTGATATATT TATTCCTAGA GGATCTGCCC TTGTCGTCAT TAGATTCATC TCCCCAAAAT 4500

GGCAACAGCA CATAGAAAGA TATAACGACA GGTTTTCTCG AATTGTTTAT TTTATGGATG 4560

ACGACCTGTT TGACCCGACT GCACTATCTA CGTTACCAAA AGAGTATCGT ACCAAGATAA 4620

TAAGGAGGTC GGCGGCTCAG CATCGATGGA TTACGCAATA TTGTGATAAC ATTTGGGTTT 4680

CAACTGCCTA TTTGGCTAAT AAATATGCAC ATCTTAACCC GGAGATTGTT TCTGCTAAAC 4740

CGTCACTGGC ACTCATTGAA ACACATCGAT CAGTAAAAAT CGCTTATCAT GGCTCAAGTT 4800

CTCATCGGGA AGAAAAATAT TGGTTGAGAC AAATC 4835

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1746 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GAAAAATGNC ATAACCGCAT TCCATCAAGC CCGTNAATAT CCCGGACTTT CATTTATTTC 60

TGAGGCGTAC AGGGAAGCAA TAACTGCTGG TCAGATATTG CTGTCTCCGG TACATTTACC 120

TGACACTGTA TTTTTCCATC CCAGTTTACC GACAGGGTTT CCCCCGGCGT CACGCCACTC 180

AGCCAGGCAA GGCCTTCGTC GGCCACCATG CCCAGTTCCC GGCCTTTTTC ACTGGTTACA 240

CTGGCACCAA ACGGGGGCTG AGAGCCATCA GCAAGACGCA GTATTGCAAA CAGACGTTTC 300

CCTTTAAGCA CGCTGAATTT CCGGTAACCA ATGGCACCTT CTGTCAGCGC CGATTCCACA 360

ACAGAACGGG TTGCTTCCAC ATCATCCGGT AAGCGCTTCA GGTCAACAGA GGTTGTATTC 420

CGGTAATAAC TGCTGATGTC AGTCACCACG CCCGTTCCCC AGCGATTTGT CACCACCTGC 480

CCGCCATCAA CCGGTACACC TCCCACACCA TCCGTGTCAA CAAGAAGACG TGTTCCACCG 540

GACATTCCCC CTGCATGTAA CGCCGCACCT TTTCCGGTAA TTGTTGCCCC ACCGGAAGCA 600

CTGACGCCGA AAGACGTATA TCCTTTCTGC AGGGATGCAA TATTCGCGGA CAAATTTGCC 660

AGCGGACTAC GATGACTGTA ATAGGCATTA ATCTGACGTT GCGATGTCAG TCCACCGCCA 720

CTGTTAAGGC CGGCGTTCAG GCTGTAGCTG TCCAGACCGT CATTGAACGT GWCAGTGTAG 780

CCGGCCATAT TCACATAACG GTCATTACTC ATACTGCCAC TGTAGCTCGC TGTCCCCGTC 840

CCCCAGCGGC ACGGATATAC GCAGGTAAGC AGAATCNTTA TCACGCCCCA GATATTTAGA 900

CCTTGAGGCT GACAATCCAA CCGCCACACC CTGCAGTCCG AAAACATTAA AGTAGCGGTT 960

GACGCTCACC GTATAATAGT CCGTTTTCCG TATGTCCCAG TATGTCTGAC GGCTGTACTG 1020

CAGGTTAAAA GAGGTGTTCC AGTCCGCCAC GTTTTTATTC AGCGTAACGG TATACATCTC 1080

TTTTTCCCGA CTGCTGTAAT CATTACGGTA GCGGGCGTTC AGGTACTGCT CCATGGTCAT 1140

ATAGTTTCGC TCTGAGAAAC GATACCCGGC GAACGTAATG TCGGCATCCG CATTATCAAA 1200

CCGTTTGGAG TAGCTCAGAC GCCAGGATTT TCCCTGAAAC GTTCTCTCTC CCTCAATACG 1260

GGCTACTGAC TGCGTGATAT CAGCGGAAAG GGTCCCCGGC ACACCCAGGT CCCAGCCGGC 1320

ACCGGCTGCC AGTGCATTAT AATCACCGGC AAGCACAGCC CCGCCATACA GCGACCACTG 1380

GTTACTGAGC CCCCAGGATG CCTCTCCGGT CGCAAATACA GGCCCTTCGG TCTCATGCCC 1440

GTATCCACGG GAACGACCGG AGACAAGTTT GTACCGGACC TGTCCCGGAC GCGTCAGATA 1500

AGGAACCGAG GCCGTATCGA CCTGAAAGTT TTCTTCCGTC CGTTCTGTTC AATAACCTCA 1560

ACATCAAGAC GTCCGCGAAC TGAACTGTCC AGGTCCTGAA TACTGAATGG CCCTGCGGGG 1620

ACCATCGAGT CGTACAGCAC CCGTCCCTGC TGCGACACCA CAACACGGGC ATTAGTCTCC 1680

GCAATCCCGG TAATCTGCGG TGCATAAGCC TTCGCATTCT TGGGGCGGCA CATTCCGGGT 1740

CAGCGN 1746

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

ENSDOCID <WO 9822575A2 I >

(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TGTACTGAGC ACGGCGAATA TCCAGTGTTC AAATTCCACT TTGCAGCGAC TGCATGATGT 60

CTGCGGCGCG GTAACAATCA GGGCATTACT GTGTTTGCTG GCGGCGATGG AGACAACCTC 120

ACGCCCGCTA CCGACCGTGC CTTCCGCCTC TTCTTTAGCC GCCGTGAGCG TGCCGCTGAC 180

CTGCTTCAGC ACATCGACCA GATCTTCGGC TTTGCTGTAT TTGAGATAGA AAACCTGGCT 240

GTTGCCGCTG CGTTCCATTT CTGAGTCCAG CCGACGGATC AGGCGGCGCA TTTTCTCCCG 300

CGTGGCCGGG TCACCACTGA CAATCACACT GTTGGTGCGT TCGTCGGCGA CAATTTGAGA 360

TTTCAGCGTC GCAGGCTGGT TCTCGCCGCT GTTTTTAGTC AGGCTTTCCA GCACGCGGGC 420

GATTTCCGAA GCAGAGGCGT TATCCAGCGG GATCACCTCT TCAGTGCGAT TANCCGCGTG 480

ATCCACACGC TGGATCACTT CCGTCAGCCG CTCCACGACG GAGGCGCGCC CGGTGAGCAT 540

AATCACGTTG GAGGGATCGT AATTAACAAC GTTGCCTGAG CCTGCGCTGT CGATCATCTG 600

GCGCAGAATC GGTGCCAGTT CGCGTACCGA AACATNACGT ACCGGCACGA CTTTGGTGAC 660

CATTTCATCG CCCGCGTATT GTCGCTGCCT TCACCAACCA GCGGCAGGGC TCGACTTTCG 720

CGG 723

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TAGAGGATCC CCGGCGTTGC GATCGTCACG AACATAGACC CACAKCCGTC CGGTAGGTAT 60

TTACCCTGAC CCGGYTCCAG TACATTTACC GGCGTGTCAT CGGCATGCAC TTTACCCGGC 120

ATCAGCACAT AGTGCTTCAG TTCATCATAC AGCGGGCGAA GCTGCTCTCC CATGATGTCA 180

ACCCAGCGCC CCATCGTATT GCAGTGCAGC TCCACGCCCT GGCGGGCATA GATTTCCGAC 240

TGACGGTACA GCGGCAGATG CTCGGCGAAC TTAGCCATGA TTATGCGGGC CAGCAGAGCC 300

GGACTGGCGT AACTGCGCTC GATGGGTTTT GGTGGCTGCG GAGCCTGAAC TATACAGTCG 360

CACCGGCTGC AGGCCAGTTT TGGGCGAACC GTTTCGATTA CCCTGAACGC GGTGTTGATG 420

ATATCCAGTT GTTCAGAGAT GCTTTCTCCC AGCGGTTTCA GTTTGCCGCT GCAGACGGGG 480

CATTCGGTTT CTGCCGGGGA GATAACCTGC CTGTCACGGG GAAGTGTTGC CGGAAGTGCT 540

TTGCGGACGG GAGAGTCTGA TGTTTTCGGC GCTGTCTCTC CGGCCATTGA GGTGAGTTGC 600

AACTGCGCCT CACCAAGCCT GTTCTGGAGC TCGGTTATAC GCGTTTCTGC CCGTGCGATC 660

TTCTTTTCTA TCTTCTCGCG GCTTTTCTCG CTGCTGCGAC CGAACAACAT TCTCTGTAGT 720

TTAGCGACCA GCGCTCTGAG TGAGCTGATC TCGCGGCATA GCCGGTTATT TCACCAGACA 780

GACGGACGAT AACAGCCTGC TGTGCGATCA GCAGGGCCTT CAGTTGCTCG ATGTCGTCGG 840

GGAGTGTGTT GTTCATTCCC CTGTTTTATC ACGGGTTATA TCCGGATGCC AGGCCGTTCT 900

GTCCGTTTGG GATGTTGCCA CGCGATCCCC TCCAGTAGCA TGGATAACTG AGCTGGCGTC 960

AGGTGCACTT TCCCTTCCCG GGTTACCGGC CAGACGAAGC GGCCCCGTTC CAGGCGTTTG 1020

GCGAACAGGC ATAACCCGTC ACGATCGGCC CACAGTATTT TCACCATTTT GCCACTGCGG 1080

CCCCGGAAGA CGAAGATATG CCCGGAGAAC GGGTCATCTT TCAGCGTGTT CTGCACCTTC 1140

GAAGCCAGGC CGTTGAAGCC ACAACGCATA TCTGTGATGC CAGCGATGAT CCAGATTCTG 1200

GTACCGGTTG GCAGCGTTAT CATCGGGTAC CTCCTTTTAT TTCGCGGATT AGCGCCCGTA 1260

ACATTTCCGG AGTGAGAGGG TCAAACAGTT TTACCACACC TGATTTAAGA TGCAGCTCGC 1320

ACCGTGGGAC GTTTCCGGGA TCACACTCAG GGCACTCATC AGGCTTGTTA CGCCAGAAGG 1380

GATTTGTAAC TGGTCTGGTC GGCTCTGGCG TATCAGTCAG AGCCACCGGG ACAGGCATGC 1440

ATTCCTGTAT GTCATCATCG CTCAGTAAGC CGTCCTCGTA CTGGCTTTTC CATTTAAACA 1500

GCAGGTTATC ATTGATACCG TGCTCTCTGG CGATCCGGGC AACAACAGCA CCGGGCTGTA 1560

ATGCCTGCTT AGCCAGACGG ACCTTAAATT CACGGCTGTA GCTGGCTCGC CGTTCTTTTC 1620

GCCATGTGCC TTCGCTGATT TGAGGCTCTG TTAATTCCTT CTTTCTGTTG GCATAAAGGA 1680

TGGCGTCAAG CTGAGCTAAT GAAACTGAAT CGGGCAATGG CCATGCGATA CCGGATGCAA 1740

TAAATCGCTG AAAAAGCGTA TGTATTGTGG AATGACTGAG ACCTAGACGC TGAGCGATGG 1800

CCCGGATGGT CAGTTTATCT TCAAATCTTA AACGCAGAGC ATCAGGCAAA TAAGAACGGA 1860

AGCAGGGAAT ATCTTTTTTT GTCTGGGAAT TCATCGTTCG TGTCCATCTA TATAGATGGG 1920

CGCGATTGTT GCCAGACAGG ACAATTTTCA CAAGACGTCG CAGATGGGGC GCTTACCAGA 1980

AATGCGCGGG TACGACAGTG ACTCGTCAAA TCTCAGTTGT AGCACACGCG GGATCAATTC 2040

CGGATTGTCT GCCAGTACCG CCTTTCGTGC ATTCATCTTA AATGTCCCTT TACTGCAAAA 2100

ATGGACATTA GTATCGGAAA CAGGAAAGGG AGGCGAAAGA CGGTTTAAAT GAGACGGTTA 2160

CCATTGTGTC GGGCTGTGTA CGTTCTCCCC GGACAGACAG CCTCAGTTCG TAGAATCTAT 2220

AAATTACTGC TACTGATGCT GCCGGGGAAA GGCGTAACGA AAAAACAGCC TCCGTTACCG 2280

GACAGCAAGG AGGCTGAATG GAGTTTACAG GATTTGCTTT TTTATAATGT CTGGCCATGC 2340

AGTAAAACCG GACAGGTTTT ATTATCATGT GAGGTATTCT GACATAAAAT CCTGGATTTT 2400

INSDOCID <WO__9822575A2 I >

TATTTTGTGA CGAATGCTGC AAAATTGCAT CTGCACTCTG ATGTAGCTTT TATCTGTTTC 2460

AGTGAAGCAT GCCCACAAAC TGAGTTATTA AGTTGTGGAA GAACAGTTTT GTCCCGCCTG 2520

CATCTCTCCT TTCAAAAACC AGTATGTCGC CATGCC 2556

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CAGTTAGTGT TAAAAAATNT CCTCTGCTNC AGAAATTACA CCCACCAATA TACAATNATT 60

AATAAATTTT CGGTTGGGTT AGGTAATGGC TGGGATTCGA TAATATCTCT TGATGGGGTT 120

GAACAGAGTG AGGAAATATT ACGCTGGTAC ACAGCCGGCT CAAAAACAGT AAAGATTGAG 180

AGCAGGTTGT ATGGTGAAGA GGGAAAGAGA AAACCCGGGG AGCTATCTGG TTCTATGACT 240

ATGGTTCTGA GTTTCCCCTG AATAAGATGA TGGATTATCT GACTGGCTGT TCATCAGTCG 300

GATAATGATG AAAACTGATG AGCAACAGGT TGTGCGGGCA ATGTGCAGGA TCCGTCACCA 360

AAGGGTGGAA GTTGCGGGCG ACTCAGATAA ACGGGTTACA TGAGCTATTT CTGGAGTTTG 420

ACGAAGCCGT CTGGAAGGGA GAAGAGGCGA TTCCATTGAT GTCTCTGGAA AACATCTGTC 480

AGTCGTGCTG CTGGAAATAT TGATAGAGCA ATGGGAATGG TTATCCAACA TTGATGAACA 540

TATTGTATAT TTACAGAAAT TTTTAAAAAC AGGACTCAGC AGGTTAAATC GTGTAAAAAT 600

TACTCATGAA TACCATTATG GGCTTACAAA GCGATGTGGT TAAGCAGATC TTATTCAGGC 660

CTGTGCAGCG TAGGATTACA ATAGGATCGA ATAACGCCAT ACAGGGGAAT GGGAGATAGG 720

CTGATTCATC CTGTGGCTAT AACCAGGAGC ATATCGGGAA TCMANTATGT TACCCCAGAT 780

GGAACACCAT 790

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCGGCCGCAG TACTGGATCT CTTTGCGGCA TGACGATGAG GGGGAGAGAA ATAAACTTAA 60

CCCAGTCATG GCAGATGAAG AACAGGCTTA CGTAAAAGGG TTATATGAAG GGATTATGCT 120

GATTGGTAAT ATAATCAATA AGCCTGAAGA AGCTAAAGCG TTAATCAAGG CAACTGAAAA 180

NSDOCID <WO__9822575A2 I_>

TGGCTGCAGA ATGGTGAGTA ACCGGCTGCA ACTTCTACCC GAAGAGCAGC GTGTTCGTGC 240

CTATATGGCG AATCCTGAAT TGACCACTTA TGGTTCCGGA AAATATACAG GATTAATGAT 300

GAAACATGcT GGCGCAGTAA ACGTCGCCGC TTCCACCATT AAAGGTTTCA AACAGGTCTC 360

GATAGAGCAA GTCATTGAAT GGAATCCTCA GGTAATTTTT GTGCAGAATC GTTATCCTGC 420

TGTAGTGAAT GAAATACAGT CAAGCCCACA GTGGCAGGTA ATAGATGCTG TCAAAAATCA 480

TCGTGTTTAT TTGATGCCAG AGTATGCCAA AGCATGGGGC TATCCGATGC CCGAGGCTAT 540

GGGGaTTGGG GAATTGTGGA TGGCGAAAAA GCTGTATCCA GAAAAATTCA ATGATGTTGA 600

TATGCATAAA ATAGTCAATG ACTGGTATAG AACGTTTTAC CGTACTGATT ATCAGGGTGA 660

AGACTAATGC GAGTGCTTGC TGCGGGCAGT TTACGCCGGG TATGGAAATC ACTTGTGTCA 720

GAGTATCAGG CCGATAATAT ACAGTGTGAT TTTGGACCAG CGGGTATATT AAGGGAGCGT 780

ATTGAGGTGG GTGAGGCATG CGATTTTTTT GCATCAGCCA ATATGACTCA CCCACAGATA 840

TTAATGtCCG CAGGanGAGC ATTGTGTATT AAACCTTTTG CCAGAAATCG TTTGTGTTTG 900

TATGTTCGGG CGAATAAATT CAATGAGAAT GACGACTGGT ATTCTTTATT AAATCGGGAA 960

ACATTGCGAA TCGGAACATC AACGGCGGGA TGTGATCCAT CTGGTGATTA CACTCAGGAA 1020

CTGTTTGAAA ATATGGGGAG TGTCGGTGAA AAAATAAGGC AACGGGCTGT AGCATTAGTT 1080

GGGcgGGAGG CATTCGTTTC CTCTTCCAGG AAATGCGATA gcAGCGCAGT GGTTAATTGA 1140

AAATGATTAT ACTGATCTGT TCATCGGTTA TGCCAATTAC GCTCCTGGCT TGCAATCAAT 1200

TGATTCAGTA AAAGTTATAG AAATACCGGA ACCTTATAAT CCGATTGCTA TCTATGGATT 1260

TGCCTGTCTG ACCGATAATG CCCTGCCACT TGCCGACTTT ITAGTTTCAC CTGTTGCCAG 1320

AGGTATACTT GAACAGCATG GGTTTATGCC TCCAGGTACG TTATAGCCCC CTGTCTTACA 1380

GCTGtCTCTT gATCAGATCT CCTGATCAAG AGACTTCATC ACCAGGTAAC CCTCAACCAT 1440

ATCCTGCATA TCCTGAAGTC TGAACCAGCC ATCCCACATA ACTACCCAAC CGGGGCGGCC 1500

TGTGCGTTTG CTGTCATGCC ATCGCCCCAG TTTCGCCAGT TTCAGACAGG CCCATTTCAG 1560

TGTCGGCGTC TGTGACGGAA GCGGTTTTCC TTCCAGCTTA ACCCACAGCA GTTTCCACTC 1620

TGTCGGCGTC AGTATTTTCT TACAGCTGTC ATTTTGTGTT TCTTCACTGA TACCTCCCTG 1680

CCGCAGGCCa GCACCCGTAC CGCGATAAAC GCCTTGATAA CCACCATGCG CTCAAGGTTA 1740

TCCCGGGTCT GCATTCGCAG CGATTCCACA CATGTACCAC CACTTTTCCA CGCCTTGTGG 1800

TATTCCTCTA TCAGCCaGCG TCGCTCGTAA TGGCTGACGA TACGTCGCGC ATCGGCGGCA 1860

CTCGCCACTT TTTCTGACGT CAGCAGATGC CAGCAGGCAC CGTCCTCTGC CTGCTCCCGG 1920

CAACAGACAT ACGTGAGCGG GAGCGCCTGG CCGCTGTTGT CGGGATTTTT TATGCTGAcT 1980

TCGTTGTAAC TGATGAACAT CCGGGCCtgg CGGGCTGCCC GCCCGCCTTT TTGCATCACA 2040

TTCAGCGTGT GGCTTCCCGC GGTTGCCAGG ACTTCCGGCA GTTCGAAGAG CTTGCCGGGT 2100

NSDOCID <WO 9822575A2 I >

GCTTCTTCCA GCCGGCGATT CTGTGCAGCA CGCACCACGA AGCGCTGTCC GTGGCTGACT 2160

TTATAATGCA GGTAATGCTA GATATCCGCT TCCCGGTCAC AGACAGTGAT TACCCGTTTC 2220

TGTATCTCCC CCAGCCGTTC GGCCATACGC TCCGAAGCCT GCTGCCAGCG GTAACTTTCT 2280

TTTTCTTCAT AGGGACGTTC TTTTCGCTGG TGCTTAACAC CATAGGTgtC CGTGACCCGA 2340

CTCCAGCGCT GCTGTTCGAT AAGACCGACT GGCAGGGCGC TGTCGGGGGC GTACATCAGG 2400

ACAGAGTGAG CCAGCAGCCC GCGCGTCTTC GGGTTAGTGG TGGTATTCCC CAGGTCATCA 2460

GATGCCGTAC TGTGGCTGAA GTTAATGGTG GTGGTGTCTT CCAGTGCGAG GAGCAGCGGA 2520

TGAGCCTCAC ATGCCCTTAC AGTGGCGGTA AATCCGGCTT CGGCAATGGC TTGCGGGGAC 2580

ACAGACGGGT TACGTATCAG GCGGTACGCA CCTTCAACCT GAGCAGTGGA CTGGGATGAT 2640

TTCACAATAG AAAGACCTGC ATGCTGAGCG AGAGAAGAGG TCAGTGACAC AAGGCGTCGT 2700

GTACGACGCG GATCACCGAG ACGGGCATGT CCAAACTGCT CGTTAGCCCA TGAATAACAA 2760

TCAGAAAGTA CCATAACAGA GTCGAATAAA ATGAAATATA AGAGAAGATC AACGGGTGAA 2820

GAAAAAGTTC AAAAAATGGC TACCGGGGAG GAAGGAAAGT ACCGGATGGA AAGAGCCCCC 2880

CTAAAGCAGA CTGACAGACA TCACAAATCC CCGGGGGGGA CTTGTGTATA AGAGACAGGT 2940

CTTACAGGGG GAGCGTCCGT CTTTTTATCA ACATCAGGCA ATGACATAAC ATTATGAACA 3000

AGCTCACAAG TCTGATGGTT AAATTTTATA ATGCTCCTTA CTAAGACCGT ATTTTTTCAT 3060

TCTGAGATAG AGTTTTTTCC GCGGGATTTG TAAATATTCA GCAACCTCAT TGATACGCCC 3120

CTGATGGATA TTAAGTGCCT CTGTGATTAT CTGTCGCTCA GCGTCCTCCA CTCGTCTGTC 3180

AAGCGGTGTC GGGGTTCCGA CGTGCATCAA CGGATTTGCT GTTTCTGCCA GCGGTAATAC 3240

TCCTACAGTA AATAGTTCTG CTGCATTGGC CAGCTCTCGC ACATTATTTG GCCACATGCG 3300

GCGCATCATC TCTTTGAGCA TCTCTTTTCC CACTTCCGGA ACAGGATGGT TAAGCCGTTG 3360

ACATGCTTTA CAAAGGTAAT GGCGAAACAG TGGTTCAATA TCATCGGGGC GTTGAGTTAA 3420

TGGCAGGCAA GCGATTTGTG TCATTGCAAA GCAGTAATAG AGCTCCGCGA TGATATGGTT 3480

GCTGGCGGCC AGCTCGACCA GCGAAGTGTC TCCAATACCA ATCAGGCGAA AAGGTCGGTG 3540

TTCCTGGCTT TGTAACTGAA CCAGATGGTA CTGCTGTTCA CGCGTCAGGT GTTCAGGATG 3600

GCTGAGCACT AATGTTCCCC CCTGAGCCAG CGCAATGAAA TCATTAAGCT GTGGTGCATT 3660

GTCTGGTGTC AGCTCGCGGT AGATAAATTC GCCTTGTGCA TTACGTCCAA ATTGGTGCAG 3720

ATAACGTGCA CCGGTCATCC GTCCTGTGCC TGGGGCACCG TAGAGCCAGA CGGCAATATC 3780

TGTTTCAGAC AACTGCTGTA AACGTCGCCG ATACTGATTT ATCCATTCAC TTCTCCCTAT 3840

CAACTCCACC TGCAACGTCT GTTGGCAATA CTGACGACGC GCAATGATTG ATTGACGCTG 3900

GCGTAgcGCC TCTTCAACCA GAGAAAGCAA TTTGCCGGGA TCAACCGGTT TTTGCAAAAA 3960

ATCCCACGCG CCTTTTTTTA CCGCATCAAC TGCCATTGGC ACGTCGCCGT GCCCGGTaAT 4020

NSDOCID <WO_ 9822575A2_I_>

AAGCAGAATG GGGATCTGTT GATCATCCTG GTGAAATAAC ATCATCAAAT CGATACCAGA 4080

GCAGCCAGGC ATACACACAT CACTTAGCAC AATACCTGGC CAGTCTGGTT GTATCCACGT 4140

CTGCGCCTCA AAAGGATTGT TACAGGCAAA AACCCGATAG CCTGACTGTT CAAGTAACTG 4200

TGTGTAGGCG TCCAGCACGT CAGCATCATC ATCAATCAGC AGAATCGAAT ATTCACTACT 4260

TAGCATCTTC CACATCCGTT AGTCTGAATT GCAGTACCAC ACAGGCATTC CTGGTCATCG 4320

TTGATGCCAG CCGTAATTCA CCTTTCATTT GCTCCATCAA CGACACACAA ATTGAAAGAC 4380

CAATACCCAG TCCTACTTCT TTACTGGTGG TAAACGGCTT CAATAACGAA GGCAACAATG 4440

CCTCAGGCCA GCCCGGGCCA TTATCGCCAA TGAATACGTT CAGCGTTTTA CCCTGCATTT 4500

GCCAGTTAAC GGTAATGACA GCGCCTTGCC CACAAACATC AAGCGCATTC GCCAGTACGT 4560

TAACCAGTAC CTGCTGGGTT CTGACCTCAT CGCCTGAAAC TGTGGCTGTA CCTTGCGGCA 4620

GAACAAGCGT AGCTTGCAAA GGGCGATGAC GCATGGCCAG AAGTTCCCAG GCCGCACTGA 4680

ACATCTGTGC TAAATCAACG GAATGGAGTG ATATTTCCAG TTCGGCGCGC CGGGTAAACT 4740

GCCGTAGTGA ACGGATAATG GCGTCAATGC GACCAATCAC CCcTTCGGCT TTACCAAGCA 4800

TCATGCTGGC CTGTTCTGTC TGGGTCTGTT cAaTGcCTGC GGGCTGTAAA CAGATACATC 4860

GACAGCGCAT TTAGCGGCTG ATTGATCTCG TGGGCCAGCG TGGTCATCGT TTGCCCGACT 4920

AnCCGCaGct TCGCTGTCTG AATCAGTTCG TCCTGGGTGG CTCGCAGATC GGCTTCTATC 4980

ACCTTTCGAT CGGTAATTTC TTGTTCAAGT TGCTGTTTTT GCACATTGAG CTGCCCGAGA 5040

GTATGGCGTA ATAATCCTGC AATTCTCCCC AGTTCATCAT TCCCATAAAC AGGAATAGCC 5100

GTTTCCGTGC CTCCCAGACC AATTTGCACA ACGGCCTGAT TCAGTAGGGT AAAGCGTTTC 5160

ACCAACCGTG AGCGGATAAA ATAATGGTTG AATACCCATG CCAGCAGTAA CGCCAGTGcT 5220

GTCGCCACCA GGATCAGCCC ACCgctAACG CGAACAATTT GTTCCATTCG TTGATTAAAC 5280

ATCTGCATTT GTTGATGAGT ACTGCcAAGT GCGCTTCCAG TAACGTTCTG AAGCGACCCA 5340

GTGTCGCTTc CCTGGTGCGA CTGGCATCCT CTAAGGCTTT TTGGGCGGTG ACATATTCAC 5400

GCATCGTAGC CGGCATTTTG TTTTTTACGA TTCCCATATC CAGCAATTCA TCGATAGTCT 5460

GCCTCAGGGT AATGGTGCCA GGCCAGTCAT CCAGCATACG TATATTTTCA TCTGCCGTTT 5520

TTTTCAGATT TTCAAAATAA CGGAGATGAG TTTCCACCTG TGTGTCGTCA TCACGTCCTG 5580

ATTTGAGTTC ATTGAGTCTG TCACGCAGAT CGTCAACAAT CTGATTTTCA ATGCGTGCCA 5640

GGGTATAAAC CTGCTGCTGT TCATTTTGCA CTTCACGAGA TCGCTTCAGG TATTGCGCCG 5700

TATCGCCyTG TCGGGAGGCG ATTTGATCCA GCAGCGTTCC CTGCTGCCAG GTGAAATCCT 5760

GCACTAAAGA ATTAAGCTCG GTAGTAAAAT CATCGTGTAA CCAGTCAATC CTCGCTGATA 5820

GCTCACTCAC CTTTTCCCGT AGTAAAAACA TGTTGTAAAG CGCACGATCC AACTCGGATA 5880

ACAGTGATCG ACTGTCCTGC AAAAtGACCG TCAGTTGTTG GCGTTCCCGG GATGACAGCC 5940

3NSDOCID <WO__9822575A2 I >

CCCGACTAAG CCGTTCTATG GTGTCGAGAT GCTGAATAAT CTGGGTACGA AGTTGCAATC 6000

GCACCGTGGT GTTGGGAGCC TGCAAAAATT CATTTAGCTG GTCTACCACC AGATTCAGGT 6060

TCCCTTCAAT AAGGAAAGCA GAGTGAATAC GGGGAAAATA CTCATCCAGC GAGTAACGAA 6120

TTTGTGAGCT TTGTTCATGC CATGAATACA GACTGACACT ACTGACAATC AGGGTCAGAA 6180

GTGCCCCCAT CAGAAATGCG CAACGTAAGC TGGTACTGAT ACTGACCTGT CTTAAACGCT 6240

GCCACAGCGT TATGTTTTTC ATTTCAGCTC TTCCAGTTTT TTTATCGCCA GGCGCTGGTT 6300

ATTCAGAAAC CAGAGTTGCC ATTCCATCAT TTGCTGCTCG GCAAAGCTTT TGTTATCGAA 6360

CTGTGCCAGC CAGACGGGAT CTTCACTGCT GGCCGCTGCA ACGGGCACTT GTGTTAACAG 6420

TGCACGTATT TCTGGTAATG GTTTCTTCAG ACGTGCCTCG GTACTGTGCA GCGCTCGCCA 6480

GGCATCTTTT AGCTGTGCTA ACCGAAAGCT AATTGCCGTA TCAAACAAGC GCTGCACCAG 6540

ACGCTGACGT TTCAGGATAA GGTGATAATT CAGCGGGGGT TGATTCATCA GGAGCTGTTG 6600

TTGCGTTGCC CGCGGATTGT CTGCGGCAAC TGGTGTCACC GGATATTTTC CTGTATTGGC 6660

ATCGGCCAGA ATACGCTGTC CTTTCGGACT TAACAGGTAG TGAATAAAGC GACGGGCTGC 6720

ATCGACGTGT GGGCTTTTCC TGAGAATTGC AACGTAGGTG GGGGATACCG CAGACCGGGG 6780

GAAATAGGTA AAAGAGAGAT GGGGGTCATT TAACAGTAAA TTAGCATAGT TATCGATAAC 6840

GGGGCCGGCA ACGCCGAGTC CGCTTTTTAT TTTAnTCGcT ACGCCAAAAC TGCGGGAGGA 6900

GATTGTCACC AGGTTTCCTG CACTTGTCAG CAACGTTTCC CATCCTTTCA CCCAGCCTTT 6960

TTGCTGTAGT AATGACTCAA CCATTAAATG GTTAGTATCT GAACGCGACG GACTACTCAT 7020

CAATAAAGCG TCCTGATAGA TCGGCAAAGC AAGATCGTCC CAGTCAGCAG GGGCAGGAAG 7080

GTGTTTTACA GAAAGCGCCG GACGATTAAT GAGCAGACCA AAACCTGATA TTGCTACTGC 7140

AACGGAGGTT GCACGGATCG ACTCCGGCAC CAGGTTTTGG CTTTCTGCGG GTGCATCATC 7200

AAACGGGGCC AGTTTCTGGT GCTCCTGAAG GTGCTGGAGC AGCATTGGTG ATGAAGTCAG 7260

GATAAGATCG ACGTTTTCTA CGTTGGCCGT ATCAAGCAAC TGTTCCAGTG AGGCACTGGT 7320

GCGGTTAAGC GTACGGATCA TTACCGACTC AGGCTCTGTT TGCCAGCGCT GTATTATCCA 7380

CGCGGTAGCT CCGGGTGAGA ATGTGGTGGC CATCACCAGT TCATTTCGTT GAGCCcTGAC 7440

GGCCCCGGCG TCCATCAGCA ACAGTAAAAG AATCATGGTT TTGATGCCGA TTTCGCACCA 7500

GCTAAAAAAT CGGTTTGTGA TCCAGGTCAT AAATATTAAT ACACCGCAAA AATCGCATTG 7560

AGACAAAAAT TACCCGTTTC AGACATTCGT CTGATAACAC GTCTGCTCAA AGAGACCGTT 7620

AATATATTAA TCAGAGATTA CCCGATAATC AGCATGAGAT TTGTTAATAT CCGCACATGC 7680

TAACAACAAA CCAGATAAAG CATAAATCTA CCTTGTCTAT GCATCAATAA AATGGGTCAA 7740

AAACAGGCTT TGATTTTATT ATTTTGTGTC AATTGTGACA CATTTTTTCA GTTTGATGTT 7800

TCATYTCAAT TATATGACTC TCATTGTCAG AATACTCCTG ATGTTCATAT CAATATAAAA 7860

TACAGGTGAA GACATGTTAT CAATATTTAA AACGGGGCAA TCGGCGGATA GTGTTCCGGT 7920

GGAGAAAATT CAGGTGACAT ATCGTCGCTA TCGTATGCAG GCGTTACTTA GCGTATTTCT 7980

GGGGTATCTT GCATACTATA TCGTGCGTAA TAATTTCACT TTATCGACGC CTTATCTTAA 8040

AGAGCAATTA GATCTCAGCG CCACACAAAT TGGCGTACTG AGTAGCTGTA TGCNTATCGC 8100

CTATGGTATC AGCAAAGGAG TGATGAGTAG CCTTGCCGAT AAAGCCAGTC CGAAAGTCTT 8160

TATGGCGTGT GGGCTGGTGT TATGTGCCAT CGTTAACGTT GGCCTGGGAT TCAGCACTGC 8220

ATTCTGGATT TTTGCGGCAT TGGTTGTTCT GAATGGTCTT TTCCAGGGAA TGGGCGTTGG 8280

TCCTTCTTTC ATCACTATTC CTAACTGGTT CCCTCGCCGG GAGCGTGGTC GGGTTGGTGC 8340

TTTCTGGAAT ATCTCTCATA ACGTCGGTGG TGGTATTGTT GCCCCTATTG TTGGTGCCGC 8400

TTTTGCCCTA CTCGGCAGCG AGCACTGGCA AGGTGCGAGC TATATCGTTC CGGCCTGCGT 8460

GGCTATCGTT TTTGCGGTAA TTGTGCTGAT TCTCGGTAAA GGTTCCCCAC GTCAGGAAGG 8520

TCTACCCTCT CTGGAAGAGA TGATGCCGGA AGAAAAAGTC GTCCTGAATA CCCGACAGAC 8580

GGTAAAAGCA CCAGAAAACA TGAGCGCCTT TCAGATTTTC TGCACTTATG TATTACGCAA 8640

CAAAAATGCC TGGTATGTCT CACTGGTTGA CGTATTTGTA TACATGGTGC GCTTCGGGAT 8700

GATTAGCTGG TTGCCTATTT ACCTGCTGAC GGTGAAACAT TTTTCTAAAG AACAAATGAG 8760

CGTCGCGTTT TTATTTTTTG AATGGGCCGC AATCCCTTCC ACGCTACTTG CCGGTTGGTT 8820

GTCAGACAAA CTGTTTAAAG GGCGTCGTAT GCCATTGGCG ATGATTTGTA TGGCGCTGAT 8880

TTTCATTTGC CTGATTGGCT ACTGGAAAAG TGAATCGCTG TTTATGGTGA CAATTTTTGC 8940

TGCCATTGTT GGTTGCCTGA TTTACGTTCC ACAATTTCTG GCTTCCGTTC AGACTATGGA 9000

GATCGTTCCC AGCTTTGCTG TTGGTTCTGC AGTAGGCTTA CGCGGTTTTA TGAGCTATAT 9060

CTTCGGTGCG TCTCTGGGCA CCAGCCTGTT TGGTATTATG GTCGATCATA TTGGCTGGCA 9120

TGGCGGATTT TATCTTCTTG GCTGCGGTAT TATTTGTTGC ATCATTTTCT GCTGGTTATC 9180

ACATCGTGGT GCAATTGAAC TTGAACGTCA CAGAGCCGCA TATATAAAAG AACACTGATT 9240

ACCTTCCCCA GGGCCGTCTC CCTGGGGAGT GGAGTATATT ATGATTTATA AGATATCTGG 9300

AAATCAGAGA TTAATATGGA AATTTTATAA GACTGATTAC AATAAATGGA GATGGTATTG 9360

TCATGAGAAA AATGGATATC TTTTGTCTCA ATCAGATAAC GCATATAATT CGCAATTGTT 9420

ATGCATTGAA AATGCTAAAA AACAGGGATA CTCAGACGAA TCGGTCTTGC CACTTTTTCT 9480

ACATATTTCC TATATTCAGG AAAAAGGCTG GAAATGGTAT CAATGTTATG ATTGTGGATA 9540

TATTGTAAAA GAAACCTCTG TTTTTTTTTC GACATACCAG GAATGTGTCA ATGATGTTAA 9600

AAGGAATATA CTAGCATCTA TGTGTAGTGG TTGTAGTGGC ACAGTAAATT TGGCCACCTG 9660

ATTAAAGGTG ATATTCTCAC CACAACATAA AACAACAAGA AAACAAAGCG TACCTTCTCT 9720

CCTGAGTTTA AACTGGAATG CGCCCAACTT ATCGTTGATA ACGGTTACTC ATACCGGGAA 9780

INSDOCID <WO___9822575A2 I >

GCTACTGAAG CTATGAATGT TGGTTTCTCT ACTCTGGAGG CATGGGTACG TCAGCTCAGA 9840

CGGGAACGTC AGGAGATCAC GCCTTCTGCT GCAGCACCAC TCACATCAGA GCAGCAACGT 9900

ATTCGTGAGC TGGAAAAGCA GGTGCGTCGT CTGGAGGAAC AAAATACGAT ATTAAAAAAG 9960

GCTACCGCGC TCTTGATATC AGACTTCCTG AATAGTTACC GATAATCGGG AAACTCAGAG 10020

CGCATTATCC GGTGGTCACA CTCTGCCATG TGTTCAGGGT TCATCGCAGT AGCTACAGAT 10080

ACTGGAAAAA CCGTCCTGAA AAACCAGATG GGCTGTATTA CACAGTCAGG TACTTGAGCT 10140

ACATGGCATC AGCCACGGTT CGGCCGGAGC AAGAAGCATC GCCACAATGG CAACCCGGAG 10200

AGGCTACCAG ATGGGACGCT GGCTTGCTGG CAGGCTCATG AAAGAGCTGG GGTTGGTCAG 10260

CTGTCAGCAG CCGACTCACC GGTATAAACG TGGTGGTCAT GAACATGTTG CTATCCCTAA 10320

AAGCAACAGC AAACAGCGAC CACTGGGGAG CCCTGCATTG CGGGATTGTA TTGTTCAGCG 10380

GGCCATGCTG ATGGCGATGG GGCCGAGGAG AGTGATTTTC ATACGCTCTC ATATGGTTTT 10440

CGACTTGTGC GAAATGTCCA CTACGCGATC CGCACGGTGA AACTGCAACT CACCGACTTC 10500

AGGGGAAACT CGGGGCCGCT GGGTAATCTC ACATAAAAGT TCTTCGGTGT CATAAACAAC 10560

GAGAGTATTT GATTCCTTTA TGGTGGCCTG GTGCAGAGCT GCCCTTTCCC AGGACCTCCA 10620

TATAATTTTT GTAGCGGCAG TCAGTGGCAC ACTCAGTTAA CTACTTTCAC TTCAGTGACT 10680

TTGAATGAGT CAGGGCTGCC GTTAAAGGTG TTAATGAAGG CTTGTATTTT CCACTTCTGG 10740

CCTGGTTCAA GATTGGATGC TGTGTCGATT GTTTGACCGA TAACGACTCC ATCTTTTAAN 10800

AGATTAAATT TTACATAAGC ATTTTTGACA ACAGAGTTTG ATTTATTTNC AGCATAACCC 10860

ACAATTGCCT TCGTCCCACT TGGGGTGTTT TCCACATGAA GGTTAG 10906

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ATGGTTATTT TTATTTCCTG CACCTTGCTT CATTTGAAAT AAAAACATAT GCATACGACG 60

CTGCCATTGA GCAGAAAAAT ACAGGAATTA ATGTTATGAG TTAACCATAA TACCTGTGTT 120

ATGAATATCT GACATAAACA AGAACAATTC ATATCTTCTG TATTCAGCAG AATAATAAAA 180

GTTCGTCTGC CATTCTCAAA CTTATTCTTC GGAATACGTT GTTTCATGAA AGAAGGGGCC 240

GGAATAAAAG CTGGTCACCG TAATGCTAAT ATTAATGCAG ACTACCGCCT TCTGGAATTA 300

ACAGTCATCA ACCAGCACAA ACCATTAGCA ATCAAACAAA TTTTAATTAA CAAAATTTTA 360

GCTAATACAA TTACTGCATT AACCACTCTG CAGTTTGCCT TCTCAATAAG TTACAGATGC 420

VSDOCID <WO_ 9822575A2 I >

CAAACAATAC TCTTTTATAT GTTATAACAT AACACAAACA ATAAATAAAG AACAGACGGC 480

ACTCCATTTC TCCACGTAAG TGAGCCATCA GAATCGCTTA TGAATGTGTA CGGCAGACGT 540

ATACTCGTGT TTTACTGCAG CAACCGGAGC AAAAGTTGCA CTTCCACAGC CTGGGTTAAG 600

TTTTTCATGC TTGTGGGCTC GTCGTCCCTC CATTTCCACC GCGGGCAAAC AAGGCCATCT 660

TTTGTCTGGC CACACAGCAG ATGGAGAGTC GAATTATGCT GTCTGACGAC ACCGGGAACA 720

AATATGCCAT GCCTTCGCAC AATGAACCCG GGCATCATCG TTTTATCTTT ATAATCGAGA 780

CAGGTATGAG GGAAAGTCGG ATGATAAGCA GATAGTGAGT GAGGCGCTGG AACATGGCGC 840

TCTGGCAAGA GAAGTGTCAC AGGTTACCTG ATGATATGGG GCAACCTGAT ATCTACTTAC 900

TTTTTTGCCT ACTCTCTTAC TTCATGCCAG CAGCGAGGGT ATCGACATTG TGTTTGAACG 960

CTGCCGTGTA GGTAGCAGCG AGGCCGCTAC TGTCGGTAAG TGCTTCCGGA TAAAGCTCTC 1020

CTCCCGCTTG TGCACCACTG GCATTGGCGA TTTGTTTCAC CAAACGGGGA TCTGTCTGGT 1080

TTTCGATAAA GTACAATTTT ACGTGCTCTC TCTTAATTTG ATTAATCAGT TTCGCCACAT 1140

TTTTACTGCT AGCTTCCGAC TCAGTGGAGT ACCCCACTGG CGACAGAAAG CGAACCCCGT 1200

AGGCGGCAGC GAAATACCCA AACGCATCAT GACTGGTCAG TACTTTACGT TTTTCTCTTG 1260

GAATAGCAGC AAACGTCTGC GTGGCGTAAT TATCCAGTTG CTTCAACTGC TGGATATAGC 1320

TGTCACCCTG TTTTCGATAA TCGCTGGCGT GCTCCGGGTC TGCTTTGCTC AGGCCATTGA 1380

CAATGTTGTG AGCATAGACA ATACCGTTTT TCATGCTGTT CCAGGCGTGC GGATCAGTGA 1440

TGGTGATCCC ATCCTCTTTC ATTTTCAGTG TATCTATTCC GTTAGACGCG GTAATTACCT 1500

CACCTCTGTA GCCAGAGGCT TTCACCAGAC GGTCCAGCCA TCGCTCCAGT CCCAATCCAT 1560

TGACAAAGAC AACATCCGCC TGTGCCAGCG TTTTGCTGTC TTTCGKCGAC GGTTCAAATT 1620

CATGTGGATC ACCATCCGGT TGCACCAGAT CAGTGACATG AACGTATGGG CCGCCAATCT 1680

GGCTGACCAT ATCGCCCAGT ACCGAGAAAC TTGCCACCAC ATTCAACTCT TTTGCAATCA 1740

CCAGTGGGCT CACTAGTAGG CTGGACAGTG CCACAACCAA AATGGACCGT TTCATCTTTC 1800

CTCCTTCATC TCGTTGCTAT GTGTAAAAAC ACTTCTTGTC AGCGACATCT GCATAACATG 1860

CCGCCATTAG AGCCAAACAG AACTGAAAAG CAGAAAAACA GAGTGCTCGT GAGGATGACT 1920

GCAGGACCTG CAGGCAAATC AGCGTAATAA GACCAGATCA GTCCAACCAG ACTGGCGCAG 1980

GTACCAATAC CCACTGCAGC TAACAACATG ATGGACAGAC GTTGACTCCA GAAACGCGCG 2040

CTGGCAGCCG GTAACATCAT AATACCGACT GTCATCAGGG TGCCAAGTAG CTGGAAACCT 2100

GCCACCAGAT TGAGTACCAC CATTGACAAA AACAGGCAGT GGATCAGCGC CCGCGACCGA 2160

CGTGACAGAA CTTTCAGGAA AGTGACATCA AACGACTCAA TCACCAGCAC CCGGTAGATC 2220

AACGCCAGTA CCAGAACCGA ACCGGAACTA ATTATGCCGA TAGTGATCAG AGCATTGGCG 2280

TCAATAGCCA GAATGGAACC GAACAGCACA TGCAGCAGGT CGACACTGGA GCCACGCAAA 2340

3NSDOCID: <WO 9822575A2 I_>

GAGACCAGGG TGACGCCAAG TGCCAGCGAG CCGAGGTAAA ACCCGGCGAA ACTGGCGTCT 2400

TCTCTCAATC CAGTGCGGCG GCTGACCACA CCAGACAACA TCGCCACAGA CAGCCCGGCA 2460

ATGAAGCCAC CGACTCCCAT CGCAACCAGC GACATGCCCG ATACCAGGTA GCCAATTGCT 2520

ACTCCCGGCA ACACCGCATG GGACAGTGCA TCACCGATCA GGCTCATACG GCGCAGTAGC 2580

AAAAAACAGC CAAGTGGCGC GGCGCTCAGG GTCAACGCCA GACATCCGAC CAGCGCCCGA 2640

CGCATAAAAC CGAAATCGCC AAATGGCTCG CACAACAGGT GCAGTAACAT CATGGCAGCA 2700

GCCCCTGCTG CGGTGGCGTG GCTGCAGCCG TGAGGGAATG GAGTATATCG GCACTTCTCC 2760

CCCATCGGTG GCCTTCCGCA CTGAGCATCA GTACATGAGG AAAGTATTTT TCTACCTGTT 2820

CCATGTCATG CAACACCGCA AGAATTGTAC GTCCTTCCAG ATGTAGCTGC CGAATAACAA 2880

CCAGCAGAGT ACGGATAGTC TGAATATCAA TGCCAGTAAA TGGTTCATCC AGCAGAATAA 2940

CCGACGGCTG CATCACCAGC AGTCGTGCGA ACAGTACGCG CTGTAACTGA CCACCGGAAA 3000

GTGTGCCGAT GTGCATCGGC GAAAATTCTG TCATACCGAC GGTATCCAGC GCTTCGATAG 3060

CTTTTTTTCG CCATAGACCG GAAATACGAC CGAACATCCC GCTGTGTGGA ATACATCCCA 3120

TCAGCACCAG ATCGTTAACA CTCAGTGGAA ACTGGCGATC AAATTCAGTC AATTGGGGCA 3180

AATAACCTAA CTGGCGTTGC CCCTGCGGTG CCATGCAGAA GCAACCACCC AGAGGTGGCA 3240

GCAGACCGGC CAACGTTTTA AGCAAGGTGG ATTTACCTGT GCCATTCGCT CCGATAATGG 3300

CAGTCAGTGA ACCGGTGTCA AAACATCCAT TCAGCGTACC CAGCGGGTGC TGTCCCGAAT 3360

AGCCAAATGC CAGTGAATGT AATGCGATCA TGTCAGTACC ACCGCCCAGG AAATAAGAGT 3420

CCATAACAGT ACCAGCAGCA CACCGACGAT ACCCAGTCGG GCTATTGCGG AAAAAGCATA 3480

AAGACTGACC ACAGTATCCC CCATCAAAAT TGTTATAGTA TAACATTATT GCTTTATGGG 3540

TGCCGATGAT AGGTAAGAAA ATGTGTCATG GCTTCTGCAG CGTAAGCATA CAGCGAGAGC 3600

AGTATTGACA GGGATGCGTT AGTCATTTAG CAGTGTAATG CGCTAAATAG NTGCGCGGAA 3660

TAGTAGATCA CTTTGAGGGT ACTCAGCCCG GATTGTGCGC TCTGATCAAT CGCCAAATCA 3720

AAACAAATCA CCAACCGAAC TGAGCAATGC CGATCATAGC ACCAATTTCC CGTGACGAAC 3780

GACACCGGAT GCAGAAAGCC ATCCATAAAA CACACGATAA AAATTATGCC CGCAGACTGA 3840

CTGCCATGCT GATGCTGCAC CGGGGCAACC GTATCAACGA CGTTGCCAGA ACGCTCTGCT 3900

GCACCCGTTC ATCTGTTGGA TGCTGGATTA ACTGGTTACT AAAATCATTC CCTGCCGGGC 3960

GTGCCCATCG CTGGCCATTT GAGCATATCT GCACACTGTT ACGTGAGCTG GTAAAACATT 4020

CTCCCGACGA CTTTGGCTAC AAGCGTTCAC GCTGGAATAC AGAACTGCTG GCAATAAAAA 4080

ATCAATGAGA TAACCGGTTG CCTGTTAAAT GCCGGAACCG TTCGCCGTTG GTTGCCGTCT 4140

GCGGGGATAG TGTGGCTAAG GGTTGTGCCA GCTCTGCGTA TCCGTGACCC GCATAAAGAT 4200

GAAAAGATGG CAGCAATCCA TAAGGCACTG GACGAATGCA GCACAGAGCA TCCGGTCTTT 4260

TATGAAGATG AAGTGGATAT CCATCTTAAT CCCAAAATGG GCGCTGACTG GCAGTTACGC 4320

GGACAGCAAA ACGGGTGATC ACGCCGGGAC AGAATGAAAA ATATTATCTG GCCGGAGCGC 4380

TGCACTGCAG GACAGGTTAA AGTCAGCCAT GTGGGCGGCA ACCGCAAAAA TTCGGTGCTG 4440

TTCATCAGTC TGCTGAAGCG GCTTAAAGCG ACATACTGTC GAGCGAAAAC CAGCACGCTG 4500

ATCGTGGGCA ACAACATTAT CCACAAAAGC CGGGAAACAC AGCGCTGGCT GAAGGAGAAC 4560

CCGAAGTTCA GGGGCATTTA TCAGCCGGTT TACTCGCCAT GSGTGAACCA TGTTGAACGG 4620

CTATGGCAGA CACTTCTCGA CACAATAATG TGTAATCATC AGTACCGCTC AATGTGGCAA 4680

CTGGTGAAAA AAGTTCGCCA TTTTATGGAA ACCGTCAGCC CATTCCCGTA GGGGAACATG 4740

GGCTGGCAAA AGTGTAGCGG TATTAGGAGC AGCTATTTAG GAGAACAGCT CGCTGACCCG 4800

GTTGACTATG ACTCAAGCCC ATGACGAAGA TAGCTTTCTG GATCAACATC GTTCAGTCTG 4860

CACGTCCCAA TCCAGCCACC AGCCACCAGC CACCAGCCAC CAGCCACCAG CCACCAGCCA 4920

CCAGCCAGGC TACAGTGCCA TCCCGACCTC CCCACGTAAA CCCAGGGACA GGCTAAAGGC 4980

AGAAAATGGG GAAGGCAGTA TGACTCTCCG TGACACAGAT GCGGGTACCT GATGGGAGTG 5040

AGATCATCTT CCCCTCCCGG TCAGTTCCCG GATCAACACC GTGAGCAGCT CTGGCGAAGG 5100

TTTTTCCAGC GTCATTTTAC CGTAACGAAA TTCAACCTTA CAGGAACTGG CACAGACTGT 5160

GCACTAAGTG GCAGTGGATA AAAGCGGAGT AAGAGCCGCC ACAGGCTCTT TCTGCTCATC 5220

AGGCATTATC TCAACAGGTA ATAATTCAAC GCCAGCGCCA GAAGAGGTTG TTACCGGAAG 5280

ACGCCGCGCC CCCCTTCGTT CAGCCAGAGC CTGAGCCATT TGACCAGGAG GTTATCATTG 5340

ATATCGTGTT CCTGGTCAAT ACGGGCAACA GAGGTGCCTA CGACGTTTTT TCAGTTCGGT 5400

TATCTATTGA CTTAACTCTT TGGCCAGTAA TGCTGCAGCC CCCGTGCCAT GAATAAACGA 5460

GTGGTCGCAG ACCACGCAAC ATGCAACATC ATTCAGATCC CCCGCTAATA TTACAGGTAA 5520

TTCAGAATCA GCAATACTTT TCCCGACCAT TAAAAGTTCT GAGTCACGAT CAGTTGACTC 5580

ATCACTTTCA GTCGGGCTCG GTGGAACAGG ATGAAGACAA TGTAATCTTA TTCTCAAACC 5640

TTCTGGCATA TGAACTATCA TATTCATGGA GGGAATTTCC TTGTCCACTA AATACTGTAT 5700

TTCTGCATCA CTTAAAATCA TCCAGGAATA TACATGCATG CCATATAAAT TTTCTTTCGG 5760

GCATTTCAGG GAGTATGGAA ACACTTCATC CAGAGGTGAT AGTTTCTGTT CCCACCATAA 5820

GTTTGTTTCA AGAAGAACAA GTATATCAGG TTTTTCTTTA TTTATAAGTT CAAGAATGGG 5880

TATATATTTT TTATTGGTCA TAAGAACATT GAATACCAGT ATACTTAAAC CCAGAAATCC 5940

ATCAGAGTCC TTTATTTCCT TTACCTGCTT CTTGCCAATT ACTGTATAAG GAATTATCCA 6000

TACCAACTGG TAAGCGACAC AAATTAAACT TATTATCCCA ACAAACAACT CTGTAAATAA 6060

GTCAAGAAAA ACAACAGACA GAAAAACATT CAAAGTACAC AGCAAAAGTA TCTGTAGTCG 6120

GGGAAAATCC CATCCCCCGA CAACCCATGA TGTATTACCG GAAACAGGGA TAAAAGTTAT 6180

3NSDOCID: <WO 9822575A2 I >

GACTGCCAGA AGGATAGCAG TAAAAATAAA AACACAAGTT ATCACAAATC GCTCCTTGTT 6240

CTGAACCGGA ACACAAAACT GTCATATACG TTTCAAAAGT AAAAATACAC TGCTGCCACA 6300

AGATTTACAG CGTAACCGGA CAGCATATCC TGATTACGGA CAATCCATGA AACCGCCTCA 6360

CCAGAAGCGT CCATCACATC CGTTTTTTCC CTGTTTTATA TTCCCCGAAA CATTTTATTT 6420

TCAGGAATCT CCGGGCCTTT ATCCCGCATC ATTGCAAAAT GGCATCTGAA TCGATCATGA 6480

TTTGGCATCC ATCTCCGATC ACAGTTTGGC ATCACAATCG ATCACGATTT GGCATGCTTC 6540

CGATCATTGA TTAGCATCCT GCCAGTCACT CCGGGAATTA ACTCTTTTCG CCACAGTCTT 6600

CATTGCCGTG TTTAAACCAA TGGAGACGGC AATGTCCAAA AAGAGAATAT CCAGGAGCAC 6660

TATGGATACC TGTTTTAAGA TCCTTCAGCT CAAGTTCGAC CAGAAGCTGG CTAACCGTTG 6720

TATCGGACTT GCAAAACACC AATGGGGATT GATCTCTATT TTGCGACACA GACGCATTAT 6780

CAATACATCG ATGGTGCGAT CAAATACCTC AGTGGTCTCA CCGTGGATCA AATCCAGCAA 6840

TTGCTCACAG ATTAAGACTC GTCGGGAGTT TTGAGCCAAC ACCAGCAGTA ACCCATATTC 6900

ACCTTGAGTG AAATCTACAG GCTGTTGATG AGCATCAACC AGCACGTAAC GGTCCGGGAT 6960

CAAGTGTCCA GCCGTTAAAA AAACCACTCT ACTACCCTGC TCGACCTAAG CCTCGGCGTT 7020

CAGCCGCCTG AACGGGTATG GCAAGGGTGA AAAGAAACAG CATCCCCACA GTACCGACCA 7080

GACGACAGGA TGATGCTGGA ACAGAAAGCA TTCGCACCTC TCTTAGAATT AGACAGTGCG 7140

TACAGGATAC GTAAGACAGG GTGACGGGGC GGCGATAAAC TCTATTTACA AAGCTGAAAA 7200

TTTTCTGACG ATGAAAAACT ATTCAACAAG GTTATCTGAG GCGTTAAAAT AACCAGCTCG 7260

ATTAACGACT AACTTGAGGT GAATATGAAT TTAAAAAATA TAATTTTAAG TACTGTTTTA 7320

TCAATCGCTA GTTGTCATGC CCTGGCTGTA GGTAATTCTC CAAATAGCGC TATCTAACCT 7380

TCATGTGGGR AAACACCCCC AGTGGGGACS AAGGSCAATT GGTGGGGTTA 7430

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGATTATTCT GGCTCAGATT CATTTTTCAT CAGTCGCTTT CCCCTATAAA CCGTAAGGTT 60

CCATAGTGTC GACGCTCTCG CTTAATTCCC ATATCGTCGA TAGTCTTATT AGCCGCTTCT 120

GTCAGGTCAG AAAAAGTATC ACGCTTCTTT GGGAGTTCAA GTCAGATTTC TCGCCGTCGG 180

GCGATGCGCT CAAAATGTTT GTCTGTATGG GGTCGCTTCA TCACGTCAAG CCATCGCGCT 240

GCCGCTCTCC GCCAGAGTAC AAGCTCTTCC AGTTGTTCTG CTTTTTATCT TATCTGTGGC 300

GATGCAGTAT CCTCCTCCGT TTGTGTAAAT CGTTGAGTGG TGAATCACGC AAAGGGGCTT 360

CTTTTTTCTG ATCTATCCCC ATATTCTTTA GCGTTCTGGT CGCAGCATCT CTGATGTCGC 420

AGACACTGAA CCTTTGTATT TTCCATGATC TTGTGGAGTT TTCGATACAT CTGCTCCGAT 480

GCTGGGTTAT AAAGATCCGC TCTTTATCAT CCTTGGCTTG TGTAAGCAAT TCTCCCCAAC 540

GTTCTGCTGC ACGCCGCCAT AACTCTCTTC TTTCCAGTTC CTCAGCTTTT TCATCATGTA 600

CCATTCGTGT ATCCCCGTTT ATCCAGTCTG AACCGCACCG GGTTTCCTGG AGAATGTTTT 660

CTCTGTGAAC TCAGGCTGCC AGATCATCGT TTCCGATGGA AGCATAATAA GCTTTTTCTG 720

CTTCTGCCGG ARGAATATGG CCCAGCTTTT CCAGCAATCG TCGATTGTCA TACCAGTCCA 780

CCCACGTTAG TGTGGCCAGC TCCACTTCTG TCCGTTTTTT CCAGCTCTTA CGGTTATTAC 840

CTCCGTTTTG TAAAGACCAT TGATGCTCTC CGCCATTGCG TCGTCATACG AGTCGCCTGT 900

ACTCCCTGTT GATGCCAGTA ATCCGGCTTC CTTAAGCCGT TGCGGACACA TAATGAGAGC 960

CTTTATCGCT GTAATTGTCA ACGACGGATG AAAAGTGATC CACTTATATC TCCACCAACG 1020

GCCCAATATT GATCCACCGT TTTACTCAGG ATTAGCTTCT GCTATAACCC CGGCCTTTCG 1080

TTTCTGTCTG AGTCGATAGC TTTCTCCTTT GATTTGAACG ACATGTGAGT GGTGTAAGAT 1140

ACGGTCCAGC ATCGCTGAGG TCAGTGCTGC ATCACCGGCG AACGTTTGAT CCCACTGCCC 1200

GAACGGCAGA TTGGATGTCA GGATCATTGC GCTCTTTTCG TAACGTTTAG CGATGACCTG 1260

GAAGAACAGC TTTGCTTCTT CCTGACTGAA CGGCAGATAG CCTATTTCAT CAATGATGAG 1320

CAGGCGGGGG GCCATTACTC CACGCTGAAG CGTCGTTTTA TAACGGCCCT GACGTTGTGC 1380

CGTAGATAAC TGAAGTAACA GATCTGCTGC TGTTGTGAAG CGAACTTTGA TACCTGCACG 1440

GACTGCTTCA TAGCCCATCG CTATTGCCAG ATGGGTTTTC CCCACACCTG ATGGCCCCAG 1500

TAATACGATA TTTTCATTAC GTTCTATGAA GCTGAGTGAG CGTAACGACT GGAGTTGCTT 1560

CTGCGGTGCT CCGGTGGCGA ATGTGAAGTC ATACTCTTCG AACGTTTTCA CCGCCGGGAA 1620

GGCTGCCATT CGGGTATACA TCGCCTGTTT ACGTTGATGA CGTGCCAGTT TTTCTTCATG 1680

AAGCAGATGC TCCAGGAAGT CCATATAACT CCATTCCTGG TCTACTGCCT GTTGTGACAG 1740

CGCAGGCGCT GCGCTTATAA GGCTTTCCAG TTGCAACTGC CCGGCGAGCG CCATCAGTCG 1800

TTGATGTTGC AGTTCCATCA TCACGCCACT CCTCTGCAGA ATGAGTCGTA GATGGAGAGT 1860

GGATGATGCA GGGGGTGTTT GTCGAAGTTC ACCAGATTTT CATCAAGATG CACGTCATAC 1920

TCTTTTTTCT CCGGAGCAGT GCCAGCATGG ACTGCTGTCT TCGAGCCAGC GATCGCAGGG 1980

ACGGGCCTGG ATTGTTTCAT GCTTTCGTTG GTTAGCGACA TCGTGCAGCC AGCGCAGACC 2040

GTGGCGGTTG GCTGTTTCAA CATCGACAGT GATCCCCATC GGGCGCAGGC GAGTCATTAG 2100

TGGGATGTAA AAACTGTTAC GGGTGTACTG CACCATCCGT TCCACCTTAC CTTTAGTCTG 2160

TGCCCTGAAG GGGCGACACA GTCGGGGAGA GAAGCCCATC TCCTTGCCGA ACTGCCACAG 2220

INSDOCID <WO 9822575A2 I_>

CGAAGGATGG AACCGGTGCT GACCGGTCTG ATATGCGTCA CGTTGCAGAA CCACAGTTTT 2280

CATATTGTCA TACAACACTT CGCGCGGCAC ACCACCAAAG AAGCGGAACG CATTACGATG 2340

GCAGGTCTCC AGCGTGTCAT AACGCATATT GTCAGTGAAT TCGATGTACA GCATTCGGCT 2400

GTATCCGAGA ACAGCAACGA ACACGTGAAG CGGTGAGCGA CCATTACGCA TAGTGCCCCA 2460

GTCAACCTGC ATCTGTCGTC CGGGTTCAGT TTCGAACCGA ACGGCAGGCT CCTGCTCCTG 2520

AGGAACCGAG AGAGAACGAA TGAATGCCCT GAGAATGGTC ATTCCGCCAC GATATCCCTG 2580

GTCTCTGATC TCGCGAGCGA TTACCGTTGC CGGGATTTTG TAAGGATGAG CATCGGCGAT 2640

GCGTTGACGA ATATAATCCC GGTATTCATC CAGGAGTGAA GCAACAGCAG GTCGCGGCGT 2700

ATATTTTGGC GGCTCAGATT TTGCCTGCAA ATAACGTTTA ACCGTATTGC GGGAGATCCC 2760

CAGTTCTCTG GCAATCGCCC GGCTACTCAT TCCCTGCTTG TGCAGGATTT TAATTTCCAT 2820

AACTGTCTCA AAAGTGACCA TAAACTCTCC TGAATCAGGA GAGCAGATTA CCCCCTGGAT 2880

CTGATTTCAG GCGTTGGGTG TGGATCACTA TTGCACCGTT CGTGACAGTA ATGGATTGTG 2940

TCAGACGGAC GACGGGCCCA TAACGCCTGC TCCAGTGCAT CCAGCACGAA TGTTGTTTCC 3000

ATGGACGATG AGACTCGCCA TCCCACGATG TATCCGGCGA ACACATCAAT GATGAACGCC 3060

ACATAAACAA AGCCCCGCCA TGTGCTTATC CCGGTAAAAT CAGCTACCCA CAACTGGTCC 3120

GGGCGTTCTG CGATGAACTG ACGGTTTACA CCGTTGCATG CGGCAACAGC TTTCCGGCTG 3180

ATTGTCATGC GAACCTTTTG CAAACCCCAT ATATTTCAGA CGATACCGTT CAACGGTAGT 3240

GAACCCACCA TCACCGCTCC CGGTATCCCG CTCATGCTGG TATACCCAGA CATGCAGGGG 3300

TTCCAGCGTA CAGCCAATCT TTGGGGCAAT GGAACAAATT GACGCCCACT ACGAGTCATA 3360

CGACTTTCCA GAACAATACG GAGCGCCCGC TGACGGACCA CCAAAGAGCC GCCATTATTC 3420

TTATTACCTT TAACTAATAA TGCCAATTCA GACCCAAACA CGGCATCATT CGCTTCAGCC 3480

TCTGCGCCAT TAATTAATGC CAGGACTTGG TCAAGAAAGC GTTGCGCTTC GTTTACATCT 3540

GTTGCTTGTC GCAGGTAATA AGGTATTCGT TCAACAAACT CGGAACGTGA TAAAGGCTGA 3600

TGCTCCAGCA AAACCTCAAG CATTGCGGGC CGCAACAAAC GACGCTCAGC ATCAACATTG 3660

GGAAACTTAA CCTCAATGGC ATATGTGGCA AAATACTTAA GTTGCTCCTT AAGCCCCAAA 3720

TTAGGCATAA GAGAATCAAT TGAGCCAGAC GCCACTGCAG CGCTTGATTC AATTGTTTCT 3780

ACATACTCGT AGGAAGGTAC AACAACATCT GGAGCCAATG TTTTAAGCTC ATGGAGTTGA 3840

CGGATAATCG GGGATAGAAC CTCATCAGGA TTACTGAACC AATCAGTGGA CCAAATACGG 3900

CTAATTCTCC ACCCCAAACG CTCCAAAACC TCTTGACGCA AACGATCACG GGCAGATTTA 3960

GCTGAATGAT AAGCCGCACC ATCGCACTCT ATACCCATTA AGTAACAACC CGGATCTTCT 4020

ACCGACAGAT CAATAAAGAA TCCTGCAACC CCACCTGAGG TTCACACTCA AACCCAGCGT 4080

GATTGAGTGC TTCCATTATA GCAACCTCAA AGTCACTATC CGGAGCCCTG CCCGTATACG 4140

NSDOCID <WO 9822575A2 I_>

TCGTGAGGGA ATCTAATTTG CCACTTTCGG CAAACTGTAA AAAACCTTTC AACGAAATAA 4200

CACCAAATTT ACTGGTTTCA CTCGTCAATA CATCTTCAGA ACGCATTGAA CTAAACACAT 4260

GCATCCGTTT CTTTGATCGA GTTAAAAGCA CATTCAAGCG GCGCCAGCMA ACATCGGAAT 4320

TGACAGGCCC AAAGCGTTAA TAAACCTTTC CACCATGCTC AGAAGGTCCA CAGGTAAAGG 4380

AAATAAAGAT TACATCACGC TCATCACCTT GAACGTTCTC AAGTTTTTTC ACAAAAAGTG 4440

GCTCTTCCAT GGCATATAAG CCATCAATTG CATCGTTAAA TTCAGTGCGA TTTCGGCGCA 4500

ATTCATCAAT AGCGCGCTCA ATCTGATCGC GTTGCCTGGA ACTCATGGCC ACTACCCCAA 4560

GAGATTCATC CAGCCGGTGT TGCGCATGAT GAAGTACAGC CTCAGCAACT GCTTGGGCTT 4620

CTTCAATATT GTGTTGATTA GAGCAACGAC CTTTTGATAC ATAAGTAAAT TTGATTCCAT 4680

ACTCTGGAGA CTCAGCATTT GGAGAAGGGA ATATCACCAA ATCACTGTTA TAAAAATGGC 4740

GGTTAGAGTA TGCAATTAAC TTTTCGTGTC GTGAACGATA GTGCCAATGC AAACGTCTCA 4800

TAGGAAACAG TGGCAAAGCA GCATCCAAAA TGCCGTCAGT ATCACTTAAA GCCGCGACAT 4860

CATCGTCATC TTCTCCGGCG GAACTTCGAT CTGAAGTGGC ACACTGAATT TGGCCACCTG 4920

AACAGAGGTG ATATGCTCAC CTCAGAACAA CACAGGTGCT CCAATGAAAA AAAGGAATTT 4980

CAGCGCAGAG TTTAAACGCG AATCCGCTCA ACTGGTTGTT GACCAGAACT ACACGGTGGC 5040

AGATGCCGCC AAAGCTATGG ATATCGGCCT TTCCACAATG ACAAGATGGG TCAAACAACT 5100

GCGTGATGAG CGTCAGGGCA AAACACCAAA AGCCTCTCCG ATAACACCAG AACAAATCGA 5160

AATACGTGAG CTGAGGAAAA AGCTACAACG CATTGAAATG GAGAATGAAA TATTAAAAAA 5220

GGCTACCGCG CTCTTGATGT CAGACTCCCT GAACAGTTCT CGATAATCGG GAAACTCAGA 5280

GCGCATTATC CTGTGGTCAC ACTCTGCCAT GTGTTCGGGG TTCATCGCAG CAGCTACAGA 5340

TACTGGAAAA ACCGTCCTGA AAAACCAGAC GGCAGACGGG CTGTATTACG CAGTCAGGTA 5400

CTTGAGTTGC ATAACATCAG CCATGGTTCT GCCGGGGCAA GAAGCATCGC CACAATGGCA 5460

ACCCGGAGAG GCTACCAGAT GGGGCGCTGG CTTGCCGGCA GGCTCATGAA AGAACTGGGA 5520

CTGGTCAGTT GCCAGCAGCC TGCGCACCGT TATAAACGAG GTGGTCGTGA ACATGTCACT 5580

ATCCCGAATC ACCTTGGGCG GCAGTTCGCA GTGACAGAGC CAAATCAGGT ATGGTGCGGC 5640

GACGTGACGT ACATCTGGAC GGGGAAACGT TGGGCATACC TTGCCGTTGT TCTCGACCTG 5700

TTTGCAAGGA AACCGGTAGG TTGGGCAATG TCGTTCTCTC CGGACAGCAG ACTGACCATC 5760

AAAGCGCTGA AAATGGCCTA GGAAATCCGC AGTAAACCAG CCGGGGTAAT GTTCCACAGC 5820

GATAGTAATA ATGCCGGTAT CAGTTTTTAT CATCACTCTG TTTGCTGTTT AACCAGACTG 5880

GTGTGATTAC TGATGCAGTG AAGACCTTCC CGCATCCTGA CTCACACAGC GATCGACCCT 5940

TTGTGTCCTG CCCTGGACCT GTCGGTTGCC GGAAGCGCCT TCATGCGAGG CGTCTCCTCA 6000

CCGATGCGCG TGACTCAAGA AGGGCCTGAC GGTTTGTCTC GTTACTGTCC TGTCCGGGTT 6060

ATCTGTCTGG AGATTCAACT CTGTTTCCTC ACAGGAGCTC TGTTATGGCA GGTAAAGTTA 6120

CGGAAACCGC TGTTGTGGGT GGCGTGGATA CACATAAAGA TCTGCACGTT GCCGCTGTCG 6180

TAGATCAGAA CAATAAAGTT CTGGGGACCC AGTTTTTCTC CACAATACGG CAAGGTTACC 6240

GGCAGATGCT GGCATGGATG ACTTCGTTTG GGGCATTAAA GCGAATTGGT GTTGAGTGTA 6300

CTGGCACCTA TGGATCAGGT CTGCTTCGCT ATTTACAGAA TGCCGGGTTA GACGTTCTTG 6360

AGGTGACTGC GCCAGATCGG ATGGAGCGAC GCAAACGGGG TAAAAGTGAC ACGATTGATG 6420

CTGAATGTGC CGCTCACGCC GCATTCTCCC GAATAAGAAC CGTCACACCC AAAACGCGCA 6480

ATGGCATGAT TGAGTCTCTG CGGGTATTAA AAACTTGCCG AAAAACAGCA ATATCAGCCC 6540

GCAGAGTCGC TCTCCAGATT ATCCATTCCA ATATTATCTC TGCCCCGGAT GAATTACGTG 6600

AACAGCTCAG AAATATGACG CGCATGCAGC TCATCAGGAC TCTGGGATCC TGGCGGCCTG 6660

ATGCCAGTGA ATACCGCAAT G 6681

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TATTCGCGCA TACGCGTTGC ACATGTTCTT TTGGCGAACG ATCATCGGCA ATACAGAGTT 60

CCCAATGGGG ATAGCTTTGA GCCAGGACAG AATCCAGACA GGCACGCAMG TAGATCTCCG 120

CTGGATTATA AACAGGAATC ACAATAGATA TAACTGGAGG GTGAGTCATA CTGGCAAGCA 180

TCAGACTCAC CWCTTCKTTG CCAGGCAACG AAGGTAATTC CACCGTTTCT ATCCATTCCT 240

CATAACCGAC AGAAGACGGG GTAACGCTGA ACGTYTCGTT ATAGAATGCT TGCAGGCGCT 300

CTATTGACAT ATCGCCATTG TSCATCAATA TGGATTTTWT GATTTTTTCT AGCGGCATGT 360

CACGATAGCT TTGGTGTTCT TTTTGAATGC GAGCCAATAG TGCAGACTCG ACTACTTTCA 420

CATCAACAGC CGCTATTTCA AACTGATTAA TTGCAAATTT TGCTGCCTGT TCTAATGGAT 480

CAAATCGTAA TGCACAAGAG GCGATTCCAG ATAGAACAAC GACTGACGCT GACCGCTCGT 540

TTATATGGCA ACGTTACTGT TTCAAACTCA TTGAACCCTT TACCTGTATC CAAATRTAAC 600

TTAGCTAATC CTTGCTTTGG TTGGGCAATT AATAGAGATA TTAAATTGAT ACCATCCCTT 660

GCTAATATTT GAGAGCTGCT CCAAATCAAT AATGAAAAAT GGATCATTTC CCTCTGCAAC 720

CCAACTTTGT GAATTATCTA TATCTATCGA GAGCTGATTT GTTGCCAGAT AGGGCAGCAC 780

AACTGTATTT TGCATTTTAC TCACTGCAGG AGAAACGTCC CATGCTTCGC ATGGTTTCCT 840

ACCAAGTAAC ATCCCATAAC GCTTAAAATG TTCTCTTGCT GACAACCCGG TCTGTTTCAC 900

\SDOCID <WO__9822575A2 I >

ATCCAAATAG TTATGCAGAT ACCAATGTTC ATCAAAGTGA GCTAGCAACT CGTCTTGGTG 960

ATTTTTAACC ATCACTTTTA TTCTCCCTTA TTGACAGGCA GGCAACTGCG CTGCTCAAAC 1020

TTCCCATACA TAATGTAATG AAGCAGCGGA TTAATGCCTC CTTGGGCCAC ATCCGGATAG 1080

GTTTGCAAAT ACCAGCGAGT ATCAAACTGC TCACTAGGGC TATAACCTTT ATCCGCCCCC 1140

ACGCTAATAA AATGCTCAAG AGCTGAGAGC CCAGTGTCTG CAACCTCTGG GTAGCGATGT 1200

TGATACCAGA GTTCATCAAA CAATCCTGAA GCGGCAANTA CTCCGCGGCA CTCTCTGTAG 1260

CTGTTGTTCT GGATGGAGTC TCCTCCTTAA ATGTTCTGCC AAGAGCACGA ACTGGGGCTG 1320

TAATCTTCCA AGAGACGGTT CT 1342

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CGAAGGAAGC AGTNTGCNGC CTGCGCTGGC GGAGTTGCGC CTGTTCCCAC CGATGATGCT 60

GTACATGAAT CCTCCGGCGA ACAGAGCGGT GAACTGGAAA CCATGCTTGA ACAGGCCGCG 120

GTCAATCAGG AACGGGAATT TGATACCCAG GTGGGGCTGG CGTTAGGGCT GTTTGAGCCG 180

GCGCTGGTGG TGATGATGGC GGGCGTGGTG CTGTTTATCG TCATCGCCAT CCTCGAGCCG 240

ATGCTGCAAC TGAACAATAT GGTTGGAATG TAATTTACGG AGTTATCACA TGAATTCGTT 300

ATCCCGCACA CAAAAACCAC GGGCAGGTTT TACCCTGCTG GAAGTGATGG TGGTGATTGT 360

TATTCTTGGC GTCCTGGCAA GTCTGGTGGT GCCTAACCTG TTGGGCAACA AAGAGAAARC 420

CGATCGGCAA AAAGCCATCA GCGATATCGT GGCGCTGGAG AATGCGCTGG ATATGTACCG 480

ACTGGATAAC GGGCGTTATC CGACCACTGA GCAGGGGCTT GAGGCGCTGA TCCAGCAACC 540

GGCCAATATG GCGGATTCCC GTAACTACCG TACCGGTGGA TACATTAAAC GACTGCCAAA 600

GGATCCGTGG GGCAATGATT ATCAGTATCT CAGCCCGGGT GAAAAAGGGC TGTTTGATGT 660

TTATACCCTG GGGGCAGATG GTCAGGAAAA TGGGGAGGGC GCTGGCGCAG ATATCGGTAA 720

CTGGAATTTG CAGGAGTTTC AGTAATCAGT GCCTGAACGC GGATTCACAC TTCTGGAAAT 780

CATGCTGGTG ATTTTCCTTA TCGGCCTTGC CAGTGCGGGC GTGATACAGA CGTTTGCGAC 840

CGCTTCAGAG CCGCCTGCGA AAAAAGCGGC GCAGGATTTT CTGACTCGCT TTGCGCAGTT 900

TAAGGACAGG GCAGTGATCG AAGGGCAAAC ACTCGGTGTG CTAATCGACC CGCCTGGCTA 960

TCAGTTTATG CAGCGTCGTC ACGGACAGTG GCTACCCGTT TCTGCGACCC GCTTATCGAC 1020

ACAGGTTACG GTGCCAAAAC AGGTGCAGAT GCTGTTACAA CCCGGCAGTG ATATCTGGCA 1080

GAAGGAGTAT GCGCTGGAGC TGCAACGTCG TCGCCTGACG CTGCACGATA TTGAACTGGA 1140

GTTGCAAAAA GAGGCGAAAA AGAAGACGCC ACAGATCCGT TTTTCGCCTT TTGAACCCGC 1200

CACGCCGTTT ACGCTGCGCT TCTACTCAGC GGCGCAAAAC GCATGTTGGG CGGTAAAACT 1260

GGCACACGAT GGCGCGTTAT CCCTCAGTCA ATGTGATGAG AGGATGCCAT GAAGCGTGGA 1320

TTTACCTTGC TGGAAGTGAT GCTCGCGCTG GCGATTTTTG CGCTGGCTGC CACGGCGGTG 1380

TTACAGATTG CCAGCGGCGC GCTGAGTAAT CAGCACGTTC TTGAGGAAAA AACGGTAGCG 1440

GGCTGGGTAG CTGAAAACCA GACCGCACTG CTCTACCTGA TGACCCGCGA ACAACGGGCG 1500

GTCAGGCACC AGGGCGAGAG CGATATGGCA GGAAGCCGCT GGKTCTGGCG AACCACACCA 1560

CTGAATACCG GTAATGCGCT 1580

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTTAACCATT ACCCAGCATT TGGTAGTTAA ATAGTCGTTA AAAGCATAAA ACATGGACAT 60

TGTGCCATCC CAGCTAAAGC ATCCATTACC GCCTGACAGG GATAAAAATA AAAAAGCAGG 120

GAACCATTTT TTCATCAGAA ATCACTTCCG TAATTACAGT TATTCATTTA GGTATGACTC 180

AGTTATAAAT CATGCTCATA CTGGCCGTGG TCTGGRAATC CCCGCCATTC AGTATCCCGC 240

TGCCATTACG AAAGGGCACT GAAGTAAAGG TGAACGTTGA ACGTGCTGTG TCCAGACCTG 300

CTGTCACTCC GTAACCATTT CCTGAACCAT TACCTAATAT AAGAGGTGTT GACATTCCTT 360

TTCCCTGATA CAGCGCTATA CCAAAATGAG TTATATTTGT TGCCAGTACA TTATTCTGAC 420

CTCCTCCCAT AGTATTTCCC GTAACTTTTA TCCAGAGAGA GCCACTCTTA TACGGACAGG 480

ATATGCTTAT GGTTTTTGTG ACTTCACCAC GTGAGTTGTC CACGTGCTCA GGATTAATAT 540

TCCCAAAATC AACAACAATA TTCTGCCCGT TATTAATGGT GCATGGGGGG ATATAAACAT 600

TCCCCCTGAT GTTAATCTGC ACATCAGCCA GTACAGCGAC CGATGTCAGA AGCAACGATA 660

TAAATAATGA TAAACGAATC ATTCCCCTCC GGAGAGCGGT ACAGAAAACA TTTTATTTTA 720

CGAGATATAA AATTAACGTA TTTTAGTTGA TACTATTACG AATATGATGC AACCAGCGTT 780

GCTGTTGCAG AGAAAGGACC GGCTATCAAA TTCTGCATAT TCCCTTTATA TCCAAGTTTG 840

GCATGAAGTG ATATAGTTTT ATCTGCATTA TTACCTGTGA TTTTTCCGGG CGTAAATGGA 900

GTCCCTAAAG TTATCGCAGT CCCAATATTT CCTGCATTAC TGTTATAAAG ATAAACGAGT 960

AACCCATCAG AAGATGTGTT TGATGTATTC TGAACTAAAA TAGCATTGTT ATAAGTGTTT 1020

GTTGCCGTTA TCGTAACCTT CATTGTTCCC AGATTATAGG GACACCGCAT ATTCACAGTA 1080

AACTCTTTTT CGTGATTTCC ATTTTGACTC AGGGTCTGAA TCTCTACATC CTGCCAGTCA 1140

ACAGTTGTGT TGCTTACAGT ACAGGCAGGA ATAATCAGTT TTCCTCTGAA GGTCAGATTA 1200

TCAACTGCAT GTACATGCTG AGACATTAAC ACTGCCCCCA GCATTACCGG AAGACACAAA 1260

CCTCTTATCT TTTTCATCTG AAATATCCTG TACAAAAATT TTGCTAACGA TATGTCAATT 1320

CAAACGTGGC TGTTGCTTCA TAATCACCGG GTACCACACT CTTCGTCCGC AGGCTTCCGG 1380

CGTTGCCACA ACATACGCGC CGAAAGGAAG CTCAAGACTG TTTCCGGTAA CCTTTTCCCC 1440

CTGGCCTTTG TTATGGGAGG TGCCGGGTTT CAGCAGACTG CTGCCATCGG TGTCCAGCAG 1500

TGCAATGCCT AACCGGCCAG CATTCACTCC GGTTACCTTC AGATGGCCCG GGAGGGCGCC 1560

TCTTCCGTCC CCTTAAAGGT CAGGGTCACA ATTTTGCCAA CTGCTGTTGC ATGGCAGTTT 1620

TCCAGCCTGA TGACAAACGA CTCTGTCGGC GAACGTCCGG GCGGATACCA GAAATCCCTG 1680

GACGCCCGGG TTTTGAAGAC GACATGTTTA TTCAGACTGT CACCGGACAC ATGGCAGGGT 1740

CTGTCAAGCA GATTACCCCT GAATGCCACA TCTGAGGCTA TTGCCTGTCC GGCAGACAGT 1800

GCGGCAAACA GTAAAAGAGC GCCTGTGCTT TTTATCATCA CATTCCCTTA CTCATATTTT 1860

ATGCTCAGAC GCAGCATGGC CGGATTGCTC CTGGCATCAG AATACTCACC CTCCTGTGTC 1920

GCCCTTTTCC TCCAGGCGGC CAGCATCTCC TCCTGCCGCC GGTCAGGCCG GCACAGTAAA 1980

AAGGTATCAC CATCGTGTAT AACAAGATGG TCACAGCCGG ATAGCTTACG GTCAGGAAGT 2040

AAAGCACTTC CGCTTCCGGG ACCGGTTACC AGTGAGCCGG AGACTGTCAT CGCAACGCCC 2100

CGTTTTCCGG GCTGAAGTGC ACCACCGTCC CCACATCCTG CCAGCCTCAG CATCAGAGGT 2160

GCTCCGGCTG CCGCAGAGTG ATTTTCCGGC CGGAGGYTTA ACGGCACCTC ATTACTCACC 2220

AGCGTGCAGG GTGAGGACAG CAGTGCACCA CTGACGGTCA GGCTTCCGGT GCGTCCCCCC 2280

CGTTCATTTA TCCGGTAATG ACGCAACTCA TCTGCAGTAA AGACGTCATC GTATATACCC 2340

CGCTCTTCAG CCCGCAGGAA AGTATGGATG AAACCACTCA GCGACAGTGC AATAAGATAC 2400

AGTACTGCTG TTGTTTTATT CACAACCATA ATATCCCACC CGCATTTAAC CGTTATTGCG 2460

GTACATTATT TCTCTTTTTT CACAGAGCAA CGGCTACCAT TACAGATAAA CGACAGTACC 2520

GGGCGACCAC CATAGTCATT AATATAAGAC AGATAAGGGG TATTATAATT TGCCGATTTT 2580

ACTGTCTGCT CTGAACGGGG AGACAGCATC ACGGTTTCAA ACTCACCTTC CTCTGCCTGC 2640

TTTTCACTTC CTCCCAGACC AATAACAGTG ACATAATAGG GCGTTGGGTT TTCAATACGA 2700

TACCCACCGC TGACTTTGTT CAGAATTAAC TGGTCCTGCC ATACTTCATT TGGTCTGGTT 2760

TTAATTGCTG CCGGGCGATA AAAAAGCTTT ATTTTGGTCT GTAAGGCTAT CTGCAGTACA 2820

TTGGCCTTTT CACTCCTCGG CGGTATTTCC CTGAGATTAA AATAAAACAG TGATTCCCTG 2880

TCCTGAGGAA GTTTACTGAT ATCCGGTGTG GTACTCAGCC TGACCATGCT TTTCGCACCC 2940

INSDOCID <WO_ _9822575A2_I_>

GGCTCAAGGC GCTGAACCGG AGGGGTGGCA ATAACCGGCC CTGTAATAAT TTTTTCCTGA 3000

TTTTCATTTT CTATCCATGC CTGAGCAAGA TAGGGCAGTT GTTTGTTATC ATTGGAGATA 3060

TCAAGCGTCA TTGACTTCTC ACTCCCGTCA AACACCGCGC GGGTTCTGTC CAGCGAAACA 3120

GCAGCGTCTG CCCCGGATAT AACAAACAGG GGGATGGCAG CCATCAGAAT CTTTTTTCGA 3180

ATCATACTTA ATTTCCACAT TCTGTAATTT CACCTGGTCC GGAAAATGGC ATAACCGCAT 3240

T 3241

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AACGTGGATC TCCAGCTGAT CGGTGCCGTA TTCCAGGTCG TAAGTTTCAC TGATGGTTTC 60

ACGCGGCAGT TTGCCCGGTT TACGGACCGG TACAAAGCCA ACGCCCAGAC CCAGAGCTAC 120

CGGAGCGCCA AACAAGAAGC CACGCGCTTC GGTGCCGACA ACTTTGGTAA TGCCCGCATT 180

TTTGTAACGC TCAACCAGCA AGTCGATGCT GAGAGCGTAA TTTTCGGGTC TTCCAGTAAG 240

CTGGTGACAT CGCGGAAAAG AATGCCGGGT TTTGGGTAGT CCTGAATGCT TTTGATGCTA 300

TTTTTGAGAT ACTCAAGCTG CTGTGCATCG CGGGKCATAA GTGTATGCCT GCTTGTTACG 360

GTGGTACTCA CGGCGCGTTT TTAAACGTAT CAAAAGTT 398

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17710 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CAGTTNCNGT TCTCATAGAC AGATTGATAA AATCGTAAAC AGCCCCTAGC ATTCCCGTTT 60

CCTTTGCACA CATATTCAGG CACGGGGATA AAGTATAAAG AATGTCGTAC TGCTGCTACC 120

AGAGCAATAT TCCCCCCTGA TGGCCGTATC AGAGATAGTA TGCCGGTATT TTGCGGGTGG 180

TTCCCGTCAG GTTATCGTGT ACCTCCACGG TCGTAGTCAC CACCGGCATT CCGGCYTTTC 240

TCAGCCTCAA AACATCAGCT GCAATACGCT GACTGCCGAA CCAGAACAGG CCGTCCAGTG 300

CAGTCACCAG CAACCCCGCC TCCAGCGCAT GCTTCAGCCG TTCACGGGGC GCTTTCACTT 360

CCCGGGCAAT CTGCTGGTAT GGCGATGATG TGTTTTCATT CCCAATCACC CGGCGAATAC 420

GATGAGACAG ATGATACCGG TATGTATCCG GCACACCGGA AAGGCTGGCC TTCAGGCTGT 480

ACACGCAGCC AAATCGTTTA TCATTGAACA CCACATTTTT CTGGCTGATG CCCCATTCTT 540

CACGCAGCGC GGCAATCAGT TGTGGTGTAC GGGTAAGCAA CAAGCGAAAA GGCAGTTCAA 600

AACTGGTGAC ATAATCCACA TTCAACAGGG CAATGCGAAG TCGTTCTTCT GGTCCGGCTT 660

CTGTCTGCCG GCACTCCTCC AGGACATCCT GCCACTGCAG GCGAAGACGG GAAGACTCAT 720

TCAGTTCTGT AAAGCAGTAT TTATCCGCCA GATAGTCAAT TCGTGTATGC ATACTGAAGA 780

GTATTCCGTA TAAAGATTCA GCTGGCAAAA CTTTATCAGT CTGTAAAAAC TAACGGAAGA 840

GTCGATATTT CTCCCGACAA TCACCGGATG ATTGTTGCAA TACCTCGTGG CATCAGAGAC 900

TGAACAGCAG TTTTTAACGC AACGTATTGC TCTGATGTAT CAGGCCGGAC AACCCGAAAA 960

CAGCCTTCCA CCCGGCATTG TCCGCCAGCG CTTATCACCG GCCAGGTCTG TTGCAGTAAA 1020

TCCGCCACTT GCGAACATGC TTCATCAACT GTGACACTGG CCCGCGGATG GCAAATGCTC 1080

GTCTGGCTGA GCAGCAACAG GCATCGCATT GTTGCTCCTC TATGTTGTTC CCGCAACCAG 1140

CGTAATACCA CCGGCGAGGA TGGACAGGCA GTGTGATTAC GCTCCGTAAT ACGTTCGTGC 1200

ACCCGTCGGT GAAAGGAACT ACAGAATGTC TGAATCTGTT GCCCGTTGAT GTATCCTTCT 1260

GTCGAATGAA GTGTGAAGTG GATTGCCAGC AGATGCGGCC AGTGATCCAC CGCCTGCTGA 1320

ACAAAACGCC GGATTTCCCC CGGCTCTGAA AGTAAGGCTT CGGTTATTTG CACTATTTTA 1380

TCTCTGTTGA ATTTGGTTAA GTCGGTGCAG ACGCATCAAC ACAAGTACGG TTCGATGCAA 1440

ACAGCTGTGA CTGGCAATAT GAAAGGAATG ATGAATCAGT CAGGATGACA AAGTGCCGGC 1500

TGACCGGAGG GGACGCAGGA AGATTCACGG GGGGACCAGC ACCAGGGAAC AGCGCCACAA 1560

TACCAGCGCT GACACGTTGA ACATTGCCAG CGTACCGGTA TCACAACACG TTTCATACTT 1620

CTGCCCCCGT GATTCTTCGA TTCGTTACTG TATCTACTGT GACACTTCGC TTTTATACCT 1680

GCGGCTGGAT CGGCCCGGCT TGATGAATCT TCACTGATCA GCTTATAAAA CCCTCTGTCG 1740

GTCATACCGG TGAAACTGGT GATATAGTTC ATGTCAATCA GGGAATTATC GGCACGCAGA 1800

AATACGCTGT CGTGGCTTGT TGTAGTCAAC ATGGTCAGAA TGTCCTCTGT GAGATTTATG 1860

AAGATTGTGC GAATGCGGGG AATCTACTGA GCTGTGCTTT CAGAACTGGC CTGTTACGGG 1920

AKRSCAGGGA TTACCGGCGG GGTAACGGGC TTCCGGATCA TACACACCAC GATTATCGCG 1980

GACAAAATCA CTGAACGCCC ATATCACCTC TTTAAGTATG TCTTCGCAGC CCGGTACATG 2040

ACGATCCAGC GCCACATCCC GAGTGGTACT ACTTTGATGC GCCCGGTGAC ACAAAGCCCG 2100

GATTGTTCCA GACATCCTGA ATCAAACGCC CCAGATTAGG GGCGTCGAAA TATGCCTCTC 2160

TGACCATTAT ATTCCGGTGT ACAGGTAGCA GGTCAGAAGT GACAATGCGT CACCTGACGT 2220

TAAAAGTCAC TACACCCAAG ATGACGTTCA ACAGCACCAT GCGATTCAAT GTAAGCCCGG 2280

GCTGTCTGTT CCAGTACACC AGGCTCAGCG TTGTATGTGT TAGCTGCATC AAATACCAAC 2340

GACAGCACTT CAGGATACAC AACCAGATGT GTAATGGAGT TATCTTCACC CAATACTTTT 2400

CCCCACGCCT GCTCAATCAG ATTTCTGAGA ACCACCACCT CACGACTCTT ACACCAGACA 2460

TCGTTATTAA GTAGCAGCAC CATAAGATAA GGAGTGGTAT CGTTAGTCAC AGCCTCCCTA 2520

CTCCAGAGAT AATATAAAGG GGTGGGCTCA ACAGATTTAT CTTTACGTCG CTTACACTGC 2580

AAATATTCAG AAATGAGTCT ATGCAGTTCA CCAGTAAAAT CCGCCATCAG AGAGGGAATG 2640

GCCTTATTAA TACCAGGGCA AGGTATTAAT TTAAATTGTA ATAATTTAAT TTCAGGATGT 2700

GTGGCTGCAG CCCGATACAG AGTTGCAAGG ACACACTTTT GCCAGAGGGC GTTACTGGAA 2760

AGCTTAACGT TTGATTCTGT ATACATAATA AATCACCTTA CAGTTACAAC AGGTCAAAAA 2820

CCGCTGTAGC CAGAGTTACG CTGGCCTGAT GCTTTAGTAC CGGGCTTCGT CAGATAATCC 2880

AGACGCTCCA ATAAGCGCTG ATACTGCTCA GGGAAATCAG GATCATGAAT ATCCTGGATG 2940

TCACGTCCAT TAGCAGGGAA ATGAATAACG CAGCCCCCTG GATTAACAAT GCAGAAATCG 3000

TCCTGAGGTA CTGATCAATA CGGAGAGGAC TCTCGCGTGT GGTTTATTGA CACCACAGTG 3060

CAGATTCGGC GAATCCGCGA TCACGGTGCG ATTTCGTTCC ACAGCACACA ATCATGACCC 3120

CGGGTTTTAT TCAGGTAAGC AGGATTGCGG ATATCCGGTG TCGCGCCTTT CTGTCACGAA 3180

CGGGGTAGGT GCGAAACACC GGATAAAATG CAGGCTGGCA ATACCTCTGA ACGCCCTGCG 3240

CAGAGCGGAT ATTTTGGATT AAGTACTCGC ACCTCCGCAG TCCTGAAACA AGTCTGGCTG 3300

GTAGCTGTAA ACAGACTTCG TACATGTTGC TCTGGAATAG ATCCCCGTGC CACAGGCTTC 3360

GCAGAACTTT TTCCCGGGAA AATGCTGCCC GCACATCACA CAATGCCACT CCAGCACGAC 3420

CGGTAATGGC GATAGAAACA TCGCCATATC CTCAATGTAA GGGTGGGACT TTTCCGGATT 3480

CAGCACCACG CAGGCCGCCT TCTGTTGCGC GCTCAGGGCA TGTAAATCGT GCTCAAACCA 3540

CGCCCCCTGA GCATCTGTCT GCAAAATCAA CCGACCACGA CAGGAAAGGC AGAAACAATG 3600

CCTGATATTT CTGCTAAGGC TGAGGCCGCA CTGATAATGT GTTCACCCGG CGTGATCCCC 3660

AGCCCCGTTT TTATACCGTT CATTCAGCCA CTCCCTCCTC ACTGAAGTGC CCTGTATGGC 3720

AGTGAGTGCA GTACCGCTCC CCATAATAAT CGTGGTGACA TTGTCTGCAG TGCCAGCTGG 3780

CTTTACGCAC CACGGGTAAG GCATCCGGTA CGAATTTCTG CAGACGCTTA ATCAGTTGTA 3840

TTTCTCTGCG CTCCGGTCTG ACATAAGGGC ACTGTTGACC GTGCTCCGTC AGCCCGTCGT 3900

CAGTGTGTTC AAACCAGGGA AGTTCAGTGT CGTATTGCGG ATGGTATCTG AGCGCACTGC 3960

CGCAAAGGTG GCAGGTGTAG CGGTCGTAAG GTGCAGTCTG TGCGGTACGG GCAGCGGTCA 4020

GACGTCCGTT GCCATCAAAT GCGAGAAAAG ATTTTGCGTA CATAGTATAT GTTCCTTACC 4080

GCCAGACGAC ACGCAGGCGT CAGCGTCCCT TTACGGGCAG CGTGGGCAGG GTGTGAATGG 4140

CGGTACAGTT AAGGGGGGGG TGGAAAATGG GCGGGCTGTT GTTACAGCAC TGTGGATGTC 4200

ACATCATGGC GTACCAACGT AAAAAATAAT CAGCAGGCCC GGATACATCG TTGTCGCCGG 4260

ACATCAGCCC GTCCTGCTGG TTTTGCCGGG CTCAGCCCCG ACTGCAGCCG AAATTACGCT 4320

CACCAGTGGC GTGAGCTTTG GTATGTTCCT TCGCCAGATA GTCAGCACGT TCCAGCACCT 4380

GCTGAAAGCC AGTGTCATCA CCGCGTTCCA GCCACACCGC CGGCGTGTCA GGAAAATGCG 4440

CCAACGTGGC ATAAGGCCCG GCATCCACCC CCAGGGCACT GCACCAGGCN TGWTTAATCA 4500

TCCCGGCCAG TGACCCCGGA TCGCGGTAAT CGCCGGCACG ACACCAGGTA TCCCGGTTGA 4560

CCAGCAGCAG GAGGTGATAG TGTTTTTTGC CCCTGAGTAC CCCGAACTCC CGGGCCCAGG 4620

CGTAATGCAG GGTGGTGGGA TGCACGCGTT TACCTTCACG NCGTTACGCT TCTGGTAAGC 4680

GTCGATTCGG GCTTTCAGGG CATTGATGAA GCGGGATATC ACAGCCGCGT CCGTAGCTGC 4740

CGGTACATCC GGGAGACGCA GATCAACCCG AAGTGCCGTC AGGCGGGGAT GAACATTCAG 4800

TGCGTGCCGC ACCGTCTCAC GAATACGTTG CTGCCAGAAG GGGTTGTATT TGTAGGTCAT 4860

GGTTAAATCT CCGTATGGTT CATACGGAAT AGCCACGTCG TAAAAAATGC GCAGAGCCCC 4920

TGACGTGGCC ACCGACAGAA CACGGCCTCA GGCGCGTTGT GATAACCCAG CTATCGTTTC 4980

CGGACTGACG GTTGAATTTC CTGCGTTGTT TTCTTAATGT AAAAAACCTG CTACGGGTAA 5040

GGCTGTGAGG AGGAAGTGAT GGTGATACGC AAAAAGAAGT GCAGGGACTG CGGAGAAGCG 5100

ACAGAGCATA ACACGGTATG TTGCCCACAC TGCGGTTCTG TCGATCCCTT CGGCTATTAC 5160

CGCAATACAG ACAGAATATT CACCCTCCTG ATGGTCCTGC TGGTTGTGGT TCTGCTGATG 5220

ACGGCTGCGG TCAGCGTGTA TGTGCTGTGG TAGTCGGAGG GGCAGGGAGC AGACGATGAC 5280

GTAAAATATC TCCGGTGCTC AGATATCACG GCCGGTCAGA CCGCAAACCA ACGGTTAATC 5340

GTAACCGGAT CAGGCAAATG TGTGATTAGC CCCCTGGCGC TCATACCCGC ACCGCAGACC 5400

ACCTTAAGTA CTTCCCGCCC GACACCATTC CCTGCTCCCG GATAATTTGT TGTCGCTATA 5460

CCGCTTAACA TCACCGATAC CACACCGGCG CAGATAGCAC CGGATTCATT GTAGAGATGA 5520

CTTAAGGTTC AGGTAACATA TTTCCAGACA GAAGCGGGAA CACGATCGTA AAGTTTGTTC 5580

ATGGTCAGTT CTGCCAGCCG GTGATCAACC GCAGAGTTGA AATTTTCCAG CTCCGCCGGG 5640

GTGAGTTTAT ACCGTGCGTG GGAAATCACT TTTTCCAGTG TCTCCCGGGA TGAACAACGA 5700

CGGAACTGAT ACAGCCAGTC TTCTTTGGTT TTTACTTCCA TTCGTCTCTC GTTACTTTAT 5760

GCTGCGGTTA ACAGGATGCC GTCAGTATAC CGCATGCAGA CACTCTCCCG CTCCCCCGCT 5820

TGCTGCGATA CAACTTAACG TTTCAGGAAT CCAGTCATCG CACCGGGAAA GGCTTTCTGG 5880

TGACAGGAAA CGTCAGGAAC AGGAGTTTCT CAGACTCCCA CTCATCGGAT CAGGCTCAGA 5940

CAGGATTATT AATACGCTCA GTTCATGTGT CATATACAGG GCATCGGGGA TGAATATATG 6000

GGTATAACTC AGAGCCTGTA CTACAGCTTT CACTGCTGAC TGATTTTACG TATCAGCGTT 6060

CATGTATCTG CACTCTGATA TAGAATACTT CTACCGGAGC TACTCTTACG TTAGCTCACT 6120

CTCACATCAG GCAACATCAC TTATTCAGCT CACTTACCTC TTACCACTCA CTACTTCTTT 6180

ATATTTATAA TATCAATCAG ACAGCCTTAT CCCCCCGGTA ATATCTGTTG CCTTCCCGCC 6240

AGCCACAGGC TTATTCACCA CAACCACCTC CGATAACAAC TCTGCAATTA TCAGAACGCC 6300

TGCTTCTCTC CCTGTCCTCA CGAAAACTAT CCCCTCTTTA TCGCGCGTGC GTGCGGAAGC 6360

ATCTTTTCGC AACAACCACC CGGGATTCCG CTACGGCTCT GCCATCGCAA TCCCCCCGTT 6420

TATCTCCGGA CAGCCACATT CCCGATTATT TTTTACGTTT CTCCCCGGTT GTTATGCCGG 6480

TGAAGGTGGT GCGTCGTTTT CATCACCACA CCGGTTGCGA TTAACAACAT CCGGAGGAAC 6540

ATTCTCATGA CCACACCCTT TTCACTGATG GATGACCAGA TGGTCGACAT GGCGTTTATC 6600

ACTCAACTGA CCGGCCTGAG CGATAAGTGG TTTTACAAAC TCATCCAGGA CGGAGCCTTT 6660

CCGGCCCCCA TCAAACTGGG CCGCAGCTCC CGCTGGCTGA AAAGTGAAGT GGAAGCCTGG 6720

CTGCAGGCGC GTATTACACA GTCCCGTCCG TAATTTCTGC CCCTTATCCG TTCACCCGCA 6780

GCAGACGCCT CCCCGGCCTG CCGTTGACAT TCTGCTGCCT GTTTTATCCC CGTGAGGAAT 6840

ATGAAAATGA AACAACAGTA CCAGACCCGC TACGAATGGC TCCACGAAAG CTACCAGAAA 6900

TGGCTGACCG GCTTCAMCCG GCACGCCGTA TCCTGGGGCG TGTGTCATCC GAATATCTAC 6960

TATTTCCATA ATCTGACGCC CGGGTGGGTG TCATTCAACG GCGAACAGTC GGAGATTGCC 7020

ATTGTTCCCG GCAGTCTGCA CCGGCTGATT TATGGTCATG ACAAACGGGC CATGCCGCCC 7080

CTGGATGATG ATCTGGTGGT GAATTTATGC ACCAGTGAGA ATCTGCTGGT TCATCATCCG 7140

ATGCTGGAAG GCATTCTGCT GTCTGAGTGC ACGCGCCTGC ATAAAAAATC ACTGGCGAAC 7200

AAACTGATCA GTATATTCCG TCAGTTTGAC GGCACGGAGC TGCGTCTCAA ACTGGTCTGG 7260

CTTTGCTGGT TTGATTTAAT GACCGGAAAC TGCCTTGACG ACTGGACGGA GAACCTGNAA 7320

CGGAAATCAG AAAAAGAGCT GGAGAAATGG ATCATTGAGC GCCAGAACCG GAACGCACCG 7380

CTGACGAATC TGATGGATCA GTACGTGCTC CTGGCATTCC GCACAACGGT TGACGATAGC 7440

CGCAACTGAT GTCTGCATGC TGCCSGCTGA AGCCATATTC ACGGGGCAGG GACGCCCCTG 7500

CTTCCGCAAC AATCCGGGGT AATGGCGACG TACGCCTGCA GAGTGTGTTC ATCGTTGTCA 7560

CAGCCGGACA AGGTGAATAC CGTTGATGAT GCGGGGATGA ACCTGCTGGT CCACCGCGCT 7620

GTCACTCAGA CGCGTCAGCG TGTATGGACG CCCCGATCGA ATGGTTCTTC CGCCAGAGTG 7680

CACAGAAATG AGGCACGGAA CGTTACCTGA AGGGTGACCG GCACGGACTG CAACTTGTTG 7740

CCATTGATGG CGCACAAGTC ACATACAGCA GAATGTCGTG ACCGCACCTT ACCGGTGAAG 7800

CGAAACGGTG CTGCCCCACT CCACCACCAT CCCGGATAAC GCCATTACGC TGTCTGATAA 7860

GCGCTTTTAC AGCGCAAATC TGGTGCAGAA AAGCGTAAAG CTGACCTGCC GGAGCAGGAT 7920

GTGGGCATGT TGCGGGCTTA CAACCTGATA CGGCATGAGG CACTAAAAGC AGCATCAGAA 7980

ATCAGCCTGA GTTCGCGTTC CGGTTTATCC CGACAGAGAG GACAGTGCCG GGCAACACGG 8040

TGTCACCGGG GAGCATCCCG AAACGACCGG AGCATCTGCG GGATGCTCTG TAAGTGGTGT 8100

TAAGGTGGGC GGTTAAGGTA TCAAAAAAAT CGTTATCCTG TGAAAGACAG TGCGCTCTGC 8160

TGAAGTGAAC GTCACTGCCG GGAAGCATCG GGTTTCGCTA CCGGACAGTC GCGGTAACGC 8220

GTTTACCGGC ATCTGTCTGT GTGGCAGGGA TGGCTGATAT TGTCGGTTAT ACCAGCGGCA 8280

GGTGCGTCCT GTTATCTGTA AAATCAGGGC GTGCCGGTAC ACAACGCCTC GTTGATGCCG 8340

GTCACTGAAC GAATCATCCT CTGACGAAAA CAACCGTCGA TACAACGCCG GCGTAAAAAG 8400

AAAACCGGAA ACCATCTTGT GCACGACAGG TACTCAGGGG GGTATAACGC CTGCGCACCA 8460

TCACATCCGG GAACAGGGCT GCTCCTCAGT GTCTTCGTGT GGCGAAGCAT CTGCAACCGG 8520

ACGGTACTGC CCTCAGAGCA ATCTCCCTGC TGCAGTGCAC AGAGTAAGCC GGAAAGCTGG 8580

TGAATGCCGC CATGACACAC TGCGACGTGG AGAAACAAAC GACACACTCC GTCCGCAGTA 8640

ACACTGAAGG TAGTCCCGCA AACCTCAGAC TTCTTCCTGC ACGTTATCAG CGGACTGAAC 8700

CCCGGTCAGC CACTTAAACC TGCTAATCGT GTTGCTGCAT ACCCGCCCGG CCGGAAGGTG 8760

TTATGAAGCC CGCCACCGGA GCGCTTCTGC AAATATCCGG GGAGATAAAA TTTTCGTGAC 8820

AGGATGACGG TCGTGCTGCA GACGTAAAGC CGCAGGAGCG GACACGACAG ACAGTGTTCA 8880

CTGTGGCGTC CTTTGCCGTC GGTATCGTGC TCACGCTGAG GTCCCGGGGG TACACCTGAC 8940

GACAAATACC TGCGATTCCC GGGACGGTCT GTTCTCCGTA AAATAAAGAA AATGCGGGAT 9000

GCCTCCCGGA CTGCAGAGAA GAGGGATTGA CAGACAGTGT ATATTGCGTA CGATTACAGG 9060

GGAAAAACAC AGTAAATATG GAGGTCAGGT CCGAAAACAA CCTACGAAAT TTCTATGAAA 9120

AACGATTGAA AAAATCATCA AATTCAGTTC GTTTTTCTAT GGTAATTTTT AAACACTCCC 9180

GATGATAACC TGTTGTATGT GCATGTGGGG AACGCACCGA AAACATCAGA ATCATCTGAA 9240

AAAAACAACG AACACACCAG AAAAACAGGA GCAACCATAA CGAAGCAACA TATTGATTTT 9300

AAACAGAATT TAAGGTTAAC AGACAAAAAA CACTTTCAAC TGAAGGAGAA ATATACACTG 9360

GCGACAGTGC AGGGTTTTTC ATGCAAAAAA AATGAGCTTT TATCTCCGGC GCATACTGAC 9420

CGGGATGCAG CCATGACAGA GCAAAAACCA TTAAATATCA GGAGGTTAAA CACACAAAAA 9480

GCTGACATGC ATCAGGGAGC AATCCCTCAC AACAGAGGCT GAGCGGCAAC GCTTCCTCAC 9540

AGGACGGCAT TCCTGAAAGG ACAGGCAGCC ACGGCTTTTT ACTGCCCGTA TCCGGTATAT 9600

TTATCTGCCG TGACGTGCAG AGGATTTTGT GTTTCCGGAA ATCAGGAAAA CAGGAGAACC 9660

GCGGGAGATA TGATGGAAAA AGAACCGGAT GATATCTGCG CAGACTGTCC GAATATTGAT 9720

GCAATAAAAC GGCACAAACA ACAGGCCGGA GCCATCAGGG AATACACTGA GTGGTTAAAA 9780

AAACAACCGC GTGCTTCTTA CTTTTTTCTC TTCCGGTTGT ACGCATACCT TCAGAATGAA 9840

GTGATATCCC GAAAACAAAA ACATTCGCTC ACCAGCGATA ACAGCCATCC CCCGGAATCT 9900

GATGTCACCC CTCCGGATTT AACCCTTCCC CGTCGCTACT ACTGTGATTA CGGTTACACG 9960

CCCTACCCCA TGATGGGCGG ACAGATGTCT GTTTTTGCCA CAACGTCAGA AACCACCAGT 10020

INSDOCID <WO 9822575A2 I >

TCGACGAATG CAGTCCCCGG AAACGCAGTT ACCGGGAATG AGACTGAAAA GCATGAAAAC 10080

GCGGTACCGG CGACATTCCC CGTCAGCCGT TCTGCAATGC CCCCGGAACC TCTGCGGTTT 10140

GCCACGGGTT TTCCATCGCA ACCACTGCTT GCCGGTCCCC GGGAAAAGCC GATGCGCACC 10200

GTGCATCCTG ACATCCACAG CGAAATTATA TGGTTCTGCT CCACTTACCT GCTGAAATCC 10260

GGACCACAGA TTACGAAGAC GATTATCAAC TCAGTATTCT CTGAATGGGC CCGCATCAGC 10320

AATGATTACC CCTCCCCCTT TTCGTGGGTG GACAGCAGGG ACAGTGAACA GTGTGACTGG 10380

TTATGGAACG CCATGCAGCT CCGGTGTGTG GGAACCCCGC TGAATCCCCT TACCCCGGAG 10440

CAGAAATACT GGTTTGCCTG CGCCACGTTT GATAACTGGG AGGGCTGGAA TGAGCAACAG 10500

ATACAGTTTT TACTGAAAAG TAATCCCAGA CGAAACAGAG CGAAGTTTAC GGTCACCTTC 10560

GGCCCTCCCT GGATTCAGCA TAAAGCCATT CTTCTTGATG AGCTGAAGAG TGCCCGGGAG 10620

CAACAAAAAA GGCGCGATGA ACGCGCTGAT GGTTCCGTCC CGCTGAAACT GTCCGGAAAA 10680

ATCCACAAAC ACCTTGAAAG TATTGCCCGG AGTCGTGGTA TCCCCCCAAA AAAACTGCTG 10740

AATGAAATGA TTGAGCAGGC GTACCAGGAC TCAGTGGTGA ACAGCCGGAA TAAACCACTG 10800

ATTTAAAATA ATTTCAGACA GATATTATCT CCGTGAATCC CCCGCCACCT TTCCGGTGCG 10860

CGGGGTTTTG TCTTTTTTCA CCGGGAATAC ATGTATGAAT CCGTCTGATG CCATTGAGGC 10920

AATTGAAAAA CCGCTCTCCT CCCTGCCTTA CTCGCTTTCC CGTCACATCC TGGAACATCT 10980

GCGCAAACTC ACCCGTCACG AACCCGTGAT TGGCATTATG GGTAAAAGCG GGGCCGGTAA 11040

ATCCTCACTC TGTAATGCAC TGTTTCAGGG GGAGGTCACC CCGGTCAGTG ATGTTCACGC 11100

CGGCACCCGG GAAGTGCGGC GCTTCCGTCT GAGTGGCCAT GGTCACAACA TGGTTATCAC 11160

TGACCTGCCC GGGGTGGGCG AGAGCNGGGA CAGGGATGCA GAGTATGAAG CCCTGTACCG 11220

TGACATTCTG CCTGAACTGG ACCTGGTACT GTGGCTGATT AAAGCCGATG ACCGTGCCCT 11280

GTCTGTGGAT GAGTATTTCT GGCGACACAT CCTGCAACGC GGACATCAGC AGGTGCTGTT 11340

TGTGGTGACG CAGGCCGACA AAACGGAGCC CTGCCATGAA TGGGATATGG CCGGCATTCA 11400

GCCCTCTCCC GCACAGGCAC AGAACATTCG CGAAAAAACG GAGGCGGTAT TCCGTCTGTT 11460

CCGGCCTGTA CATCCGGTTG TGGCCGTATC GGCCCGCACC GGCTGGGAAC TGGATACGCT 11520

GGTCAGTGCA CTCATGACAG CGCTTCCCGA CCATGCCGCC AGTCCCCTGA TGACCCGACT 11580

GCAGGACGAG CTGCGCACGG AGTCTGTCCG CGCTCAGGCC CGTGAACAGT TTACCGGTGC 11640

GGTGGACCGG ATATTTGACA CAGCGGAGAG CGTCTGTGTT GCCTCTGTTG TCCGTACGGC 11700

CCTGCGCGCT GTTCGTGACA CCGTGGTCTC TGTTGCCCGC GCGGTATGGA ACTGGATCTT 11760

CTTCTGAACC TGTTGTGGAT GATGTCCTCC CTGCCTCTGA GTCTGCTCAC AAAAGCGCTG 11820

TTTTCGTTAC TGTCTCTCTT GTCCGTGCAA TAGCTCAATA ATAGAATAAA GCGATCGATA 11880

ACTATTTCAT CGATCGTTTA TATCGATCGA TATGCTAATA ATAACCTTTA TTACCAACAT 11940

NSDOCID <WO 9822575A2 I >

GCGCAGATAC GCACAGACAG ACATTCAGGG GACGACAGAA CAACACTTCA GAAACTCCCG 12000

TCAGCCGGAC CTCCGGCACT GTAACCCTTT ACCTGCCGGT ATCCACATCT GTGGATACCG 12060

GCTTTTTTAT TCACCCTCAC TCTGATTAAG GAAATGCTGA TGAAACGACA TCTGAATACC 12120

TGCTACAGGC TGGTATGGAA TCACATTACG GGCGCTTTCG TGGTTGCCTC CGAACTGGCC 12180

CGCGCACGGG GTAAACGTGG CGGTGTGGCG GTTGCACTGT CTCTTGCCGC GGTCACGTCA 12240

CTCCCGGTGC TGGCTGCTGA CATCGTTGTG CACCCGGGTG AAACAGTGAA TGGCGGAACA 12300

CTGGTAAACC ATGACAACCA GTTTGTATCC GGAACAGCTG ATGGCGTGAC TGTCAGTACC 12360

GGGCTTGAGC TGGGGCCGGA CAGTGACGAA AACACCGGCG GGCAATGGAT AAAAGCGGGT 12420

GGCACAGGCA GAAACACCAC TGTCACCGCA AATGGTCGTC AGATTGTGCA GGCAGGAGGA 12480

ACTGCCAGTG ATACGGTTAT TCGTGATGGC GGAGGGCAGA GCCTTAACGG ACTGGCGGTG 12540

AACACCACGC TGGATAACAG AGGTGAGCAG TGGGTACACG GGGGAGGGAA AGCAGACGGT 12600

ACAATTATTA ACCAGGATGG TTACCAGACC ATAAAACATG GCGGACTGGC AACCGGAACC 12660

ATCGTCAACA CCGGTGCAGA AGGTGGTCCG GAGTCTGAAA ATGTGTCCAG CGGTCAGATG 12720

GTCGGAGGGA CGGCTGAATC CACCACCATC AACAAAAATG GCCGGCAGGT TATCTGGTCT 12780

TCGGGGATGG CACGGGACAC CCTCATTTGC GCTGGTGGTG ACCAGACGGT ACACGGAGAG 12840

GCACATAACA CCCGACTGGA GGGAGGTAAC CAGTATGTAC ACAACGGTGG CACGGCAACA 12900

GAGACGCTGA TAAACCGTGA TGGCTGGCAG GTGATTAAGG AAGGAGGAAC TGCCGCGCAT 12960

ACCACCATCA ACCAGAAAGG AAAGCTGCAG GTGAATGCCG GCGGTAAAGC GTCTGATGTC 13020

ACCCAGAACA CGGGCGGAGC ACTGGTTACC AGCACTGCTG CAACCGTCAC CGGCACAAAC 13080

CGCCTGGGAG CATTCTCTGT TGTGGAGGGT AAAGCTGATA ATGTCGTACT GGAAAATGGC 13140

GGCCGTCTGG ATGTGCTGAC CGGACACACA GCCACCAGAA CCCGTGTGGA TGATGGCGGA 13200

ACGCTGGATG TCCGCAACGG TGGCACCGCC ACCACCGTAT CCATGGGGGA TGGCGGTATA 13260

CTGCTGGCCG ATTCCGGTGC CGCTGTCAGT GGTACCCGGA GCGACGGAAC GGCATTCCGT 13320

ATCGGGGGCG GTCAGGCGGA TGCCCTGATG CTGGGAAAAG GCAGTTCATT CACGCTGAAC 13380

GCCGGTGATA CGGCCACGGA TACCACGGTA AATGGCGGAC TGTTCACCGC CAGAGGGGGC 13440

ACGCTGGCGG GCACCACCAC ACTGAATAAC GGTGCCACGC TTACCCTTTC CGGGAAAACG 13500

GTGAATAACG ATACCCTGAC CATCCGTGAA GGTGATGCAC TCCTGCAGGG AGGCGCTCTT 13560

ACCGGTAACG GCAGGGTGGA AAAATCAGGA AGTGGCACAC TCACTGTCAG CAACACCACA 13620

CTCACCCAGA AAACCGTCAA CCTGAATGAA GGCACGCTGA CGCTGAACGA CAGTACCGTC 13680

ACCACGGATA TCATCGCTCA TCGCGGCACG GCCCTGAAGC TGACCGGCAG CACCGTGCTG 13740

AACGGTGCCA TTGACCCCAC GAATGTCACC CTCGCCTCCG GTGCCATCTG GAATATCCCC 13800

GATAACGCCC CGGTTCAGTC AGTAGTGGAT GACCTCAGCC ATGCCGGACA GATTCATTTC 13860

ACCTCCGCCC GCACAGGGAA GTTCGTACCG GCAACTCTGC AGGTGAAAAA CCTGAACGGA 13920

CAGAATGGCA CCATCAGCCT GCGTGTACGC CCGGATATGG CGCAGAACAA TGCTGACAGA 13980

CTGGTCATTG ACGGTGGCAG GGCAACCGGA AAAACCATCC TGAATCTGGT GAACGCCGGC 14040

AACAGTGCGT CGGGGCTGGC GACCACCCGT AAGGGGATTC AGGTGGTTGA AGCCATTAAC 14100

GGTGCCACCA CGGAGGAAGG GGCCTTTGTC CAGGGGAATA TGCTGCAGGC CGGGGCCTTT 14160

AACTACACCC TCAACCGGGA CAGTGATGAG AGCTGGTATC TGCGCAGTGA AGAACGTTAT 14220

CGTGCTGAAG TCCCCCTGTA TGCCTCCATG CTGACACAGG CAATGGACTA TGACCGGATT 14280

CTGGCAGGCT CCCGCAGCCA TCAGACCGGT GTAAGCGGTG AAAATAACAG CGTCCGTCTC 14340

AGCATTCAGG GCGGTCATCT CGGGCACGAT AACAACGGTG GTATTGCCCG TGGGGCCACG 14400

CCGGAAAGCA GCGGCAGCTA TGGCTTCGTC CGTCTGGAGG GTGACCTGCT CAGAACAGAG 14460

GTTGCCGGTA TGTCTGTGAC CGCGGGGGTA TATGGTGCTG CTGGCCATTC TTCCGTTGAT 14520

GTTAAGGATT ATGACGGTTC CCGCGCCGGC ACGGTCCGGG ATGATGCCGG CAGCCTGGGC 14580

GGATACCTGA ATCTGGTACA CACCTCCTCC GGCCTGTGGG CTGACATTGT GGCACAGGGA 14640

ACCCGCCACA GTATGAAAGC GTCATCGGAC AATAACGACT TCCGCGCACG GGGCCGGGGC 14700

TGGCTGGGCT CACTGGAAAC CGGTCTGCCC TTCAGTATCA CTGACAATCT GATGCTGGAG 14760

CCACGACTGC AGTACACCTG GCAGGGGCTC TCCCTGGATG ACGGTAAGGA CAACGCCGGT 14820

TATGTGAAGT TCGGGCATGG CAGTGCACAA CATGTGCGTG CCGGTTTCCG TCTGGGCAGC 14880

CACAACGATA TGACCTTTGG TGAAGGCACC TCATCCCGTG ACACCCTGCG TGACAGTGCA 14940

AAACACAGTG TGCGTGAACT GCCGGTGAAC GGGTGGGTAC AGCCTTCTGT TATCCGCACC 15000

TTCAGCTCCC GGGGAGACAT GAGCATGGGT ACAGCCGCAG CCGGCAGTAA CATGACGTTC 15060

TCACCGTCCC GGAATGGCAC GTCACTGGAG CTGCAGGCCG GACTGGAAGC CCGTGTCCGG 15120

GAAAATATCA CCCTGGGCGT TCAGGCCGGT TATGCCCACA GCGTCAGCGG CAGCAGCGCT 15180

GAAGGTTATA ACGGCCAAGC CACACTGAAT GTGACCTTCT GATAATTCGG CATTGTCTCT 15240

CTGTGGTCCC GGTCATCATG ACCGGGACCC GGACAGGTGC AAACGCTTCA GTGCCACATT 15300

CACTGGCATT CACAATAACA TGATATTCAT CACGGAGTGA CTATGTTACA GATAGTCGGT 15360

GCGCTGATTC TGCTGATCGC AGGATTTGCC ATTCTTCGCC TTTTGTTCAG AGCATTAACC 15420

AGCACAGCGT CTGCGCTGGC AGGGTTCATA TTGCTGTGTC TGTTCGGCCC GGCTTTACTG 15480

GCTGGCTATA TCACTGAACG CATAACCCGG TTATTCCATA TTCGCTGGCT GGCAGGCGTA 15540

TTTCTGACGA TTGCCGGAAT GGTCATCAGC TTCATGTGGG GACTTGATGG TAAACATATC 15600

GCACTGGAGG CTCATACCTT TGACTCTGTA AAATTTATTC TGACCACCGC TCTCGCCGCT 15660

GGTCTGCTGG CTCTTCCCGT GCAGATAAGA ACCATTCAGC AGAACGGGCT CACACCAGAA 15720

GATATCAGCA AGGAAATTAA CGGGTATTAC TGCTCTTTTT ATACTGCTTT TTTCCTTATG 15780

GCGTGTTCTG CATACGCACC ATTGATCGCA TTGCAGTTCG ATATTTCACC CTCACTGATG 15840

TGGTGGGGCG GGTTGTTGTA CTGGCTGGCT GCATTAGTGA CGCTGCTATG GGCGGCCAGC 15900

CAGATCCAGG CGCTGAAAAA ACTGACCAGT GCCATCAGCC AGACACTGGA AGAACAACCG 15960

GTGCTCAACA GTAAATCGTG GCTGACCAGT TTGCAAAACG ATTACAGCCT TCCTGACTCA 16020

CTGACGGAGC GCATCTGGCT CACGCTCATT TCACAACGGA TTTCCCGGGG AGAACTGAGG 16080

GAATTTGAAC TGGCAGACGG AAACTGGCTA CTGGACAATG CCTGGTATGA AAGAAACATG 16140

GCGGGTTTCA ACGAAAAGCT GAGAGAGAGC CTGTCATTTA CCCCTGATGA ACTGAAAACC 16200

CTCTTCCGGA ACCGCCTGAA TTTATCACCG GAAGCGAATG ACGATTTTCT CGATCGTTGC 16260

CTGGACGGCG GTGACTGGTA CCCCTTTTCA GAAGGCCGCC GTTTTGTATC ATTCCACCAC 16320

GTGGATGAGC TTCGTATCTG TGCCTCCTGC GGGCTGACAG AAGTACATCA TGCCCCGGAA 16380

AATCATAAGC CGGATCCGGA ATGGTACTGC TCCTCTCTTT GTCGCGAAAC AGAAACACTG 16440

TGTCAGGACA TTTATGAACG TTCTTACACC GGTTTTATTT CCGATGCAAC GGCGAATGGT 16500

CTGATTCTCA TGAAACTGCC GGAAACCTGG AGTACAAATG AGAAAATGTT TGCTTCCGGA 16560

GGGCAGGGAC ATGGGTTTGC CGCTGAACGG GGAAACCATA TTGTCGACAG AGTCCGTCTG 16620

AAAAACGCAC GGATCCTCGG TGATAATAAT GCCAAAAATG GAGCAGACAG ACTGGTCAGC 16680

GGAACAGAAA TCCAGACGAA ATATTGTTCA ACTGCAGCCC GTAGCGTCGG TGCGGCATTC 16740

GACGGACAGA ACGGACAGTA TCGTTACATG GGAAATCATG GTCCCATGCA ACTGGAAGTC 16800

CCCGTGATCA GTATGCCGGC GCTGTGGAAA CCATGAAGAA TAAGATCCGC GAAGGTAAAG 16860

TACCCGGTGT AACCGATCCC GAAGAAGCGT CCCGGCTGAT TCGTCGGGGA CATCTGACTT 16920

ATACCCAGGC CCGTAATATC ACCCGGTTCG GGACCATCGA ATCGGTCACT TATGATATTG 16980

CCGAGGGGTC GGTTGTCAGT CTGGCGGCCG GAGGGATCAG TTTTGCCCTG ACGGCATCGG 17040

TCTTCTGGCT CAGCACCGGC GATCGCGATG CTGCCCTGCA GACAGCTGCT GTCCAGGCAG 17100

GAAAAACCTT CACCCGCACA CTGGCTGTCT ACGTCACAAC CCAGCAACTT CACCGGCTCA 17160

GTGTTGTTCA GGGTATGCTG AAGCATATTG ATTTTTCGAC GGCCAGCCCG ACTGTCCGGC 17220

AGGCGCTTCA GAAGGGGACC GGTGCAGGAA ATATCAGTGC CCTGAACAAA GTGATGAAGG 17280

GGTCGCTGGT GACATCTCTG GCACTGGTAG CTGTCACAAC CGGCCCTGAC ATGATCAAAA 17340

TGTTGCGGGG ACGGATCTCC GGTGCGCAGT TCATCAGGAA TCTTGCCGTG GCATCTTCCT 17400

GTGTGGCAGG TGGTGCTGTC GGGTCAGTGG CGGGCGGGAT ATTGTTCAGT CCACTGGGAC 17460

CATTTGGTGC ACTGACAGGG CGTGTGGTTG GCGGTGTTCT GGGGGGAATG ATTGCCTCCG 17520

CTGTATCAGG AAAAATTGCC GGAGCGCTGG TTGAAGAAGA TCGCGTCAAA ATTCTGGCAA 17580

TGATTCAGGA GCAGGTGACA TGGCTTGCCG GCAGTTTCCT GCTGACCGGA CATGAGATTG 17640

AAAATCTGAA CGCGAATCTG GCCCGTGTTA TCGATCAGAA TGCTNCTGGA GATCATTTTC 17700

GCCGCCGGTA 17710

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

AATAACCAAT AGATGCTTAA GTTTACGATA TGCCTCAACC CGCGTCTGCT CTAAGCTGAT 60

AAGGCCAGTT TTGTAGAGAT CCGCTGCCAA GGTTGCCTGC GTTTGCACAT CCATGTAACC 120

GGCGGTGATT TCATTCATGG CATCGTTATC TTGACCAGTC AGCTTAGCAC GCTCCTGTTC 180

AAGCTGCTTG GTTAGGGCGT CAACTCGGCT CTGTAATGAG ACTACGGCCG GTGCGGTTTC 240

CTTCATATAG CTGCGCAGTT GTTTTAGCTC CGCCTGTTGA CGCACCAGCT CTCCTTCAAT 300

CTGGCTGACC ACTCCCAAGC GTGCGCTGCT GGTAGATTCA GGGCTGAGAA GTTGGTGGCT 360

ATTCTGAAAT GCTAATACTT TAGCTTTTTC ATCCTGTAAG CGTTGATATG CTCTATTTAC 420

TTCTTTTTCA ACAAAGGCCA ATTGTTCGAG CGCAACCTGA TGACCTAATT TGTTAATAAA 480

ACGCTCCGAT TCTTTGAGCA TTAACTCAAC AACTCGCTGA CCGTATTGGG GATCAAATGT 540

CTGCAACTCA ACGGTAAGTA CTCCTGATAA TTCATCAAGG TGTAACGTCA AATGTTTGCG 600

GTAATAATCA AGAAAATCTT CCCTACTGAC TCCCTTATGC AACCGCGAGA AATAATCTGC 660

ACTATCACTC TGGAAATGTG CTTTAAGTGC AAGTTCTTTG TCCAACTTGG CCAGCATATC 720

CCATGACTTC ATATAATCCT GAACGAGTAA TATATCCTGA TGATTACTAC CACCTATCCC 780

TAACATTGAT AACGCATCAG GCAACATTTT AACTTGATCG GCTTGTTTAA TCATTAATTC 840

AGCCCGGSTC ACATAACGAT CGGAAGCAAT GAAGCCAAAA TAGAGCACTG CGATAGAAAA 900

GCAGATAACT ACCCAAAGAA AACTGCCTAG CTGTAAACTT TTCTTCCACG AGCGGTGTAC 960

AATTTGATAT CCTCTCGAAT CAATCAAAAA TAGTTTTGGA TTATTGCTCA GTTTTCTTAA 1020

CTTTCGCGTA AGGCGAGATA TTGAGGATGA AGAATTCGGA GATGTCATAA TCAGTTGCTG 1080

CTCAAAGTGA CTGGTAAATT TTGATGGCAT CATCAATATT ATCAAAAACT TCTAATTTAC 1140

CATCACGTAA CAAGATGCCC ATATCGCATT GTTGTCGTAG ATTTTTCATA TCATGCGAAA 1200

CCATAATCAA ACTAGCTGTT TCTCGCTTTT TGTTAAATAC ATCAATACAT TTTTGTTTAA 1260

AACGTGCATC ACCTACTGAG GTAATTTCAT CGGTAAGATA TATATCAAAA TCAAAAGCCA 1320

TACTAACAGC AAAAGAAAAT TTTGATTTCA TGCCGCTAGA GTATGTTTTA ATAGGCAGCT 1380

CATAATGTTG TCCAATTTCA GAAAACTCTT TAACCCACTC TTCTACGGGG CTTGTATCGC 1440

GTACACCATG AATGCGGCAA ACAAATCGCG TGTTTTCACG ACCAGTCATA CTACCTTGAA 1500

JSDOCID <WO_9822575A2 I >

ATCCCCCAGC TAGTGCTAGA GGCCAAGATA CTCGGCAGAG ACGAGTTACT TTCCCCCTGT 1560

TAGGCGTATC CATCCCTCCT AACAAACGTA ACAAAGTAGA TTTYCCKGCT CCATKGATAC 1620

CTAGAATACC TATATTACGG TCCCTTGGTA GCTCAATATT TACATTCCTC AGGACATAAT 1680

TTCGTCCAAA TTTAGTTGGA TAATATTTTG ATACATTATC AAGAATAATC ATTTTTCTTA 1740

ACGCTAACTA GCAATCAATT GGCGATGCCG TAATCGGTAA CAACTCATAG CAAAAGTGAG 1800

CAA 1803

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGGACCCAAG GTAAAAACNG GTAAAAAAAA CMATTGACCG ATTAAACTTT ATTTCTCTGC 60

CCGCATTAGT CTGGAGAGAG GATGGATGTC ATTTTAATTT NACTAAAGTC AGTAAAGAAG 120

CAAACAGATA TCTTATTTTT GATCTGGAGC AGCGAAATCC CCGTGTTCTC GAACAGTCTG 180

AGTTTGAGGC GTTATATCAG GGGCATATTA TTCTTATTGC TTCCCGTTCT TCTGTTACCG 240

GGAAACTGGC AAAATTTGAC TTTACCTGGT TTATTCCTGC CATTATAAAA TACAGGAAAA 300

TATTTATTGA AACCCTTGTT GTATCTGTTT TTTTACAATT ATTTGCATTA ATAACCCCCC 360

TTTTTTTTCA GGTGGTTATG GACAAAGTAT TAGTACACAG GGGGTTTTCA ACCCTTAATG 420

TTATTACTGT CGCATTATCT GTTGTGGTGG TGTTTGAGAT TATACTCAGC GGTTTAAGAA 480

CTTACATTTT TGCACATAGT ACAAGTCGGA TTGATGTTGA GTTGGGTGCC AAACTCTTCC 540

GGCATTTACT GGCGCTACCG ATCTCTTATT TTGAGAGTCG TCGTGTTGGT GATACTGTTG 600

CCAGGGTAAG AGAATTAGAC CAGATCCGTA ATTTCCTGAC AGGACAGGCA TTAACATCTG 660

TTCTGGACTT ATTATTTTCA TTCATATTTT TTGCGGTAAT GTGGTATTAC AGCCCAAAGC 720

TTACTCTGGT GATCTTATTT TCGCTGCCCT GTTATGCTGC ATGGTCTGTT TTTATTAGCC 780

CCATTTTGCG ACGTCGCCTT GATGATAAGT TTTCACGGAA TGCGGATAAT CAATCTTTCC 840

TGGTGGAATC AGTCACGGCG ATTAACACTA TAAAAGCTAT GGCAGTCTCA CCTCAGATGA 900

CGAACATATG GGACAAACAA TTGGCAGGAT ATGTTGCTGC AGGCTTTAAA GTGACAGTAT 960

TAGCCACCAT TGGTCAACAA GGAATACAGT TAATACAAAA GACTGTTATG ATCATCAACC 1020

TGTGGGTTGG GGTGCACACC TGGTTATTTC CGGGGATTTA AGTATTGGTC AGTTAATTGC 1080

TTTTAATATG CTTGCAGGTC AGATTGTTGC ACCGGTTATT CGCCTTGCAC AAATCTGGCA 1140

GGATTTCCAG CAGGTTGGTA TATCAGTTAC CCGCCTTGGT GATGTGCTTA ACTCTCCAAC 1200

TGAARTTCAT CATGGGAAAC TGGSATTACC GGRAATTAAW GGTGATATCA CTTTTCGTAA 1260

TATCCGGTTT CGCTATAAGC CTG 1283

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TCAACCTGAC CAACCACTAG AATCAACTCA CGTCCGTCGT TAGGGGGCTC ATATTCTTGT 60

GTACTCCCCA CATTGTATTT ACTGACTCGT GATGATTGTA ATTGCGCTAA TAATGACTCT 120

GCGCGTGCTT CTTCTTTCGC ATCTAAAACG TACGTAGTGA GTAACTGCTC AAGCTTACTC 180

GGACGGCGGC TATCAAAATA GATTCCAACG GGGTCAATCG AGAGTGATGA AGGTCGACAT 240

AAATTAGACC CCAATCCGTT GGAGCGGATA AAACCATCTT CAATCCGGAT CACTGATTGC 300

AGTTCAGGAT AACGGTTTCC CCACACCAAC ACCTGTTCAT CATCTTTTAA CTGTGAGGGC 360

ACAGTACGAA CAAAACAAAG TTCATCTGCC AAATACGCAC AAAATGTGCG TATAAAAGCA 420

CGCTTCCACA GAGAAAAACC AACGAGATAA AGACGACGCC AAGGTTTGGG CTCTACCTGC 480

TGCTGAGCCA AAATCGCTAC AACATCTTCT ACCTCACAAC GTTTTCCCAA TATAGGATCT 540

AAATAACGCG GATAACGGAT CAACGCCGCC GCAACTAAGC GGGGCAATGA AATAGATGAA 600

ACGCCTTCGG CTGACATTGC TTCTTCACGG CGTATACAAC GTTTACTGTC ATGCGTTAAC 660

CCCCACCCAG CATAAAATGG CATACCGAAG CAATATACAG GTTTGCCCAA CAGCAACGCT 720

TCCAAAGCCA ACCTGCGATG AAACTGTGTA CACCGCATCC ACCATACGAA TTATTCTATG 780

CGGATGGCAA GTTCACTCAC CACCTCAACA TCAGCCAGTC GAGGATCACG CCCCACTAAA 840

CGTGCTAACA CGCCGCTTTT TTTGCTAAAG CGTGTATCTG GGTGTGTTCG CAACAATAGA 900

CGCGCATTAG GGTGATTACG GCGAGCCTCG ACCACCATAG AAACAAAATC AGCTTCGCAA 960

GCAAGAGCCC CAGAAATTGA CAAGTCTCCC GCTACTTGAT CCACAAGCAA AATACGCGGT 1020

CTTGGATCAT CCAGTAAACG TGCTAAGTTT GAATGAGCCG TGAGGTGAAT AACTCAGGTT 1080

GTATATGTGT CGGTAAATCT AAAGAAGGCC CGTCAGTAGC ACGGGACAGA GCCATTAAAT 1140

GTATGCTCAG TGCTATTGGG TATAGCAGTT ATACTTGGTG ATTCCTAAAC GCAAAATATC 1200

MGAGATCAGA TGCTCCAGCG CGCGCAAAGT AAAGCCGTAT CCAACAGGTT CCAATAATAA 1260

GCTGTTCTAA TTGACTCGTC TGATGTGCAT CATAATATAT CCCCAGAGGG TCAGCAATAA 1320

GAGAAACCGC CTTTCCTCCT TTTGCTGGGT GCCCGATATA GCCAATAAAA CCATCTTCAA 1380

GTTGCCAATA AGATATTCCT AACTCTTGAG CTTTCTGTTT AATCTGCTTA GTATTAGATT 1440

JSDOCID <WO. 9822575A2 I >

TTTTTCCCCA GCCAACTAAA ACGTCATTTT TAGAAAAAGC CTCGTCTCCT TTCATATAAA 1500

GCAATGGGTG ACCAAGCATA GGCTCAATAT TATTTTYTCT GGCAAGAATC CCTTTCGATC 1560

CCGTATATAA ATACATGTTG TCTCTGTGAA CTGAAGATTC TCTACAATGG TGTATAAAGT 1620

GTGATTTAGA TGAACAGCTC TGCGCTCTCT AATGACTTTG CAATACTATC TTTTGCTGAA 1680

GTGAGAATGT CCGCCTTTAA CTCGGGCCAC CTAATACCAA TTGTAGGATC ATTCCATGCA 1740

ATGCCTCTAT CACTGGCAGG GGCATAATAA TTAGTTGTTT TATACAAAAA TTCGGCCGAT 1800

TCAGTCAGTG TTACAAAACC ATGGGCAAAT CCTTCCGGAA TCCATAATGT CGTTTGTTTT 1860

CCCCTGAAAG ATGAACGCCA ACCCATTGTC CGRAGCTCGG TGAGCTTTTG CGAATATCTA 1920

CCGCAACATC AAACACTTCA CCGGCTACAC AACGCACTAA CTTGCCCTGG GCATGGGGAG 1980

GTAACTGATA GTGCAAGCCA CGCAGTACCC CTTTAGAAGA TTTTGAGTGA TTATCCTGCA 2040

CAAAGGTAAC TGGATATCCT ACAGCCTCTT CAAACAACTT GTGATTAAAA CTCTCAAAGA 2100

AAAAACCACG CTCATCTCCA AATACTTTTG GCTCAAAAAT AAGCACACCA GGAATTGCTG 2160

TCTTGATTAC ATTCATCTAT ATGCCCACAT TTAATTAAAT ATTTTTAGGG GAAGCATATT 2220

CCCTCCCCCT TCTCAATTAC ATCACGCCTT ATCAATCATT TTTAATAAAT ATTGCCCATA 2280

GGCGTTTTTT GCCAACGGAG CAGCAAGYTC ACGAACCTGG TCGGCACTAA TAAACTTCTG 2340

GCGATAAGCA ATCTCTTCCG GACAAGCCAC TTTCAATCCC TGACGCGTCT CGATGGTCTG 2400

AATAAAGTTA CTCGCTTCAA TTAGGCTTTC GTGGGTACCG GTATCAAGCC AGGCATAACC 2460

ACGCCCCATC ATTGCCACCG ATAGATTGCC TTGCTCCAGG TAAATACGGT TCACATCGGT 2520

GATTTCCAAC TCACCACGCG GCGATGGCTT GAGACCCTTG GCAACGTCCA CAACGCTGTT 2580

GTCGTAGAAA TAGAGGCCGG TGACTGCGTA STACTCTTAG GCTCCAGTGG TTTTTCTTCC 2640

AGTGAAATAG CGGTACCTTG ATTATCAAAT TCGACCACTC CATAACGTTC CGGGTCGTGC 2700

ACATGATAGG CAAATACAGT AGCACCGGTC TCTTTGGCCG CGGCTGCCTC CAACTGTTTC 2760

TGTAGGTCAT GACCGTAGAA GATGTTATCC CCCAGCACCA GTGCACACGG GGCTGAACCA 2820

ATGAATTCTT CACCTAGAAT AAAAGCTTGT GCCAACCCGT CTGGGCTTGG CTGAACCTCA 2880

TATTGTAAAT TCAGTCCCCA GTGGCTGCCA TCACCCAGCA ATCGCTGAAA GGANGGAGTA 2940

TCTTGTGGAG TGCTAATGAT CAAAATATCG CGAATTCCAG CCAGCATCAG GGTGCTCAGC 3000

GGCCGCAGTA CTGGATCATC GGCTTGTCAT AGATGGGCAA CAACTGCTTG CTCACCGCCA 3060

TAGTAACCGG ATAGAGACGT GTACCAGATC CACCGGCCAG AATAATACCT TTACGTTTAG 3120

TCATGATGCT TGTTTCTTAT TTTTAAATTA CATAAGAATA AAGTGGCTTG AGCCGCGCCT 3180

TTCTGTTTTA TCCTCACCTG TGGTTTACTT CCCCATGATC TCAGTCAACA TCCGCTCAAC 3240

ACCGACTGAC CAGTCCGGCA AAACCAGATC AAATGTACGC TGGAATTTTT TAGTATCAAG 3300

TCGGGAATTA TGAGGGCGTT TCGCCGGGGT CGGAAAGGCG CCTGTCGGCA CTGCATTAAG 3360

CTGTGTGACT GCCAGTTCAA CTCCTGCGTC TCTGGCTTTG TCAAACACCA ACCGGGCGTA 3420

GTCAAACCAA GTGGTAGTAC CGGAGGCAGC CAAATGGTAC AGCCCGGCAA CGTCGGGTTT 3480

GCTCTGTGCA ACTCGGATTG CATGGGCGGT ACAATCGGCC AGCAACTCAG CTCCAGTTGG 3540

AGCGCCAAAC TGATCATTAA TGACCGATAT CTCGCGACGC TCTTTGCCAA GACGCAGCAT 3600

AGTTTTGGCG AAGTTGGCAC CGCGCGCAGC ATAAACCCAA CTGGTACGAA AGATAAGGTG 3660

ACGTGAGCAG AGTGCCGCAC CGTGTTCCCC TGCCAGCTTG GTTTCGCCAT AGACGTTGAG 3720

CGGGGAAATC ACATCGGTTT CCACCCAAGG ACGTTCACCA CTTCCATCGA AAACATAGTC 3780

GGTGGAATAA TGTACTAGCC ACGCACCTAA TGCTTCAGCT TCTTTGGCAA TAACCGCCAC 3840

ACTAGTTGCA TTGAGTAACT CGGCAAATTC CCGCTCACTC TCCGCTTTGT CGACTGCAGT 3900

ATGGGCCGCT GCGTTAACAA TCACATCCGG CTTGACGAGA CGTACCGTTT CAGCCACCCC 3960

TGCAGAATTG CTAAAATCAC CGCAATAGTC GGTGGAGTCA AAATCAACGG CAGTGATGTG 4020

CCCCAGAGGC GCCAATGCAC GCTGCAGCCC CCATCCACTT TCTGGCCACA CCAGACTCGC 4080

CAGCAAAAAA GTGAGTGCTG TCAATAACTC AACCAGCGGA TAACGCTTGC TGATTTTCGC 4140

CTGACAGTCG CGGCAGCGCC CTTTGAGCAT CAACCATGAG AGCAGCGGAA TATTGTCACG 4200

AACGCGGATG GTCTGCTGGC AATGCGGACA GTGCGAACGC GGTAGCGCAA GGCTTATTTT 4260

TGACTGCGCA CTCGGCATTT CACCATGAAA CTCCGCCATT TGTTGGCGCA GCATGATGGG 4320

GTAACGCCAA ATCACCACAT TCAAAAAACT GCCGATGATC AATCCTCCGA CGGTTGCCAG 4380

TATGGGCATC GCCGCGGGGT ATTGCTGAAA AACATCAAAA AGCATGGTTA AAGGTTATTT 4440

GTTGTAACTT GCCGGATGCG GGCCTGCGGG TGTATGCCAT ACGGCTTTCC TTCAGGCCCG 4500

ATGCGCCTTA TTTCATGCCG GATGCGGCGC GAGCGCCTTA TCCGGCATAC AGGCTTACTC 4560

AGCTGACATC TTATGCTCGG TAACCTGATT AATGGTTTCC GGCCCTTGCT GCGGTTTCGG 4620

CAGATTAAGC GCCGCCAGTG TCTCGTAAGC CGACTGGCTC ACACCGCCCT CGAAGTTCAT 4680

CTCGCTCGCT CCCGGCAACT GGTAAGCATT CGCGCCCGGA TTCCATTTCT TAAAGAACTC 4740

CGAAAGATCC GTCTGGGCGA CCCAGGATGC ACACAGCATC AGCTTGTCGG CAGCGTTACC 4800

GTTGGATTCG GCACAGTAAT TTCTTTCGCC AAACTTGGTT TTGCCAACCT CATCGCCGCG 4860

TGCTTTACGG TGCATCAACT GGAACAGGTT CCAGCCTTTC ATCCCTTCAC GATCGCTGTA 4920

GAACTTAGGC AGGTCACCTT CTGGATACCA CTGTTTGATA TCAAAGTTTT TCTCTGCCCA 4980

CTCTTTCAGC TGTGCGTACA TCAGCAGACG GTCACCCGCA CCGCCGCGCG CCCATGCCTG 5040

ACCGTTGCTC TCCTCCAGAT ATTCCGGCGC GACGGTAATG TCGTCAGCGA CACGGTTCAT 5100

CTTGCCGAGA TAGCGATCCT GCATGTACAG CGCCAGCACG TTGTTCGCTA CTTCAGTTGC 5160

GCCAGGAACA GTCAGCGGCG TTTCGGCGGC GTTGTGACCA ACTTCGTGCC AGATCAGCCA 5220

GTCGTTCAGC GGCGTCGTCG GCAGCGTGGT GCTGTTCGTC GAGAAGCTGC TGTTCATTAC 5280

CGGATAACCA GAGTGCGCAT CACCGATGGA GATCTGCACA TCGTTGGTGA AACGATGCTT 5340

GTGGCCCGTC AAGTTTTTAT AGGTAAACAT CCGGTGCTTA CCGTCTTCAT CATTACGACC 5400

GTAGAAGTCA TTCATCGAGC TGGCAAAGGT ATCCAGATCT TTAGCGAATT CTGCTACGCC 5460

ACCAGTGAAA TTGCTGGCCT CAAGGTTCTT CTTCGGCGTG GTGTAGACGA AAGCGTCTGA 5520

CTCCAGCTCG CCCAACGGCG CAGGGGAGTT CAGAGCGTTT TTCCATGCGC CATCTTTATA 5580

GAACGGCGCT TTCACCACAC CAGTAAAGGT GAATTCGGCT GACTCATTCT GTGGGCTGTT 5640

GCCCTTGATA TAAATCAGAC CACCGTAAGG AACCGTAAAC TTCACCTCAC CATTGGCTTT 5700

CAGCTCATAG GTTTTCGTCA CTTTTGGCGG ACGGTTCAGA GCGACTTCAT GCTTCTCACG 5760

TCCGGTAAGG TCGTCGGCCA GCGCCACGGT GACAGTCACA GGAACTGATG CAGAAGACTC 5820

AATGGTGACC TCTTTCTGAG CCGGAGCCCA CAGGCCAGTA GACTGCATGT TACCCGCAAA 5880

CCATTTGGTC GGATTCGAGT ACAGGCTGAT GGTTTCAGTA ACCTTCTCAC CTTCTGCCGA 5940

TACCGCTCCC GGATACTTCT CGACATCAAC TTTGATGTTC AGATCCCACC AGGAACGACC 6000

CAGCATCAGG CGCGTCAGCG GTTTTTCCAT ATAGTTGAGC GGATAGCTCG GGTTCATCAT 6060

GCCCGCTTTA TTAACGCTCT TCTCGCCGTA GATCATGTTG TTATCGACCA GCGATTTTTT 6120

CAGCTCATCA GAAACACTGC GTGCCGCCAG TATAGGCATC GTTGGCGTAG CAGTTCAGGA 6180

ACTCGGTGAA CGTTTTAAAG CCCAGCTCGT CATCCTTGTC GTTTTCATAG CGATATTCAA 6240

TTTTATTCCA CAGCCAGACC GACATGTTCT GGTACAGACG TTCCAGATCG ACGCTGCTCA 6300

GACGCTCACC TTTGCGACCA TTGGTCCGGA AGTAGAGCTC ATGCTGATAC AGACGCTGAA 6360

TGTTGGTGCC TAAATCCGCA GCCTGCACCA TCGCTTTTGC CGTGTCGGCG TTAAGGCTTA 6420

GTTGCGTATA CTGTGGAACA TACATGCCAC CAGTAACCGG AACCCCCGTG CCAGGACGAT 6480

ATTCCAGACA GTTGACCTCG TAGTGGTAAG TTGGGTCCTT ACACTCCTTT AATCCAGGAA 6540

ACTTCTCAAA GATTTTTGCC TTCGCAGCCT TCAGAGAATC CTCTGTTTTA TGATCGGCCT 6600

CATCAATAAA GGCATAACGC GTTTCCTGTT TGCCATCTAC ATCTTCCAGC CAGCTGGCAA 6660

CTTCCAGCTT CGGTTTGTCA TCAGGTTTGT TTTCTACCTG ATATTTCCAC TTAACTTCCC 6720

CTGTCTTACT ATCGATGGTG TACGGCAGCG CACCATCTAC GGCAGGATAA CGTTCATAGA 6780

CCCAAATGCC CGTTGCGCGC TGCTGACGAA CGCGGTTCGG ATACCCTTGC GGATCC 6836

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

3NSDOCID <WO_ 9822575A2 1_>

GGAAAAACNC GCCGTATATT AGCCCGCGCG GAAAAAGCCC CGTNACGGGC AAACGCAGCA 60

AGGTTTTATC CCAGCGCAGG CGCATGGCAG GATTTTTGAG TAGCCGTTGC CCCAGCACCA 120

GAAGCCCCAG CAATCCCGCC AGCCAGTAAA CGCCGCTGGT CTGTAACGTG TCGCTCATGG 180

CGATGAGCGT GCGGGTGGAG GCGGGCAGCG CGTGTCCGAG ATGATCAAAC TGTTCGATGA 240

TTTTTGGCAC CACTGCCGTC AGCAAAATAG TGACCACGCC CGTTGCCACC ACCAGCAGTA 300

CCAGCGGGTA GAGCATGGCC TGCAGCAGGC GTGAATTTCC AGNACCTGCC GCTGTTACGG 360

TGTAACCCGC CAGGCGATTG AGCACCACGT CGAGATGTCC GGATTTTTCT CCGGCAGCAA 420

CCATCGAACA AAACAGGGAA TCAAAGACGC GGGGATGTTC GCGCAGGCTG TCCGACAGGK 480

TGTAACYTTC CTGAATCCGC TGCGCAGCGC CATTCCGAGG CTTTTTACAT GCAGTTTTTC 540

ACTTTGCTCA CTGACCGCCT GTAAGCAGGT TTCCAGCGGC ATTGCTGCCT GTACCAGCGT 600

TGCCAGTTGG CGCGTGAACA GCGCAAGATC TGCCGCCGCC ACGCGACGAT GTGCGTGCCG 660

CCGACGCTGC AACATCCCCC CTGACGAAGT ATTCATCCGG GCTTCAATAT GCACGGGGAT 720

AAGCTCTTTA CCGCGCAACA ACTGGCGGGC ATGACGCGCG GAATCCGCCT CAATCATACC 780

TTTGGTTTTG CGACCATTAC GCTCCAGCGC CTGATAGTAA AACAGTGCCA TTACGCCTCC 840

ATGGTTACCC GCAGAACTTC ATCGAGAGAG GTTTCTCCGG CGAGCACTTT CTCAATGCCG 900

TTGCTGCGGA TACCCGCAGA GTGTTGTCGG ACATAACGTT CCAGCTCCAG CTCCCCGGCC 960

TGACGGTGGA TCAAATCACG CAATGTGGCA TCCACCACGA TCAGCTCATG GATGGCAGTC 1020

CGTCCGCGAA AACCTTTGTG ATTACAGGCG GGACAGCCCT GTGGATGGTA CAGAGTGACG 1080

GTACGGGCGT CGGTAATTCC CAGCAGGCGT TTTTCTTCGT CGGTGGCAGG CGCGGCCTGA 1140

CGGCAGTCGG AGCACAGCGT GCGGACCAGT CGCTGCGCCA TCACGCCCGT CAGACTGGAA 1200

GAGAGCAGGA AAGGCTCCAC GCCCATATCC TGCAAACGTG TGATCGCCCC CACCGCTGTG 1260

TTGGTATGCA GCGTGGAAAG TACCAGGTGT CCGGTCAGTG AAGCCTGAAC AGCGATTTCT 1320

GCGGTTTCGG TA 1332

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CCCAACGTTT ATCGTATTTC ATTAAAGTCC CTTGCCCGAT GCTATCTCGA GTTACATGAC 60

GAAATCGCTG ATTTGGATGT CATGATTGCG GCAATTGTCG ATGARCTGGC GCCTGAACTG 120

ATTAAACGTA ATGCTATTGG ATACGAAAGC STTCGCAGTT GCTGATCACG GCAGGAGACA 180

SDOCID <WO _9822575A2 I_ >

ATCCCCAACG ATTAAGATCA GAATCAGGTT TTGCGGCACT GTGTGGTGTC AGCCCTGTTC 240

CCGTATCTTC AGGAAAAACG AATCGTTATC GACTTAACCG GGGTGGAGAT CGTGCTGCAA 300

ATAGTGCACT TCACATCATT GCCATCGGAC GTTTGCGAAC TGACGATAAA ACGAAGGAAT 360

ATGTCGCCAG ACGAGTAGCG GAAGGGCATA CAAAAATGGA AGCAATACGC TGCCTGAAGC 420

GCTATATCTC ACGCGAAGTT TATACATTAC TGCGTAATCA AAACAGGCAG CTCAACAGCA 480

TCCCGATAAC GGCTTGACTC TTAGAAGGGC GTCCAGGGCA GCCACTATAC AAGCAGGCAG 540

TTCCGGCAGT TACTGTGGCG TTACCAGATC AAACAGAGTC TGAGTCGACG AGGAAATTGC 600

TGGGATAACA GCCCGATGGA GCGCTTCTTC AGGAGTCTGA AAAACGAGTG GATACCGGTG 660

ACGGGTTACA TGAACTTCAG CGATGCTGCC CATGAAATAA CGGACTATAT CGTTGGGTAT 720

TACAACGCGC TCAGGCCGCA CGAATATAAC GGTGGGTTGC CACCAAATGA ATCGGAAAAC 780

CGATACTGGA AAAACTCTAA AGCGGTGGCC AGTTTTTGTT GACCACTACA TTTAGTGCGA 840

CACGGGAAGC GCGATATGAA CGATACGATA CATCAATGGT TTATTGCGGT GATAACCTGA 900

AGGGTGAGAT TGAGGCTATT TATAATAGTC TTGAGAGGCG TCAGGTTTAG AGCAGGAATG 960

CTGAGTAGCC ATCTTATCGA TTGTTTTCGA GCGTAAGATG GCTGAATGGA ATGGCTATTA 1020

TTGCACAGTC CTTAATTATA ACATTCATAC CGACATGATT ATCTTCTGTC CGGAAGAATC 1080

AGAGGCTGCG GTTTCAGACT GTCTGCCGGT ACATTCCTCT CTCCGTTAAA AACCATAACG 1140

GGTTCATTAT CTTCGTCTGT CAGCAGATTG AATGGCGGTA TATTTTCAGT ACGAATGCCG 1200

GTCAGCCACT GAAAAATACC TGCGAAATGA CGGGCACTGA TTTTTCTGCT GACGGACTGA 1260

TGAGACGTGA TGTCACTGGC GGTAATAATC AGGGGAACGC TGTAGCCTCC CTGCACATGA 1320

CCATCATGAT GAACAGGATT AGCACTGTCG CTGACCGACA GACCATGGTC AGAAAAGTAA 1380

AGCATGGCAA AATGACGGGA ATGCCGGCGA AGGATACCAT CAAGCTGCCC GAGAAAGTTA 1440

TCCCAGTTTA CTGATGCTGG CGAGGTAACA GGCAATTTTT CGGGGATACT GCCCCAGGTA 1500

ATGATTCGGC CAGGAGTTAA GCCGGTCACA CGGGTTCGGA TGAGACCCCA TCATGTGCAG 1560

GAATATCACT TCGGAGAGGA TTTATCCGCC AGTGCACGTT CTGTTTCCTG TAACAACAAC 1620

ATGTCATCCG TTTTACGGGA AGCAAAGCTG CCTTTCTTGA GGAAAACGGT ATGCTCCGCA 1680

TCAGAAGCAA TAACAGAGAT GCGTGTATCA TGCTCCCCCA GCTTTCCCTG ATTGGATATC 1740

CACCATGTGC TGTATCCTGC TTTTGCTGCC AGCGCCACCA CGTTGTTGCC GGAGTCAGGG 1800

TTCTGCTCAT AGTCATAAAT CAGTGTCCGG CTCAGGGAAG GTACGGTACT GGCTGCTGCC 1860

GATGTATAGC CGTCAATAAA TAAACCGGGA GCAGTATTCA GCCACGGTGT GGTTGGCACG 1920

GGATAGCCAT ATACCGACAT ATAATCCCTG CGCACACTCT CACCAGTGAC GATAACAATC 1980

GTGTCATACA ACGGTACACC CGGCAGGATT TTCCAGTTGT CAGCCCCGTG CTGATTCAGT 2040

TGTTTATAAC GCTGCATTTC ACGCAATGTG TCAGTTGTCC CCACAACAGT TCCTTTAACC 2100

ENSDOCID <WO_ 9822575A2 ! >

ATCCGCAACG GCCAGCTGTT TACTGAGCAT AATACGAACA GCAGCAGTGC CAGCCAGTTA 2160

CGGTGACCGC GGTGGTGTGT TCGCCAGAAA ATCACCATGA ATACCAGAAT CGCGGCACTG 2220

ACCAGAAAAT GATAAACAGG AATCATCCCG GTAAACTCCG CTGCCTCATC AGTTGTGGTC 2280

TGCAGCAACG CAACAATAAA ACTGTTGTTG ATTTTACCGT ACGTCATACC GGCAGGCGCA 2340

TACAGTGCAC AACAGAACAG AAATAACAGC GCTGTAATGG ATGTGAGGGT ATTTCTGTGT 2400

GCAAGAAGCA GAAGAAAGAA CAGCAGCAAC ACATTCCCGG TGGTATTCTT CTCAGTGTAT 2460

CCGCATGCAA TTGTGGTTAT GACAGAAACA ACAAAAAAGA ATAAAAACAA TATAATCCTG 2520

AGAGTGTTGC CCGGACAAAA CAGTTTTCTG ATATTCATCG GAGTATATCG ACAACATTAT 2580

TATGAAGAGA ACAGGATAAT AAAAATCAGA AGTTATCTGT GAAACAGATA ACAGACANCC 2640

CTGCAGTATA ATATTACTGC AGGGTGTTCC TTTTTAATTA CAGAAATACG TAATTATCTT 2700

AATTGCAGAA ATATGCGCAA TTATCGTTCA GAAGCAGTGT CGTCAGAAGT TATAAGTCAC 2760

ACCAAGCAGG ATGTCATGAC TTTTAACATC AACCTCTGAT TTATATTTAT CCCCTTCTGT 2820

ATCCTTGTAA TACAGGGAGG ATTTACCAGC ATCCAGATAG CGATAGCTGA GGTCAAGAGC 2880

GATATCCGGG GTTACGTCAT AGCGAACACC GGCCCCAATG CTCCATGCGA AGTTGTCAGC 2940

AGAGCCTGAG CGTGATATAG AATAACGCAC TCGCTCACCG TAGCCATAAT CCCAACTACC 3000

GCTACCTGTT GATTCCTGAT GAATTCTGGC GTAACCAATT CCGGCAGACA CCCATGGCGT 3060

AAATGCACTG TCGTTTCTGA AATCATAGTA CGCATTCAGC ATCAGGCTGT TGACTGACAC 3120

CTCATTCTTC AGGTCACTAT GTCCCGCGTG GTCCTTATAG AGGTTGTATG TTGTGTCAGC 3180

TTTTCCACGG GCGTAAAACT CCAGTTCTGT ACGCACAGGA ATACTGAACT GCGGATGCAA 3240

GTCATAACCA AACGCTATAC CTCCACTGAA TACCGTGTTA TGGCCATCCC CCCCCTATAC 3300

TTTGATGTTT CCTCTTTATT TTCGGACAGG AAACTCTGGT CAGAAAGAGA TACTGCTGAA 3360

GTACCTGCTT TACCGGTCAG ATAAAAACCG CTTTTACCTT CCTCAGCACC CGCATTTGCT 3420

GCAANCATAC AGGCAGCGGT AACTGCTGAA ACAGCAAAAA CTTTTTTCAT TTCAATTAAC 3480

TCCATTATTT CACTATTTTT GTAAATAGCA CTCCTAATAT TTTAAAACCA GTCAAAAGAT 3540

AGTATCAAGC AAATTATTCA TGTCTAATGA ACAGATAAAA TCGACTATGT GTCGGCAAGA 3600

CTCTGCTCCA CCGATATTCC TCTTATTTCC GCCTCGATGA AATACCCCCG TTACCTTATT 3660

TGTACCCCTT ATAATGGGAT GTTGGCCAGC CAGACCCGGC ATGATTAGTT CTCCCTGTCG 3720

ACTATGCTCC GGGAGGGATG TCACCGGGTC TGGTGAGGCG CGGATAACCG CTAATAGGGG 3780

AAGGTCAGGT ATTTTACACC GGGACCGTCA GGGCAAGATA ACGAAAGCCA GCTCCCCGCA 3840

TGAACTGACG CCAGATAGTT TCTGTCCATT GCTGCTTTTC TCATCTTACG TCTTAACCCT 3900

GCCTTGAATA CCTTATCTCT CGTCAAAATA TTAATAGCGA TATGCCGTAT CCCTGAAAAT 3960

AATCCCGCTG CGTTTCCTCT TCTTACTTGC AGTCGTCTTC ATTCATTACC ACGTCCAGAC 4020

GCCATGCAGC TTATTCTCCA CGTGCCAGTG ATTTCGGATC GCTGTGACGA ACTTCTCTGC 4080

GGTTAAATCA GCAGAACTGA TATAATATCT GACCATTATT TCTGACTCTT GCTTTTGTTC 4140

TGCTATTATT GACCGAAAGG AGACTGCCAG GCATATTTTT TCAGCCCTTT CCATTCAAAC 4200

GTGAATTCAA TCAGCTCATC AGGGACNTCG CCAAACCATA TGAAGACGGG ATCCTNCTCT 4260

GCCGTGACTC TTGTCACTAA TTGCGTAACA GTCATGCTCN GGGATAATTA AATCTTTCAG 4320

CGGAAATAAA AAGATTATCA GATATGGGGA TGACACCACA GCACCGCTGA GGCCAGTATG 4380

GATAAACCAT GTACCTTATT AACCAAA 4407

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TTTTTTGCAA GAGAATTTCC CTGAACCTGA AGCTCATCAT CGCCATCTCC GCCGTTCAGG 60

TAATTATTAC CTGCTCCCCC AATTAACTTA TCGTTGCCAT CACCGCCATA GAGCTGGTCA 120

TCTCCGTTTC CACCACTCAG TGTGTCATTA CCTTTATCAC CATATAAGCG GTCATTCCCG 180

TCATTTCCTT CTATATGGTC ATCACCATCC GCGCCATGGA AGATATCAGC AAATTTACTG 240

CCAAAAAACT TGTCGGCACG CGTGGTCCCA ATAAGTTCTT CCACGGAATA TAAGTTATCA 300

GTCTCTGTTA AATTTTTACC ATTGATATGA GTGAATTCAT AACTCCGATA TTGCGTTTTT 360

TCAGTTCTTT TTCCAACTGA AACCTCCTGC TCCTTCACAA CTTCCTGTAA AACCTTAACA 420

TCACCACCAA GTACACGTGT TACCGTGTAA TTACCCGCTT CGGTTGCTTT TGTGCCATCA 480

ATGGTCAGAT AACCGGTGTC TGTTTTATCA TAATAAACAA CATCATGTCC TTTACCTGCG 540

TAGATATTGG CTGAGCCGGC AGATAAAAAG ACCTTATCAT CCCCGTCTCC CAGGTGTGAC 600

TCAATACGAA TTTCCCGATA CTGGTTATTA CCGACTGATG CATGCTGAAT CAGGTTAGAG 660

TAATCATATA CAGACCCCTT GTCCTGNAAC CCCCTTCACC GTCCATTTAT CAACACCCTT 720

GACTAATAAC TCGGTAATAT ATTCATATTT TCCGGACTGC CTCCTTTCAC GAATTTCCTC 780

ACCGGGAGTT TAACAATGGG CGTAACNAAT TTGCAATAAC GTGG 824

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

3NSDOCID <WO__9822575A2_I_>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GNGGCCGCAG TACTGGATCA TCACCGAAGT TTCGCGCGGA AAAGCGTTAG AGAAAGATCT 60

AATGCTTCAT GATGGTGATG GACTTTTCCT GATGGTGAAA TCCAGCGGGA AATGCTCTGG 120

CGTTTCCGTT ATCAACATTC GACAACAAAG CAGCGGACAA TGATGGGACT CGGTGTCTTT 180

TCCACACTTT CACTTGCTGA TACCCGAGGG CTAAGAGTGG ATTATATTTC CTTATTAGCC 240

AACAGAATCG ACCCGCAAAT TCAAGCTAAA GCCGTAGACG AAGAGCAATA TTTGAAAAGG 300

TGGGCACCTA CGTTACCAAT ACTGGCTTAA TGGCTACATA CGGCGGTCAG GGTCAGTTTA 360

CGCTTACAAA ATATAAAACA ATTTGATACA AAATATTCCT CTTATTCTAA ATAAAAGTAT 420

CTTGAAAACC TTCCAACTGG AAGGTAGATT GAATTTATGC TAAACATAAA GAGGAATTGC 480

TTATGAATTA CGTTATCCGC ACTACCACCG TCGTCTTTAG TCTCATGCTG GGCAGGTTAC 540

GCAACTGCTG 550

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CACTAAAGGC CCTGGATGTT TTTCGCTCAT TAGTAGACAT CTCGCTGATA ACGGCGCTCT 60

ACGCGCACTC ACTTAAAAAT TCATCCGCCG CTTCGGTGTC CATGCCACCA AATTCGGCAA 120

TCACTTCCAG AAGTGCCTGC TCAACGTCTT TCGCCATGCG ATTAGCGTCG CCGCAGACAT 180

AAATGTGGGC ACCATCATTG ATCCAGCGCC ACAGCTCCGC GCCCTGTTCG CGCAGTTTGT 240

CTTGTACGTA AACTTTTTCT TTTTGATCGC GCGACCAGGC AAGATCGATA CGTGTCAGCA 300

CGCCATCTTT GACGTAGCGC TGCCAMTCCA MCTGGTACAG GAAGTCTTCC GTAAAGTGCG 360

GATTACCAAA GAACAGCCAG TT 382

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TAAATCAGCA GAACTGATAT AATATCTGAC CATTATTTCT GACTCTTGCT TTTGTTCTGC 60

TATTATTGAC CGAAAGGAGA CTGCCAGGCA TATTTTTTCA GCCCTTTCCA TTCAAACGTG 120

SDOCID <WO 9822575A2 I_>

AATTCAATCA GCTCATCAGG AACATCGCAA ACAATATGAA GACGGATTTC TTCTCTGCCG 180

TGACTCTTGT CACTAATTGC GTAACAGTCA TGCTCTGGAT TATTTAATTC TTTCAGCGAA 240

AATAAAAGAT TATCAGATAT GGGATGACAC ACAGCACCGC TGAGCAAGTA TGTATAACCA 300

TGTACTTATA ACAAAAGGAG ACGTAAGAAG GGGAACGGGT ATCAGAGGGC CAATCAAAGC 360

AGGTATAATG AACGCCAGTA TAATTGTCCG CAACCCAGAA ATATATTATT GAACTGGTTA 420

TCTCCTGCGA ATGCATATAC TGCAACGGCC GTTAAAATAG CATTATATCC ATAAAGCCCG 480

GCAGAGATTT TATCAGGAGA AAGCTCAGGA ATACAGAATG ATACCACCAC ACTCAGAAAC 540

GAAGCGACAA CCGTAATCAT CAGTAGTTTC CGGCTCCCTG CAAGTAGTCC CAGCATAACA 600

AGAATACCGC CGACAGCATC AGGAAACATA AAAATCTCCA TAAAGCTACC AGACAATGCC 660

ACCGGATAGT TTTTCAGCAA AACAGAACCT GCACTTCGCC CGAAGGTACT GACATATCAT 720

GAGGCATTAT TCCGGAATGT AATAACCACG TAGCGATAAT AAAGGGGGCG GTCAATACGG 780

GTAACCCTCT GAGCACTGAC GACAACAGGG GAGTAAACAA AACAATACCA AGAGTTCCGA 840

CGATAAGTAC AGCAATTCCG GAGACTGACA CAGGGACAAG CATGCCACAG GCTATGCCAT 900

ACAGAACAGC ATTATATCCC CATATACCTT CATTAATCTC CTCATCAGGA TACCGCAAAC 960

ACCAGGCAAA GAACGGAGAA AGTGCTGCAC TGATGGCTGA GAAATACAGT ATTTCGGGGT 1020

GCCCCATATT AAAAGAGGCT ATTCCAGTCG CCAAAAAAAA GAACAAGCCA GAAACAACAT 1080

TGTTCTGTAA TAATACCTGT GAATACCCCT TACTAAAGGC GGTTATCACC TGTTTTACTC 1140

TCATGTAAAA TGTCACACAC ACCTCATACA TAAACCATTC TCCGCTTCTG CGGGACAGTA 1200

CCGCCCCTGA CTCCACCTCA CAGCGGATTG TGTATTTTTA AACAATCACA GTCTTCTCAT 1260

ATACTTTCCA TTCTGAAGCT TATCTCTTCC TCCGTGATAA GCTTCCGTCG CGGGATGTGT 1320

TATACGCCCT GTAAGACAGT TATAAAGGAC ATCAATGCCA TAGTTAATGA YTACCGAATT 1380

CCGGTGGATA GTCAGTACTG GTTTGCCACA AAACAGTGCA GTCACACATG ACAGGAGAAG 1440

ATATGAGCCG GATACCGCTG CTCTGAGACT TAACGCTCAT GTAAACTTTC TGTTACAGAT 1500

TCTTCCAGGG ACTAAGAAGA TAACTGANTT ACGTTCGCAT TCCAGTSTTT ATTTCTGCAG 1560

TGACAGCCAT ACCCGAGCTT AATGGAATGT GCTTATTCCC GGTTGACAAA TCATTCTCTT 1620

CAACAGAAAC AATGACATTA AAAACGAGTC CCAGTTTCTG GTCTTCTATT GCATCTAAAT 1680

TTATATTTTT TACCTTACCC ACCAGATAAC CATATCGGGT GTAAGGAAAA GCCTCCACTT 1740

TAATGATGGC ATTCTGCCCG ACGTTAATAA AACCAATATC TTTATTTTGT ACCAGAGCAG 1800

TAACCTCCAG CGTGTCATCT TCCGGAACGA TGACCATCAG TGTTTCCGCT GTTGTAACAA 1860

CCCCACCTTC AGTATGAACC TTCAGTTGCT GAACTTTTCC CGAAACAGGG GCCCTGATTA 1920

CTGAAGCCTG TTGACGCTCT TCATTTTTCT CTAACTCCAG AGTTAATAAC TCAATGCTGT 1980

AGTTGTTTG TCTTAGCTTG TCTAAAATTT CATTTTTAAA AAGCTGCGTG ACAAGCTGAT 2040

ATTCTTCTTT TGCAGACAAT ATCTCACTCT CAATTTGCTC CAGTTGCGAT TTATAAACCC 2100

GTAATTCATT TGCTGCCTCA ACATATTTAT TCTCCTGCTC AAGTACAGCA TGTTTTGCAA 2160

TTGCCTGTTT ATGCAACAGG CTCCTGAAAT CATCCAGACG GCTTTTTTCA ACCCTCGATA 2220

CATTTTCATA ACGGTTTATA CGGGCAAGTA TTGTTAAWCG CTCTGCTCTT TTCTTATCCA 2280

GATTCAGTTC TTTTTGATAC TTCTGATTTT GCCATGTGGA AAACTGTTCT TTTATCAAAG 2340

AAGTTAAACG CAGTACTTCC TCTTCAGATA CATTCTGAAA ATAAGGCTCA TCAGGAAGTT 2400

TCAGTTCAGG AAGTTTATTT AATTCAATTG ACCGGCTCAG AATTTGATAC CGAATTTGTT 2460

CCAGCCTGGC CTGTAACAGT GATGACTGCG TTTTTAACGT ATCAGCTTCA GCTCCCAGCG 2520

CTGTAAGCTT TAATAACACA TCCCCTTTCC GGACTGACTC TCCTTCTTTT ACGAYAATTT 2580

CTTTAACTAT CGAGTTTTCA ATAGGTTTAA TTTCTTTNTA CGCCCACTGA GTGTTAATTT 2640

CCCATTTGCA GTGGCAACAA TTTCCACCTG GCCTAAAACA GATAAAATGA AAGCAATAAC 2700

CAGAAACCCC ATAATAAAAT AAGCAACCAG ACGCGGCCGT CTGGATACCG GCGTTTCAAT 2760

TAATTCCAGA TGAGCGGGTA AGAATTCATT TTCGTCCTTT TCACGTACCG GAGTATCTAA 2820

CTGCTTCCGG ATTTTCCATG TTTCACTCCA GACAAGTTTA TAGCGCAACA GGAACTCGCT 2880

GAACCCCATT AACCATGTTT TCATATTCTT CTGTTCTTTC TGTTAGTCTG ACTGTAACTG 2940

ATATAAGTAA CTGTATAAAC TTTCCGGTTC AGAAAGCAGC TCCTTATGTT TACCCTGTTC 3000

AACAATTTTC CCTTTTTCCA TGACAATAAT GCGGTCTGCA TTTTTTACTG TAGACAGACG 3060

ATGAGCAATG ATTATAACCG TTCTGCCCTT ACATATTTTG TGCATATTGC GCATGATGAC 3120

ATGCTCCGAC TCATAATCCA GAGCACTGGT TGCTTCATCA AAGATGAGTA TTTTAGGGTT 3180

GTTCACCAGC GCCCTTGCAA TTGCGATGCG TTGACGTTGA CCTCCGGATA ATCCTGCCCC 3240

CTGTTCCCCG ACAATGGTGT TATACCCCTC ACGCAATTCA GAAATAAAAT CATGAGCACC 3300

TGSTAATTTC GCTGCATAAA TAACTTTTTC GACGGACATG CCAGGATTAG CCAGTGAAAT 3360

ATTATCAATA ATACTGCGAT TAAGCAGCAC ATTGTCCTGC AACACAACCC CCACCTGACG 3420

ACGTAACCAG TTAGGATCGG CCAACGCAAG ATCATGTCCA TCAATTAAGA CCTGGCCATT 3480

TTCAGGAATA TAAAAACGTT GAATTAATTT AGTTAATGTG CTTTTTCCTG AACCAGAACG 3540

TCCGACAATA CCAATAACCT CCCCCTGCTT AATACT 3576

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

VSDOCID <WO_ 9822575A2 I >

TCAGCCCGGT GAGCGGGTTT GACAATTCCG CACTCACCAT TGGGCTAAGG GTTATCAGGT 60

GGGGTTAAGG AAATGGCAAA ACCTACCCCC GTCCAAACTC CAGTCGCTGC ACATTCACCA 120

TCCCTGGCTT CTCACCTGCG CTGACATCAA TTTGTGTCAC CGGCAGCGCA TATTTTTCAT 180

CCAGTGCTTT TAACCAGTTC AGCAGGTCAT TAAACACCAC AGGTTCTATC CAGACCTGGA 240

TATTCTCCCC GCGCTCGGCA ATCCGTTTGA TGACCACCGA GTGCGCGGAA GCTGTCACTG 300

ATGACCCGCG ATACCTGTGC TGGCGTTGTC GTGCCGGATT TTCGCGCCGC AATAATATCC 360

GGCGCGGCGC TCTTCAGTCG CGCGTTCATC GCCACCAGCT GCTGCAACAT CGTCTCCTGT 420

TGCTCAATCC GTTCGCTCAA CGGCTGCCAG ATGAGAACGT AATATCCGGC GCTAAACAGG 480

AACACTACCG CTGCCAGTAA CATGCCTTTT TCACGCGGCG AACGCCCCGC CAGGTGTTGT 540

GTCAGCCAGT GTTCGCCACG GCTTAACTGG CGTTCACGCC ATTGCTGAAA ATAGTGAATA 600

AATTTATCGC GTAACATGTT ATTTCCTCCG CAACGTTACG CCGCCGGAAA CCGCATCACC 660

CTCTTTCTGT AACGCGTCCT GTTGCACAAC ATAATCTGCC GCCAGTGCGC TACGAGTTTA 720

TCGAAGCTGG CAAAGTTCGC AGCCCGTAGC TGGAGGTGAA GCGTCTGGCG TTTTTGATCA 780

AAGGTGAAAC ACGCATTTCG ATGTCGGTAA GTGACGCTGA TTTCAGGGTA CTGGCGATCG 840

CTGACAATTC TGCGAGCAGC CGGGTATCGT CGGTCTGTGG GCGATATTTT TTCAGCGCCA 900

TCGTCACCTG AGAGCGTAAA TTCACAATCC GCTTCTGCTC CGGGAATAGC GTTAAGAACT 960

GTTTCTCCGC CTGGGTGCGG CTTTGCGCCA CCTGTTCGCT GACGCTCCAT AACGTCACGC 1020

CCCGTTCCAC TACCAGCGCA ACCAGAATCA ACAATATCGG CAGAATCATC ACCCGCCAGC 1080

GCGCCCACTG TTTTCGGTAG CTGACACGAG GCTGCCACGG CCCTGTTAGC AGGTTCCCTT 1140

CCGGTTCGCC ATAAGTGGTA ATGGCGGGCA GAGCGTAACG GTCAGCGTTC GGCGTCTGCA 1200

CCAGCCCATG CAGACAGTTC TTCCGGTGCA ATGCCGACCA CGGTTAGTGA AAGCGGTAAA 1260

TCCTGCTCAT TGAGCTGTGC TCGGAACATG ACCGGAGCCA GCGCCCGCCC GGCGCTCCAT 1320

CCCCGGCATT CATCGATGCG GMAGATAACC CGTTGCGCAT CGCCAGCCAT AAACCCACAA 1380

GGAATGGACA TCCAGTCCGG CGCGACGATA GCGCGGGTGA TGCCGTTTGC CTGCAACCAC 1440

TGCGCAATGT TGCGCATATG CTGCTGGTGA ATCACAGCTA CGGTTGCCAG TTGCTGGTCG 1500

ATTTTCAACG GGGCGAAATG CAGTTCATCG ATATCCTGGT TCAGCTCTTC TTCCAGCAAG 1560

GCGGGCAGAA TCGTCGGTAT CTGCTTGCGG GGCACATCAG GCAGTTCAAC CTGCCAGACG 1620

CTGATCCATT CGCCGGGAAT GTAGAGTCGA ATCGCATCAG TTTGCAGCCA TTGCTGGAGA 1680

CATTCATCAG CAACGTCAGG CCAGATGCCG CACTCCACGT CGGCGGTACG ACGCTGCCAA 1740

CGGATGGGAG CGGAAMGNCA AAGCGGGAAA AAAATCTCAA GCATGGAACT CACTCACTTT 1800

CTCCTGTCTG ATGCCAGAGA ACAGAAAAGT GTTGTGGGCC CATGCGGACA ATTAACGAAT 1860

TCATCGTCAG TTCAATCTCA TTCACGGTGA TATCTGAACG CAGCCAGAAG TAATTGCTGT 1920

CCACGCTCAG GACGGTTTTT AGCTGTTTTT TAGTACGCTC ATCGACGTCA GCAAGTAACG 1980

GCTGTGCAAG AAACTGATCG ACATCTTCCC AGCCCTTCGC ATGACGTTGT TGTAATAACG 2040

CTCGCGCCTG AACAGGGCTT AACCACGGGT CAAACAGCGC CTCAAGAATC ACACTTTGCG 2100

TGACGTCTAA GGTATTGATG TTGATTTGCT GGCGGGTCAT CGGCAGCGCA CAGACCAGCG 2160

GTTTCAGTTT TTGATAAAGC CCGGCGTCCA TTCCCTGCAC CACGCGCATC TCGCTGATAT 2220

CAGCCAGCGG TTGATTAGCG GCGTAAAACG GCACCGAACG GGCGAGATAC TCGCTGTCTT 2280

CACGGCCCAG ACGCGTCTGC ACGCTGCGGT CTTCGTCAAT AAACTCCCAC AGGCTTTCGG 2340

CTATCAGTTC GGCCCGATAA GCAGGCACAT CCAGGCGCGT GATCAGGGCA ATCAGTTGTT 2400

GTACCGCGAG CGGACGCGAC GCCGTCGTCG GCTGAGCGAG GGCATTCAGG TTAAAGCAAG 2460

CCTGTGCGTC ACGCAGAGTG ACGGCGATTT GCCCTGCGGC AGTGGGAAAA AACGCGGGCC 2520

GGAAGCCCNA CGTGCGCCAG ATGCACGCGC TTTTCATTTT TCAGGCTCAG ACTGAGTGCG 2580

CTCAACGCCA GGCTTTCCGC ACTGGCGCTG TACGACAGCG CCTGCTGGTA CTCCTGCTGG 2640

TGCGCGTTCG CCCAAGTTGT TTCTGCATCC GCCCGGAAAG CGTGATGGTC ACCAGCATCA 2700

TAACCGCCAG CAATACCAGC ACCACGACCA GTGCCATTCC GCGTTTTGGT GGTGAGGTGA 2760

TCATGATAAT TGCGGCCCGC GTAACAACCA GATGCGTTCA ATTTCGCCCC ATTGTGGCGA 2820

ATGCAGGGTT ATGCGTACTG CCACGGGGAT CGCCTGCACT GATGACCAGC TCTCCTGCCA 2880

GCGCGTGCCG TCGTAGAACT GCAAACGGAG CGAATCCGCC GGGATTAATT TTTGCGTTGT 2940

TGGCTTCACG CTGCCTGCCG CATCGGTCAG TGGCCAGGCT AACCGTTCGA GATAACCACC 3000

ATGAATGCGG TAACCGACGG TGAGCAGATT ACTGCGCGGC AGACGCATCA ACGGATTAAC 3060

CACGCCGCCA CGTACAAAAC GCATCCCTTC ACTCTCAGAC GCCAGCACGC CAGCGCCCGC 3120

CAGTAACGCT RGTTCACGCT GGCCCTGATC GCCTCTTACC GGACGCGGCA TCATTTGTGT 3180

CAGATCGTGG GTCAGAAAAC TCATCGTTTG CTGCATGAGG TTTAGTTTTT GATCGTGTCC 3240

GGCGACGGCG CTATTCACGC GTGTAACCCG TTTGTCACCT GCTGCGCCAT CATTGCCAGT 3300

GAGGCAAAAA TGGCTATTGC CACCAGCATT TCCAGTAACG TGAAACCAGC GCGAGTCCTT 3360

CTCACTGTTG GTCTCCCACG GCGCTAAACC ANGCGCGTCG TGACTGAATC ACTGACGAAA 3420

AGTCNTCATG AAGACTGACT TCAATATCCA CNGCATGGAG CAGCGCATTA NCGGTATTCA 3480

GTGGTGTTGG TTCGCCAGAA CCAAGCGGCT TTCCTGCCAT AATCGCTCTC GGCCCTGGGT 3540

G 3541

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

SDOCID <WO 9822575A2 I >

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTACTGGACA TCTTTGATGA ACAAGCTCCT CAGTGTAAAT TGTACGTCTC TGATCGTAAT 60

CTTCCTGAGG GCGTTGAACA TCTATCCGCT GAATTTATAC CCTATACTCC TGAGTCGGCA 120

GATTTTCTGA TTCAACGTTT TTTCTCTGAA ACTATCCATA TTGAAAGTGC AATTGTTGTT 180

ACAGCACTTA AAATTGCCAA TCAGATTGCT CTATCTCAAA ATGAGACCAA GAATGTGTAT 240

CTGCTTGGAT TTGATTTTAC GATAAAGGGG GGGTTCACTA GCAAGATCCC CTGCGCAGCC 300

TTGCATGCCG AACCAGAATA TCAAGAGCGA ATTATCAGTA GTCAAGAACA GCTATTGCAG 360

ATGCTCCTTG CAGAAAAAAC ACGCCTGAAT ATCAATATCA ATCATGTTGG TAATAAGCCT 420

TACAGCGTAT ATTCTGTTGA TGCATTTAAT CAAGTGTTCG CTGCCCGCCA TCGTGGAGTC 480

GTGCTGCCCA CACATGCCCA GATTTCCACT ACATCATCAC AAAATGGGGT GAAGGTGATC 540

GCAGAGATTA CTACTAATCA CTTTGGTGAT ATGGACCGAT TGAAGTCAAT GATTGTAGCG 600

GCCAAGCAGG CAGGGGCTGA CTATATCAAA CTGCAGAAGC GTGATGTTGA AAGTTTCTAT 660

AGCAGGGAGA AGCTGGAGTC ACCGTACAAC TCTCCTTTTG GCACCACCTT TAGGGACTAT 720

CGGCATGGCA TTGAACTCAA TGAAGAGCAA TTTTCCTTTG TCGACTCTTT CTGTAAAGAG 780

ATTGGTATCG GCTGGTTTGC TTCTATTTTA GATATGCCCT CGTATGAGTT CATTCGGCAA 840

TTTGAACCAG ATATGATCAA GCTACCATCA ACTATATCTG AACATAAAGA TTATTTGGCT 900

GCTGTTGCTT CTGATTTTAC TAAAGATGTA GTAATTTCAA CTGGTTATAC TGATGAGGCC 960

TATGAGCGTT TTAYCCTKGA TAACTTTACC AAGGTTAGAA ATATTTATCT GCTGCAATGC 1020

ACCTCGGCTT ATCCCACACC GAATGAAGAT ACCCAGCTAG GTGTGATAAG ACATTATTAT 1080

AATTTGGCGA AAAAGGATCC ACGTATTATT CCTGGTTTTT CCAGCCATGA TATTGGTAGC 1140

CTTTGTTCCA TGATGNTGTC GCAGCCGGTG CAAAAATGAT TGAAAAGCAT GTTAAATTTG 1200

GCAATGTGGC TTGGTCTCAC TTTGATGAAG TTGC 1234

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ATGGGACCTT TCTTCAATGA TGTTGCCGAG TGGTTAGAGT CATTAGGTCG TAACGCTGTG 60

AATGTTGTAT TCAATGGAGG AGATCGTTTT TACTGCCGTC ATCGACACTA TCTGGCTTAT 120

TACCAAACGC CGAAAGAATT TCCTGGTTGG TTACGAGATA TCCACCGGCA ATTTGACTTT 180

3NSDOCID: <WO 9822575A2 I >

GATACCATTC TCTGTTTTGG TGACTGCCGT CCATTGCACA AAGAAGCAAA ACGTTGGGCG 240

AAGTCTAAAG GGATCCGCTT TCTGGCATTT GAAGAAGGAT ATTTACGTCC GCAATTTATT 300

ACTGTTGAAG AGGACGGTGT AAACGCGTAT TCATCGCTGC CGCGCGATCC TGACTTTTAT 360

CGTAAATTAC CAGATATGCC TGCACCACAT GTTGAGAACT TAAAACCCTC GACGATGAAA 420

CGTATTGGTC ATGCAATGTG GTATTACCTG ATGGGATGGC ATTACCGACA TGAATTCACT 480

CGCTACCGTC ATCACAAATC ATTTTCTCCT TGGTATGAGG CTCGTTGCTG GGGGCGTGCG 540

TACTGGCGTA ACTATTTTAC AAAATAATGC AACGTAATGT ATTGGCTCGG TTAGTGAATG 600

ATCTGGACCA ACGTTACTAT CTTGTTATTT TACAAGTTTA TAATGATAGC CAAATTCGTA 660

ATCACAGTAA TTATAATGAT GTGCGTGATT ATATTAACGA AGTTGTATAT TCATTTTCGC 720

ATAAGGCACC GAAAGAGAGT TATTTGGTGA TCAAACACCA TCCGATGGAT CGCGGTCACA 780

GACTCTATCG ACCATTAATT AAGCGGTTGA GTAAGGAATA TGGCTTAGGC GAGCGAGTCA 840

TATACGTACA CGATCTCCCA ATGCCGGAAT TATTACGCCA TGCAAAAGCG GTTGTGACAA 900

TTAACAGTAC AGTGGGGATC TCTGCACTGA TTCATAACAA ACCACTCAAA GTGATGGGTA 960

ATGCTCTGTA CGACATCAAG GGGTTGACGT ATCAAGGGCA TTTGCACCAA TTCTGGCAGG 1020

CCGATTTTAA ACCAGATATG AAACTGTTTA AGAAGTTTCG TGAATATTTA TTGATGAAGA 1080

CGCAAATTAA TGCTGTTTAT TATGGTGTAA AATCAAAAAG CAATAGAAGG TCCGCATTCC 1140

TAAACGGTAG CAGATGATGG TTTTCATGGG CGTTTCAGGT TACTCAATCA GCCAACAACC 1200

GCAGCGAAAA CCCTGCTTTC TCGACCAGTT CAGGCCGGTT TTACCTCCAA TGCTTTCCGT 1260

CAGAACTGAG ATTTCAGCCA GTTGCCGGAT AAGTGTGTCG ATTTGCAGCA GTATACTTTT 1320

TCGTACAGCC AGAATGTGGC AGACTGAGGT GGAATAGATA ACGTCCGTAT GCCCGCTCAC 1380

CACCTCCGGG CGGGAGTGTG TGGTATCTGA CATCATCATT TTTCCTTTCT GTTTATAAAT 1440

GAAAACGCCA GCCGTGTTCA GGCTGACGTC AGGGAAGTGA AATCGGGTGA GTGATCTTCA 1500

CTGGTTCTGG TGCAAAAGTT ACTGTTGGCG CAGGGTACGG ATACCCTCCC TGGCCTGTTC 1560

GATACAGGGC AACAGTGCTG CCGAATCTGT TTTATCCTCA TCGTTGTCGA AGATAATTCC 1620

CGATTCGCAG TCGATATTGT CCTGCAGCCA CGTAATCAGA ATATCCAGCG CTGTTTCCGT 1680

GGTTAATGAT TTCATGTTGT GAATTTCCGG ATTACCAGTC GAAAGTGGGT AAACCTGGCA 1740

GACATCTGGC ACTGGCATCC AGATGAATGA GACTGACACC ATAACGCCGG ATGAGTGTGA 1800

CGACCAGACG ACGGAACGTA ACAGATAACC GGTACCGGTA AAATGAATCC ATTCTGATTC 1860

ACCAAAGTCA CTGGTCTGGT GTAACAGCGA GTACAGCCAG GCGTTGTCCT TTTCCGTGAT 1920

ATGTGCGGTA CTGCAGCGTA TGCCGGAAAG AGTCGTAAAC GGTTGTGGAG TGCAGGTTGA 1980

CTGTTGGTCA GATTCATCCA CCACGCGGAG TGAATAACCG TTTTCAGCGA CCTTGTTAAT 2040

CAGTTCAGCG AGATTAATAC CATCGACGTC AACGACAATG CGCCCCATAT TCAGTGCCTG 2100

TACGTTAACG CTGTCGGCTT CCGGCGTCAG GGAAAGTTTC ATTGTTTCAC CTCCGGGTGC 2160

TTACCCAGGA TAATATTATT TACCGCTCTG TAATTGTCGC GGGTCATCAG GCCGGTCGCC 2220

CTGCGAGCCC GGAGGATATC GATGCTGTTT ATTAACTGAG AGCGGGTACA GGCGCTGAAT 2280

CCCGGCTGGT CGGTACGCAC CAGCGCGTAT TTTTCCACGA GAAAGTTCAC CGCATCACAC 2340

AGTGAAATGC CTGCCTCAAT ATGCTGCTCG ATCACACGTT CATCGGCAAA CGGTGTGTCA 2400

TTCAGTGTGA GGCCGTAGTG CTGGTCCAGC AGTCGGGACA GAAGTATCTG CCAGATTTCA 2460

ACAGGAGACG GGCGAGAACT GGCCGCCTGC CCGGGTAATA CAGGTAATGT TTTCATACTG 2520

AAGATTTTCC TGATATGCAG ATATAAAAAT GGGAAAGTGG CGTGGTGAAA ACACCAGGCC 2580

GTAGCAGAAG GCTATTCTGG AGAGTTAATT TTTCATTTCG GGCGTCGGAT AAACAGCCAG 2640

ATAAACGTAA CCACAACTGC TGAGGGTATC GGCTTTGCAG GTCAGCCCTT TTGCATACAG 2700

CGTGACGGTA TGCTGATGGC GGGGATTCAG TTCACCGCTG GTGAGCATGA GTTCCAGTTG 2760

TTTCATCAGC AGCGGAAAGG CCTGGTCCAG GTGGTACGCA TCTGCATTGC TGTATAGGCC 2820

TCTGATACCG GCGCGGTCGG CAAGGTAATG CAACCGGTTA CCCTCCTGCA CCAGACGTGC 2880

CCCGAAACAG GGCGTCACGG TGCAGGGCAG CCCCCACCAG GGGCGGTCGT GATTGTCGTC 2940

GGGAAGTGTT GTCCCGGGGA GTGTGTCTGA CACGATAAAA TCCCTACAGA AAATCGGCTA 3000

AGAATGCTCC GGTATTGGCG ATAATTCTGC TCATCAGAAT TCCCACTCAG TTCAGGGTGA 3060

CGCTCATCAG CCGGACATAC GGGCCAAAAC TGTCCTTACG GCGTTCAGCA AACACGGCCA 3120

GCACACCGGG AATATCCTGT ACTTCACGAC CGGTATACGC CTCAGCACTG CCGTGCCAGC 3180

GGTACTTACC GGTGCAGAAC GGAAATAGAC GGGATGCAGG ATGCTGTTGG TGAATACGCA 3240

TGGCTTCACC ACGGGTGATG ATTTTCATAA TGGGATACCT CTGAAGACAG AAGATAAAAG 3300

TGAAAACAGG TGTGATGTGG TTGTGACGGT GACGGGTTAA AGCAGACCGT GTTCCGCAAA 3360

GGAGAAAACC TGACTGCCAC CAACTATCAG ATGGTCCGGT ACCCGGATAT CCACCAGGGC 3420

CAGTGCCTGT ACCAGACGTT CCGTGATAAG GCGGTCTGCC TTACTGGGGG TGACTTCACC 3480

GGACGGGTGA TTGTGTGCCA GTACCACGGC GGCGGCATTG TGGTACAGGG CGCGTTTAAT 3540

CACTTCCCGG GGATGGACTT CCGTGCGGTT GATGGTGCCG GTGAAGAGGG TTTCACCGGC 3600

AATCAGCTGA TTCTGGTTGT TCAGATACAG TACCCGGAAC TCTTCACGCT CCAGTCCCGC 3660

CATCTTCAGA ATCAGCCATT CCCGTGCCGC ACGGGTGGAG GTGAAGGCCA CGCCGGGTTC 3720

ATGAAGATGG CGGTCCAGGG TTTTCAGGGC CCGCAGAATG AGACTGCGCT CGCCGGGCGT 3780

CATCTCTCCG GGCAGAAAGG AAAGTTGTTG CATTGTGCTT CTCTCCATTC AGTCGATGAT 3840

GCGCATAATG GCGCTGCATT CCGGATGCTG CAGGGCGTAA TCCCGCAACC GGTAATAATG 3900

GATCGTCATG GCATAACACT CCGTACGACA GGCATGATGA CTGTACGTCA TCAGACAGGC 3960

GGCAATGCCG GCGGCTTCCG GGCTCATTTC AGCGCGGTTA CCGTTCATGG CATTGAACAG 4020

NSDOCID <WO__9822575A2 I >

TACCCAGTTT TCGTCATCAT CGTCATCCGG TTCGGGTGCC ATAAATGCCC CGCCGTTGTT 4080

CAGGGTGTAC AGATTCCAGA TACCACCGCA GTAGTCTTCG CACAGACGGT CCATCCAGCC 4140

GAAGACACGG GGCTCCAGGG TCACCCACTG TGGAATGAGG CCAAAGTGCT GCGGCCAGAA 4200

GCTGATGCGC TGTTCATCAG GGACTATGGT GGCAACCAGC TGAGGCTGGT CATTCCCTGA 4260

TGCAGCGGTT ACGGAAACAG AAGGAGTGGT GGAATTATGC AAGACGGTTG TCATGAGATT 4320

ATTCCTTATA AAAAGTAAAT GAATGGAAGA AACCCCGGGG GAAGGGACAG ACGTGAGTCA 4380

GAACTGCGCT TTCAGGGAAA CGGCATCAGC GCATACTCTC CAGCAGCGTT TCAGCCATCA 4440

CCCACAATGC GCGGTTGAGC TTAATGTCGG TGTCGATGCT GTGAATGGCA CGGGTATGGA 4500

TACGTTTTCC TCTGGCACTG CGACCGGAAA TTCCGCCTTT CAGCATATTC TCCTGAATGG 4560

TCTGATAAGC ACTCCACAGG TCCTTACCGT AATCCTCCCG GCGTCGTGGT GTCAGAATGT 4620

CGGCGGTGGT GACGGGCTGA TGTTCGTCAC CATAACGGTA AGTCAGTGCC GCCTGTGCCA 4680

GCGCCTGGCG TGCCGGTGGC GGCAGAATCA GCGACTGCAT GGCATCACGC TTTTCCTCAA 4740

TCCGGTCAAA AACCCCCACC ACCTCGTAAG CCCCTTCAAT AACTTTCTCC ACCACATTTC 4800

CCCGGTGCGG AACACGCACT TCCCCCAGAG ACTGACCACA GACGCATCCG TTCTGGCAGA 4860

CGAACCTGAA GTAACCCGGC AGCATCTGGT AGCTGGAGGT ACCGTCATGA GAGTTGAGCA 4920

GAATAATTTC AGGGACATGT TCTCCGTTTA TCTCTCCGGC CCGCCGCAGA CGCAGCATGT 4980

GTTTGGTGTA TTCCCGGCGG TCCGGGTCAC GTACGCGGGT CTGGCAGGCG AAGAATGGCT 5040

GAAAGCCTTC CCGCTGCAGG CTTTCCAGTA CGGTGATGGT GGGGATGTAC GTATAGCGTT 5100

CACTGCGGGA GGTATGCCGG TCTTCACCGA AAATACCCGG TACATGGTGC ATCAGTTCTT 5160

CGTGTGTCAG CGGACGGTCA CGGCGTATCT GGTTCGCATA ACCAAAACGA CTGGCTAGTC 5220

GCATAATTTG CTCCTTATCG GTGGTTAAGA TTTACTGGTG TAATAAATGA AAAAGCCACG 5280

TCTCCCGGAG AAGACGCGGC CTGACAGATG AAATGAATGA CGTTTATTGT CTGAGAAGCC 5340

CTTAACTGGC GAGCTGAGTA TTAAGCTGTG TTCCGGCATC ACCAGCGCAA CTGACCTTCA 5400

GCATTACGGA TAACCAGCCG GGAATATGTT CCCTGGTCAT CTTCAGTAAA CACATTGCGG 5460

TAAGCTGTTA TGACAGCAAC CGCCTGCCCG TATGAGAAAG ATCCTTCAGC CAGGACATAC 5520

TCTGTGTGTA ACCCGGCATA TCTGGTTTCT CCTGATAAAT AGCCTCTGCC ATACGTTGTG 5580

GCAGAGGCTG AAGCATGAAA CTGACTTCAG GGATCAGTTA ACATTTTTTC CGGAAACGGT 5640

AATCAGCAGT GGATGGTAGT CCTGGGGATC GAAAACCGAT AACGGCAGAC TGACACGATG 5700

GCCGTTACTT TCTTCAGTTG CTTTAATGAT TTCGGTTGTG GCGACATTTT CCACGCACTC 5760

CGTTTCCAGA AATGCGTCTG TGGTTCGCGT GGCATTACTG TCACCAAAGG CTTCCGTTTC 5820

CATTTTTCTG GTCACCAGCG TCTGACCATA TTTGTCTTTG AGTTGCAGAG TGATGGTGAG 5880

GGGGCCAAAT CCTTCATCGT TTCCGCCATT ATCCAGCCGG AACTGGTAAG CACAAATATT 5940

NSDOCID: <WO 9822575A2 I >

TCCCGGGAGC CATATCGTAT CTGTATTGCG TATACTGATG TAACGTTGAT CCTGTGCCCG 6000

GAGTGGGGCA GACCACGTTA ACCCCAGAAT GAAGGCGGTA ATCATGCAGG TTTTGAACAG 6060

GTGAATCATG GTATTTACCT CTCTGAGTCA TGACGATTAC ACTGACAAAT CAGGTGATAA 6120

AACGTAAAAG GCGCAGAATA GCCGTTATGC CGGTAACTCC GGGGGTAATG TTTCTTCCAG 6180

TCGGTTAACC ATATTGCCGA GATGGGATGC ATCATATTCC ATGACGGGGC GTTGCCTGAT 6240

GATACTGACC ACCAGTGGTT TGATTAACAT GTTGGTCGCG GCCCGTTGTT GTATACCGGC 6300

GGCGAAAATG ATC 6313

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGTTGGCCGC TTGCGCAGAT AAAAGCGCGG ATATTCAGAC GCCAGCACCG GCTGCAAATA 60

CGTCTATTTC AGCAACACAA CAACCAGCTA TCCAGCAACC GAATGTCTCC GGTACCGTCT 120

GGATCCGTCA GAAAGTCGCA CTGCCGCCTG ATGCTGTGCT GACCGTGACA CTTTCTGACG 180

CGTCGTTAGC CGATGCACCG TCAAAAGTGT GGCGCAGAAA GCGGTGCGTA CTGAAGGTAA 240

ACAGTCACCA TTCAGCTTTG TTCTGTCATT TAACCCGGCA GATGTTCAGC CGAACGCGCG 300

TATTCTGTTG AGTGCGGCGA TTACCGTGAA TGACAAACTG GTATTTATCA CCGATACCGT 360

TCAGCCGGTG ATCAACCAGG GCGGAACTAA AGCCGACCTG ACATTGGTGC CGGTACAGCA 420

AACCGCCGTG CC 432

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GGGCTGATTA CGATTTTATC AATCTGTCTA TAGAACATGA ACTGAATGAA GGAATAGCTG 60

GCAGAGAGAG GTTATGCCGG ACTGGCGGAT AACCGGAACC GGTTGGCAGA GGTGGTTACC 120

CGTAAATTGC AGGACAGCTT TTATATGAAC TTTCCTGGGA TGCGCTGAAC ACGGCATACA 180

GTGAACACCC AGAGTGGTTT TCCGGGCTTG TCTCCGGGGA TGAGAATTAA AAAGTGGATT 240

ATGCTGCTAT AGCGCGGCGT GATTTCCTGC AGGGATTTCC ATTTATAAGA ATACGCCGCT 300

3NSDOCID <WO_ 9822575A2 I >

TCGGGGAATC TCCGGTTCTC CTGAGAGTTA CGATTGTTTT TTTACTCAAA TCCACAACAC 360

CTGAACTGGA ACTTGTGTTG CATCCCTGAT TGTTACTCTG CAGGAAACAT CTTTTTTACC 420

ATCAAAGGAT GACTGTTTTC CTTTCTCCCC TCCGTAAAAC ACAACTTCGA TCACATTTCT 480

GACATTTTTT CCAGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTAA 540

ATTTCAGCAC TGACATTCCG CTTACGTTAA TTTACACTGA ATACCCCACG AGGAGAATAT 600

GCAGCACCGG CAGGATAACT TACTGGCGAG CAGAACGTCG TTGCCTGGTA TGGTTTCCGG 660

TCAGTGCGCA TTTAAGCTCC GCACTTTCTC TCCGGTGGCA CGCTATTTTT CCCTCCTCCC 720

CTGCCTTTGT ATTCTTTCGT TTTCGTCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG 780

TGCAATTCAG CAGCAACAGC AACAGTTGCT GGATGAAAAC CAGCGCCAGC GTGATGCGCT 840

GAAGCGCAGT GCGCCGCTGA CTGTCATACC GTCTCCGGAA ATGTCTGCCG GTACTGAAGG 900

TCCCTGCTTT ACGGTGTCAC GCATTGTTGT CCGTGGGGCC ACCCGACTGA CGTCTGCAGA 960

AACCGACAGA CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCACGG GGCTGACCGC 1020

GGTCACGGAT GCCGTGACGG ACAGCTATAT ACGCCGGGGA TATATCACCA GCCGGGCCTT 1080

TCTGACAGAG CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT 1140

GCAGCAAATC CGGGCGGAAG GCGCTGACCT TCCTGCCCGC ACCCTGAAGA TGGTTTTCCC 1200

GGGAATGGAG GGGAAGGTTC TGAACCTGCG GGATATTGAG CAGGGGATGG AGCAGATTAA 1260

TCGTCTGCGT ACGGAGCCGG TACAGATTGA AATATCGCCC GGTGACCGTG AGGGATGGTC 1320

GGTGGTGACA CTGACGGCAT TGCCGGAATG GCCTGTCACA GGGAGTGTGG GCATCGACAA 1380

CAGCGGGCAG AAGAATACCG GTACGGGGCA GTTAAATGGT GTCCTTTCCT TTAATAATCC 1440

TCTGGGGCTG GCTGACAACT GGTTTGTCAG CGGGGGACGG AGCAGTGACT TTTCGGTGTC 1500

ACATGATGCG AGGAATTTTG CCGCCGGTGT CAGTCTGCCG TATGGCTATA CCCTGGTGGA 1560

TTACACGTAT TCATGGAGTG ACTATCTCAG CACCATTGAT AACCGGGGCT GGCGGTGGCG 1620

TTCCACGGGA GACCTGCAGA CTCACCGGCT GGGACTGTCG CATGTCCTGT TCCGTAACGG 1680

GGACATGAAG ACAGCACTGA CCGGAGCTGC AGCACCGCAT TATTCACAAT TATCTGGATG 1740

ATGTTCTGCT TCAGGGCAGC AGCCGTAAAC TCACTTCATT TTCTGTCGGG CTGAATCACA 1800

CACACAAGTT TCTGGGGGGT GTCGGAACAC TGAATCCGGT ATTCACACGG GGGATGCCCT 1860

GGTTCGGCGC AGAAAGCGAC CACGGGAAAA GGGGAGACCT GCCCGTAAAT CAGTTCCGGA 1920

AATGGTCGGT GAGTGCCAGT TTTCAGCGCC CCGTCACGGA CAGGGTGTGG TGGCTGACCA 1980

GCGCTTATGC CCAGTGGTCA CCGGACCGTC TTCATGGTGT GGAACAACTG AGCCTCGGGG 2040

GCGAGAGTTC AGTGCGTGGC TTTAAGGAGC AGTATATCTC CGGTAATAAC GGTGGTTATC 2100

TGCGAAATGA GCTGTCCTGG TCTCTGTTCT CCCTGCCATA TGTGGGAACT GTCCGTGCAG 2160

TGACTGCACT GGACGGTGGC TGGCTGCACT CTGACAGAGA TGACCCGTAC TCGTCCGGCA 2220

WSDOCID <WO 9822575A2 I >

CGCTGTGGGG TGCTGCTGCC GGGCTCAGCA CCACCAGTGG CCATGTTTCC GGTTCGTTCA 2280

CTGCCGGACT GCCTCTTGTT TACCCGGACT GGCTTGCCCC TGACCATCTC ACGGTTTACT 2340

GGCGCGTTGC CGTCGCGTTT TAAGGGATTA TTACCATGCA TCAGCCTCCC GTTCGCTTCA 2400

CTTACCGCCT GCTGAGTTAC CTTATCAGTA CGATTATCGC CGGGCAGCCG TTGTTACCGG 2460

CTGTGGGGGC CGTCATCACC CCACAAAACG GGGCCGGAAT GGATAAAGCG GCAAATGGTG 2520

TGCCGGTCGT GAACATTGCC ACGCCGAACG GGGCCGGGAT TTCGCATAAC CGGTTTACGG 2580

ATTACAACGT CGGGAAGGAA GGGCTGATTC TCAATAATGC CACCGGTAAG CTTAATCCGA 2640

CGCAGCTTGG TGGACTGATA CAGAATAACC CGAACCTGAA AGCGGGCGGG GAAGCGAAGG 2700

GTATCATCAA CGAAGTGACC GGCGGTAACC GTTCACTGCT GCAGGGCTAT ACGGAAGTGG 2760

CCGGCAAAGC GGCGAATGTG ATGGTTGCCA ACCCGTATGG TATCACCTGT GACGGCTGTG 2820

GTTTTATCAA CACGCCGCAC GCGACGCTCA CCACAGGCAG ACCTGTGATG AATGCCGACG 2880

GCAGCCTGCA GGCGCTGGAG GTGACTGAAG GCAGTATCAC CATCAATGGC GCGGGCCTGG 2940

ACGGCACCCG GAGCGATGCC GTATCCATTA TTGCCCGTGC AACGGAAGTG AATGCCGCGC 3000

TTCATGCGAA GGATTTAACT GTCACTGCAG GCGCTAACCG GATAACTGCA GATGGTCGCG 3060

TCAGTGCCCT GAAGGGCGAA GGTGATGTGC CGAAAGTTGC CGTTGATACC GGCGCGCTCG 3120

GTGGAATGTA CGCCAGGCGT ATTCATCTGA CCTCCACTGA AAGTGGTGTC GGGGTTAATC 3180

TTGGTAACCT TTATGCCCGC GATGGCGATA TCACCCTGGA TGCCAGCGGC AGACTGACTG 3240

TCAACAACAG TCTCGCCACG GGGGCCGTCA CTGCAAAAGG TCAGGGCGTC ACCTTAACCG 3300

GCGACCATAA AGCGGGAGGT AACCTGAGCG TCACAGCCGG AGCGATATCG TTCTCAGCAA 3360

TGGAACGCTT AACAGCGACA AGGACCTCAG CCTNGACCGC CGGCGGCAGA AATTCACTCA 3420

ACAGAATGAA AAACTGACTG CCGGCCGGGA TGTAACGCTT GCCGCGAAAA AACATCACAC 3480

AGGGTTACCG GCCA 3494

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GNCCCAAGCT TAGGTTCGCG GCCGCAGTAC TGGATCTATT GCCAGCTTCA CCGCCAGACT 60

GTCAGTCAGT ACATCACCGT ATTTCTGCTG GCAGGTTGCC GGGCGGCTGC ACAGTCACTG 120

ATCAGTTGCT TCTGCTGTGC CGTACTCAAC TCTTCGTACT TTTTGATAAT ACCGCCGCAG 180

TCACCGCCTT TCGCCTGACA GGACTTCATT TCAGCAGAGC AGGCATCTAT CTGCTTATTG 240

CTCAGGTAGT TATTCTCAAC AACAACCACA GGGGATTAGA AGCCTTTTAG CCTGAAATAT 300

TTTGCGAGAG CACATCCAAT ACCAATAAAT GAGCCAATCA CACATCCGAT AAACAAAACA 360

TGCCGAATCT CTTTCAAACT AATATTTAAA TTACCTGTTA TCAACCACTC CACCAAAGAA 420

AAAAACACAT CAATACATAG GAATGACACC ACTATAGAAA GAAATGCGAT TATAAAAATA 480

ATAAACAATT CTGATAAGTG CTGAGAATTG CCGCTCATTT TTTCACCTCC GGAATGTAAG 540

ACTCAATCTT TTTACCTTCA TACTCAGAAG CAAAAGAAGC CGACACATCC CCAGCTATAC 600

CAGGAATCCT ACTGGGTGTC ATTTCTTTTG ATAGCCCCAA TTCTCCTTTA ATATCGGTAT 660

ATTTTTGAAG TGTTGGATTA AATTTCGGGT CCCAGCCGTC TTTTAACCAG TTAGCACCAC 720

TATTAATGCC CCATGAAAGG CCTTTACCAA TGCCATATCC AATAGCAGAA CCAGCACCAT 780

TGATCAACGC ACCAGATGTT GGGGCTTTTC CTTCGAGCCA GTTTCCTAAT GCTCCTCCAG 840

TTGCATTCCA GCCAACTGTG CCTACAACTC CATTCCCTGC ACTAATCACA TTAACCCAAC 900

CACCGATAAT CGCTGTTGTA GGATCTATAG TTCCATCCGT CAGATAGCTA ACACCTGCAT 960

TAGCTCCTGC CCCTAATCCC CACATGGCCT GAGCACCGCC AGTAAGAGAG CTACACTACC 1020

AGTGGCCAAC GCTCCGGCAT ACGCTTTATT GACTGCTTCT CCTCGCTTAC AGGCTTCACC 1080

GCCTGGGGCA TCGTTACAGG AAAGTACATC TGCGCCATGC GTCTGAGCAG CTTTGCTCTG 1140

CTCGGACTCT GTGCCACCAA CCAGGTTATT CTCAGCAATG TTCTTCCCGA CACCAGCCCC 1200

AGCAGCCGCG CCAGCCACAT CGCCACTGGC AATGCCGCCA GCCATACCCG CTGACAGCGT 1260

TGCCAGCGTG CTTACGGTTT GCTTCTGATC TTCTGTCAGT TTCGACGGAT CTACGTCCGG 1320

ATAGAGGCTT TTCGCAATGG CTGACGAGAT CACTTCACCA GTACCCGCAC CAATTGCGCC 1380

TGCTGCCGCA CTGTTGCCCT GAAGGGCTGC TGTCACACCA CCGAGAATGG CATGGGCAAT 1440

GGCTTTTGCC GCTGTATTGT CATCAATACC CGCGTGATGA CCGATGATGT TCGCCAGCTC 1500

CGGCGCCGAA GCTCCGGCCA GAGCACCTGC TAAATTACCC CCCGCCAGCC CCTGAAGTGC 1560

AGCCGTTGCA GCCTGGATAC CGCGCTGCAT ATCGCTGCCG GTACCATACT TTTCCTGTTC 1620

CTTTTTGTAT TCCGGCGTAT CACGCAGTTT TGCCAGATAT GCCTGCCGCT GTTCTTCCGT 1680

CGCATCCGCC GGAACAGGCC CATATTTATC CTGCGCAGCT TCAACGCATT CAGTTCCCCC 1740

TGCGTCCGCG CAATATCCGC CACCTGACTG CCTATGTCAC TGATAAGCCC CACTGTCTGC 1800

AGACGCCTCT GCTCCTTCTC CTTGTCAAAT ATCGGGCTGA TACTGTCATT AGCGTGCGCA 1860

GGGTCACGGC TCAGGTTCGC CAGATTCTGC TTCTGATTGC CCCTGTCCCG GATGGTGATA 1920

GTGCCTTCTG CCACTGCGGC CTGAGTCGTT CCTTCCGCAT GTCCGCTGTG ACCTCCGGCG 1980

GATATCATGC CACCCGGCAT GTTACCCTGA AATTTATCCC CGAAGCTGCC ACCACCGCTC 2040

AGACTGATTC CACTGTGACT GACTTTATAA TCCGCTTCGT TGTGAAGGTC ACTGAACCCC 2100

AGCGTTCCGG TATCCAGGTG GTTTTTATCC GGTGTGGCAG TGGAGGCAAT CACCGCACCA 2160

NSDOCID <WO 9822575A2 I >

TCCAGTTGGG TATGTTTACC CACTGTGATG TCGAAGCCGC CGTCACCGGC AAACATTCCG 2220

GTTTGTTCAG CAACGGAGTC AAAGCGGCTC TTCATCTTAT CCCGGGAGGC AGCGATGTAA 2280

CCTGAGCCGG TCATGGAGCC AAAGGTAAAA CTGCCGCCGG CAGCCACGCT GGTCTGTTTA 2340

CTGTCGTACT TACTGGTGTC CTGCTGGCTG CTTATCAGCA GGTCGTGGCC CACATCGGCG 2400

ATAATCCTGT TGCCGTTGAC CTGAGCACCG TTCAGTACCG TATCCCGACC ACTGTTGATG 2460

GTGACGGTTT TACCGCTGTC TGTTGTGGTT TCAGTCCACT CAGTACCGTT ACCTTTCTCG 2520

CTGCCTTTTG CCGCATTAAC GCTGGCAAAG ACACTGATAC CGGCACCTTT ACCTGCACCG 2580

ATACTGACAC CCACGCCACC GCCACTGCTG CTGTTCCTGC CCGTTGTTTT TTGTGTGTTT 2640

GCCGCGCCAC TCAACAGAAC ATCATTCGCA GCATCCAGGT TTGTGTTACC ACCGGCCTTA 2700

AGCTGGCTTC CGGCAATCAC AATATCTCCG CGGTTATCGC CCCTGTTTTT ACCGGTTGCG 2760

ACAACAGACA GATTATTCCC GGCATTCAGC GTACTGCCGG ATACTGTGTC ACTTTCAGAA 2820

TGTTGTTGTG ATTTCGATTT CTGGGTGGTG AGCGACAGGC TGACTCCCGT CGCATTCGGG 2880

TCACCGGTTG CGGAGGCCAT TGCCGCAGCC TGTCCGGCCT GCACACCAGA CAGCGCTGTC 2940

TTTGTAGCCT GCAGGGTTTT CAGACGGCTG TCACTGCTCT CCTTCGTCTC CTGTGCACTG 3000

GTGACCGCAT TATTGATGGC ACTGCCCACT GTGCCGGAAA GGGCAACCGT CAGCCCGCTT 3060

TTCTTCTGCT CAAATTTTTC GTCCACAGTA CGACGGTCAT GCCCCGGGTC AACCACCACA 3120

CTGTCACCGG TAATGCTGAT ATCCCGGTTC GCAATCACAT CCGAACCGCT GATATGAGCC 3180

TGTTTGCCCG CGGTAATACT GACATTACCG GCAGTGGAGC CGATGGTACT GGCACTCTGA 3240

CTCTGCGTTG TCCCGGCCTC GCGGCGGTCG TGCGTTGTCT TACTGCTGCC AATGGTGAAG 3300

CCAATACCGC CGGTACCCAT CAGACCGGAT TTCTTCGTTT CCTTAAAGCG CCAGGACGTA 3360

TCTGTACTGG TGGCAGCAAG AACATCAACA TGGTTACCCG CCGCCAGTGA CACATCCCGG 3420

TCAGCCACCA CATCCGAACC CTCTACCGTC AGGTTATCAC CGGCGTTAAC GGTCACGCGG 3480

TTCCCCGACA GCAGGGAACC TGYTTCACGG GAGGCACTGT CCTCACTGAT GGTGTGGGTG 3540

GTTTTCTTAC TGAGAAAACC TCCGCTTTTT TTCTTCGTTT CCAGATAGTG ATAGTCACTT 3600

TCTGTCGCCG TGGTCAGGGC AACATCACGA CCGGCATTCA CGCTGATATT GCCGGTTGCG 3660

GTAACGGATG ACGCAACAGC GGTGATATCC CGTCCTGCGG TGACGGTGGT GTCACCACCK 3720

CTGGCGATTT CCGTTCCCTG CTGACGGACT GTCTCGTTAA TCTCTTTCTT TTTCTTCGAC 3780

GTATAGCTGT CGCCTGCGCC GGCAGACTCT GCCACCAGGT TCACATCACG TCCGCCCCGG 3840

ATGACCACGT TATTTTCCGC AGCCATACCG GCAGCCTGAC TGGCAATATC ACGACCGGCA 3900

ACAAGGAGGA GGTTATCGCC CGCCGTCACC GTGGACACAG CTGCGTGGCT TTCATGACTT 3960

TCTGACCTGC CGTTGCGACT GTTTTTGCTT TCCCTGACTG CATTCAGACT CAGGTCGTTA 4020

CCTGCAGAAA GCAGGGCGCT GTGCCCGGCA GAAACAGAGG ATGCTGTGAC ATCCAGATTA 4080

TGGCCTGCAG CCATCGCCAG GTTACCGCCG GCGCTGATGC TGCTGCCCTG TGAGGTGGTG 4140

GATGATGAAC TGTTGTCATC AGTGTGCCAG AAACCGGACT GACTTTTGCT CCCGCTTATC 4200

AGGTTTACGG CAATGTTGAT GTCATTACCC GCAGACATTC CAAGGTCTCC ACCGGACGAG 4260

ACCGTTGCCC CGGTAATATC AATGTTTTTC CCTGCATCCA GTGAAAGTGA ATCAGTGCCT 4320

TTAATGGTCG CAACCGGACC GGTGTCCGTA CCGCTGAGAT GCACACCACC ATATCGGCTG 4380

TCACTGCCCG CATTCCATTG CTGACGCCGG GTGATATTGC TGATGTTGCC ACTCACGCTT 4440

TCCAGTTGTA CGGTTTTACC GCTGATGACT GAGCTGATAT TGCTGATATC CCCGATGGCG 4500

CTCAGGTCCA GGCTACCGCC CGCGCTTATC AGCCCTGCAT TCAGGTTGTC GATATAGCCG 4560

GTACTGTCGA GCGAAAGGTC GTTCTGTGCG TTGATGCTGC CGCCGCTGTT GGTGATATTG 4620

CCGTCCGCAA GCTGCACGTT GTTCCCGCTG ATAACGCTGC CGTTATGCAG GGTGATATCT 4680

TCCGGCGACA GATACAGTTT CGGGACCATG ACTGTCTGTC CGTTGATGGT GACTGACTCC 4740

CACCACAGCA TGCTGCCGTC AAGCTGAGCA ATCTGTTCAG CTGTCAGCGC CACACCAAAC 4800

TCTAATCCCA GTCCTTTCTG TTGTCTGGCC GCGTTATCCA TCAGATACCG CATCTGTTCC 4860

GTGTCTGAAC CCAGTCCGTT GAGATAACGT GAACCCGTCC GGCTCAGCAC CGCGTTACTG 4920

ACATACCGGG TATCAAAGAC CGCATCCCCC AGGAAACGAT AATCTTTTTC CGGTTTCAGC 4980

CCGAGGCGGT CAAGAAAATA CGATGAGCCC AGAAACTGTT TTTCATCGGT ATACGACGGA 5040

GCCGTTTCAC GTGGCGCCTG ACCCGGTTTC GCTCCAAGAA GCTCATACAG TCCGGCAAAC 5100

AAATGGCTGT CCACCTGTCC GAGACCATCC AGTTTCGGGT TCACCGTAAT CAGATACGGA 5160

CTGTCCGGGT CCGTGGACGG AACCAGGTAT CCATTGTTGC CGGAAGGCAG TGGCCAGTCA 5220

TCACTGATAC CGGTCTGACC GGTCAGTGGC GAACCTCCGG CAATATTTTT CAGGGCACCT 5280

GCCAGTTCAT CGTGCCATTG CGGAGAGCCA ACCACCACCG GCTCATACTG CTGCAGCGCT 5340

GTCTGTGTCA GACTGTCTCC GCCGGTCTGC TGACTTAACG TATTCAGTAC AGGTGCAGAG 5400

ACCACCGGAC TGACACTACC TGCATGTGCA GTGGTTGTTC CGTTATTGAT ACTGCTGGTA 5460

AAACGGGTCT TAACATCCCC GCCCGCCTGA ATAACGGAAT AATACGTCTT ACCGGGCGTG 5520

TAATCTTTTT CCCGGCCATC CAGTGAAAAT CTGATGGTAT TGTTTTCAAA TTCCGGTGAC 5580

AGCAGGGGCA GTTTATCCAG AGAGCCTGTT GCATAGCTAC CGTAAAACGT TTTCGGGTCG 5640

TAGCGGTATA CCAGATATTC ATTCTCTGTC CCCGTCTGCC AGCTCTGATT GCTTAACTCT 5700

CTGCCCGAGA GTGCGATATC CCCATTCGCC AGGATAAATG ACGCCCGGTT TTCCAGTCGT 5760

TCAGCCTCAG CAGAAAGATT ACGCCCTGAC GCAATGCGGC CTGCCGGATT ATCAGCACCG 5820

GTTACTGTTG TGATGTTCTG GCTGCTGAGA AAGCGCTGTG TGGCACTGTC AGCAAACGGA 5880

GCGTAATAAT AAAGCGTATC CATTGTGATA TTGCATGCCC CGTGCCCGTT GCAGGGCGTA 5940

CCGTGCTGAT TTTCAACTTC ACGGGTGAAA TAGCCATAGC TGCCGTCAGG AAGAAGGGAA 6000

AGGGGAATAT CAACCAGAGC ATTTCCCATT CCCTGAATGG ATGAGGGGTT AGTCCGGGTT 6060

GTTGTTGTGG CAGAAAATCC CTCCCGCTGG TTCAGAAGAT GCCCGGTTCT TACAACAATA 6120

TCGCCCTGAT GCGTCTCAAT ATTCCCGGAA GTATTGATAA TCTCTGTGTT TGCACCGCCG 6180

GAAGCATCCT TCTGTACCCA CAGACTGTTG CCGGCCAGGA TATCACCATG CTGGTTATGC 6240

AGACGGTCTG TAAACAGCTT CAGGTTATTC CCCGCATAAA TCAGCGCACT GTTCAGCAGG 6300

GTACCGGCCA CATTCATTGT CAGACTGCCT GCCGTGCCGG TAAAACCACT GATGGTGATA 6360

TCACTCCGGC TGTTCAGACT CACATCGCCA CCGGCCTGAA GTGAACCCGG TGCGTTAAGG 6420

AAAAGACGCT GTGCGCTGAA AACACTGTTG CCTTTACCGG CAGTCAGCGT TCCATTGTTG 6480

GTGAATGCCT CTCCGGCACC GAGCACCATG GCATCACCCT GCATGACACC GCCGTTGGTG 6540

ATGGCATTTT GCGACGTGAC GGAAAGGGTT TTCCCTGCGG CCAGGGTACC GTAATTCGTG 6600

AGGGCAGCAA TCAGTTTCAG TGTGACATCA CCGGTGGCCA CCACCTGCCC CTGACCACTG 6660

AAGTCCTGAG CGTCAAGCAG CAGGTTGCCT GCACTGTACA GCCGCCCTGT ACCATTTTGC 6720

AGCAGTGAAC TGCCCTTGAC GCCAAGCCCG GAGGTTCCCA GCAGGGTACC GCTGTTGCTG 6780

AATGTGTGGT AATTCACCAG CAGGTCCGCA CCCTGAAGCG TACCGGTATT ATTCAGCGTG 6840

GTTCCTTTAA CGTCGGCACT GCCGGTGGCA AGTACGCGTC CGCCGTTGAC AGTATTCACC 6900

ACATCCAGCA GCAGGGTGGC AGCCTGTACC AGTCCGCTGC CGGTGTTCGC CAGCACCTGC 6960

GCCGTCAGCG TGAGGTTACT GCCGGAGAGG ATTTTGCCGT CGTTCTGCAG ACGGTCAGTG 7020

GCGTTCAGGG AAACCCCGCC ACCACCCTGT ATCGTGCCCT GGTTACTCAG GGTCGCAGTA 7080

CTGACATTCA GTGCATTCCG GCTCATCAGA ACACCACCGG AACGGTTGTT CACGCCACCG 7140

GAGGCGGCCA GCGTCAGCGT TTCGCCCTGC AGATGCCCGC CGTTTGTGAG TTGTCCTGCC 7200

GTGATGGTGG TGGCATTTCC CTGTAATTGC CCGTCGTTTG TGACACTGTC TGCCTTCAGC 7260

GTCAGCACAC CTGCACTGAG CAGTTTTCCG CTCGCGTGAT TGTGCAGCGT CTGATTCACC 7320

GTGAGCGTGA GAGCATCCAC ACCGGTGATG TCACCCGCAC TGGTCAGTGA GTTCGCCTTC 7380

AGGGTCAGAT TTTTTGCAAT CCATTGTCCG CTGTTGCTTA AATTCAGTGC ACTGAGCGCC 7440

ATTTCACCGT TCGAGGTGAC TTTGCTGCCT GCTGTGCTGA CGAGCTCACC CGTCAGACGT 7500

GCAGTCAGGC TGTCAGCCGC CTGGATCGCC CCGCTGTTTG CCAGACTGTC TGCGGTGATC 7560

AGCACCCGTT TGCCCTGCCA GTGTCCGGAA CTGGTAATAC TGCCTGCGGT GATTGTCAGA 7620

TCGCCGCTGG TCAGCAATGA ACCTCCGTTA TTCATCAGCG CAGGTTGAGG GGATGCCATA 7680

CGGGCGGCAA GCGTCAGCGC GGCTATCCCG GTGAGCGTGC CACTGTTGGT GACACTGTTC 7740

TGGCGAATCG TGACATGGTT ACCCTGGACA GTGCCGCTGT TATCCAGTGA GTTTCCATCA 7800

AGGGAGAGCG TGCCGGCCGA AAGCAGACTG CCCCGGTTGT CCATGGTGGC TGCTTTCAGC 7860

GTGGTGTCAC CCTGGCTCAT GATATCGCCG GTACTGGTCA ACTGACCGGT TGCCGAAGCA 7920

ENSDOCID <WO_ 9822575A2 !_>

GTAAGGTTAC CGGTTGCCAG CACGGAACCA CTGTTCGCCC AGTTGTCCCG CYTGCACGGT 7980

GAGATTCTGT CCCTGCGTGG TCCTGCGGTA TGCAGTGTTT TACCCCGGAG GGTGAGGTCG 8040

CCCGCCGTCA GCCAGCGCCC GTTACTACCC TGTGAGAGGG TGTCGCCAGC AAGCGCCAGT 8100

GCACCGGCGC CCTGCAACAG GCCGTCACCA TCCAGCGTGG TCGCCCTGAC GCTCAGCGTG 8160

TCAGCGATGA TTTTTCCCGG ATTGCTGAGG GAGACAGCAT TTAACATTAA ACCATTATCA 8220

CCGGTGATAA GCCCGCTGTT GCGGATGTCC GGTATATCCA GCGTCAGGTC TGCAGCACTG 8280

TACAGCGTGC CGTTCTGCTG ATTATCAAGC CTCTGTGTGT TAACGGTAAG TGAGGCCTCC 8340

CCCTGCAACA GACCGCTGTT GGTCAGGGTC TGTGACTGTG TATTCAGGGC GGAACCAACA 8400

AGTACGCCGC TGCTGGTCAG TTCCGGCGCA CTGAGGCTGA GCGACGGGGC ACTGCTTTTC 8460

CCGCTGTGGG TGAGCTTTTC ACTGGCGTTC ACCACCATGG TCTGTTGTGC TGCCTGCGTA 8520

CCTGCAAGAC GTGCATCTCT GGCGTTGATG CTGAGATTTT TACCGCTCTG AAGCTGTGCG 8580

CCCGCTGCGG TACTCAGTTT GTCTGCCTGA ACCCGGAGGG TGTCACCGGC ACTGTTTTCC 8640

CCGTCCAGCG CCACTGTTGT CACATTCAGC GTCATCGCAG CATCGCTGTG GGTGACCGAT 8700

TTTTTACCGG AGCTCAGCGC CTGCGCACTG ACCGTCAGCC CTTTGCCGCC GGACAGCACA 8760

CCGTTCTGTG TCACATCCTG CGCCTTCAGC ACCAGTACAT CATCGCTCAC CAGCGAACCT 8820

GTACTGGTCA GTTTCCCACT GGCCGTGATA TCCACTTTGC CCTTCGCGCC AGTGCGGCCG 8880

CTCTGGGTAA AGTCGCGGGT ATTCACGGTC AGGGGACCGC CACTGAGCAG GGAGCCACTG 8940

TTGCTGAGCG TTGTACTGCC GAGCGTCAGG GAAGCCCCCT GAACAGCACC ACTGTTATTC 9000

AGCGTGCCGG CATCGAGTCC CGCATGACCT TTCGCCAGCA ATATTCCGTC CTGTGTCAGC 9060

GTGGTGGCGC TGGCCGTGAG ATTCTGCCCG GCGGTTATCT GTCCCTGTGT TGTCAGCGTG 9120

TCACTGGCGA CAGTCACGAT ATCGCGGGCC GCGTTAATCT GGCTGGCGGT ATCCTGTGTG 9180

ATGTTTTTCG CGGCAAGCGT TACATCCCGG CCGGCAGTCA GTTTTTCATT CTGTTGAGTG 9240

ATTCTGCCGC CGGCGGTCAG GCTGAGGTCC TTGTCGCTGT TAAGCGTTCC ATTGCTGAGA 9300

ACGATAATCG CTCCGGGCT 9319

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ATGAGGCGAT TAAAGCAACA TTGGGCAGTG ATAATGCCCC CACCCAGCCA CCTAACGCAG 60

CGAAGAGTAA TACATCGCCC ATGCCTAATG CTTCTTTACG CAGAACTATT CCGGCTATCC 120

JSDOCID <WO__9822575A2_I_>

AGCGSAGGGA GTAAAAAGTG ATAAATCCCA CCAGTACGCC GGTAACTGCG TCTTGTAGCG 180

TTAACGGACT CTGTTGCGCC CATGCTGCAA TCAGCCCGGT CCACAATACG CCCTGAGTAA 240

AAACATCGGG CAGCCATTGG TTGTCGAGGT CAATGACGCT CGCGGCAATC AGCCAGGCGG 300

ATAATATCAT CACCGCCAGC CCCCATCCAC TTTCTGGCCA CACCAGACTC GCCAGCAAAA 360

AAGTGAGTGC TGTCAATAAC TCAACCAGCG GATAACGTTG CTGATTTTCG CCTGACAGTC 420

GCGGCAGCCC TTTGAGCATC AACCATGAGA GCAGCGGAAT ATTGTCACGA ACGCGGATGG 480

TCTGCTGGCA ATGCGGGACA GTTGCGAACC GGGTTAGCCA AGGGCTTTAT TTTTTGGACT 540

GCGGCACTCG G 551

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CATTTACCAA ACCCCGTTCG AATATCTTAT CTATTGCCCA TCTCATATTA AATATAACCG 60

ATAATTTGGT GGATACTAAT AGTAATTACC TTGTTATTGA AAATATAATT ATTGTTATTT 120

TTAGCCTCAT TAATTAAATT GAAAAATCCT CTCTAATTTT TGTCAGATTA GGGCTGTAGA 180

AAGGATCGAG TTCAAGATGT TTACCCCATT TGCTTTTCAT AAAGTCCACT TCCCTGGCAA 240

ATCTGGCTAG TTTCTCCGGT GAATCTTCGG CTCCTCGACT AATCGATTCA TAGTGGTAAA 300

GCTCGGCATA AGGTGTCCAG AGATTACGAT ACCCCGCTTC GNGTACTTTC AGACAGAAGT 360

CCACATCATT AAAAGCAACA TGCAGATTCT CTTCATCCAA CCCGGCAACT TCCTCATAAA 420

TATCTTTGCG AATAAGCAGG CAAGCCGCCG TGACGGCCGA GAGAGTTTGT GTCAACAACA 480

AACGGCTGAA ATAGCCCGGA TGGTGGCGAG GATAATGTTT ATGGGAGTGT CCAGCTACAC 540

CACCAATACC GAGAATCACT CCGCCATGTT GTAAAAGTAT CATTACTGTN ATAGG 595

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TGGCAGTTGA ACAGATTTTC ACATCAGCAA CAGATTAGCG AACGGGACTT GGCATTAGCC 60

GAGCGTTTTA GTGAANGTTT AGCTCTAACA CGTCTATTAG AAGAGCGCAC GCAGNATTAT 120

3NSDOCID <WO 9822575A2 I >

CACTGAACTA GAGATTGAAA AACAATTGCT TACCACCAAG TTGTCTGGCG TAGAGCAGCA 180

GTTAAGGGCT GAGCAAGAGT CGCTTCAGCA GGCCCAGTCT GCATTGCTCT CAGCAGCAAA 240

AGAAAAGCAA CATCAACTTG ATGAGTTGGA ATCGGTGCTC AATGAGCGGT ACAGTGAGAT 300

TGCAACCTTA ACCCGTTGGC TGGAAGAACG TGATCAGGCA CTCCTTAGTG CAGCAAGTGA 360

ACAACAACAG ACCAATGANA CCATATAGAG CTCAGCCAG 399

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1013 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

ATACTCTGCT TGTTGAGCAG CCATTACGTC GCTTTGTGAC GCAATATTAG ACTCGTGCAC 60

TGCTATTAGT TGAGTCAGTT CATCACATTG TTTAGAAGCC GCAGCCAAAG CAAGAGTTTG 120

CTCATCTATG CTTTGCTGCA ATGTTTGTTG CACAAGTTGC CCTTCTTCCA GCTGTTGCTG 180

TAGATTTGCA CTTACCTTTT TCAGTGCATC ATATTCCAAG CCTAACGTAT CGTGCTGTGC 240

TTCCAGTAAT CCATAAGCAT GCTGCAACTG GTTTTTAGTT TGCTGCTCAC CGTCAAGCTG 300

TTGCTGCAAT GCATTAGCCT GCTGTTGCAA CAAGTTCACC ATATTGTCTC GCTCGGCCAG 360

TGTACGAACC TGTGTATCCT GGATATGTAG CGCTTGTTCC AACTGAAGCT GTAATTCGGT 420

AATTTGCCGC GAATGTTCGC TCAATGCTCT GTTGCTCTTG CTGAGCGCGA GAGTAAGGTG 480

AGATGCACGC TGTGTTTCTT CACTCAATTG TAACGTCAGG GTATTGACCT GTTGCTCCAG 540

TTGATGGCGA GCTTGCTCCT GGCTCGTGAT GCGACTCTGT TGCTGCTCTA GTTGATGCAG 600

AGCTGTATGC AACTCATCGT TGGCTTGTAT TCGCTCCTGC GACCATACAC TCAAGTTTGT 660

TTGGGCCTCA TTGAGCTGTT CTTGCAATAA TGCCACCTCA GATGTCAGCG AATTGATATG 720

TTGCTGGGCA AAAGATAGCT CATCAGATTG CACTTGAGCA TGTGCAAGCT GCTTTTCCAT 780

TTCTAATATG CTGTTATGTT GTGCAGTAAT GCGCTCGGCA AGACGCCCCC TTTCCAATGC 840

CTGCTGTTCT ACCAATAGCT GCCGTTCAGC CTGAATGTCA TCTTGTTGTG TAGACAACTG 900

ACGTTTTAAC TGGGAATTCT CCCAACTCTC GCTACAAGAT TTNCCCAAAC GACAAAAGAT 960

GTCTTGGACT TGTNTGGGTT ACACGAGCAT TTTCTGAGGA TTTTATACCA ATN 1013

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

NSDOCID <WO_ 9822575A2 I >

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GATATCCACA TCGAGACGTT TGAAAAGAGT CTGGTGATCC GTTTTCGTGT TGACGGCACA 60

TTACATGAAA TGCTGCGTCC GGGGCGCAAA CTGGGCTCGC TGCTGGTGTC GCGTATCAAG 120

GTGATGGCGC GGCTGGACAT TGCCGAAAAG CGCGTGCCGC AGGATGGACG TATTGCGCTG 180

TTGCTGGGCG GCCGGGCGAT TGACGTGCGT GTATCAACCA TGCCTTCCGC CTGGGGGGAA 240

CGGGTGGTGC TGCGACTGCT GGACAAAAAC CAGGCTCGCC TGACGCTGGA GCGTCTGGGT 300

TTAAGTCTCG AACTGACTGC GCAGTTGCGC CACTGTTACA CAAACCGCAC GGCATTTTTC 360

TGGTGACGGG GCCGACCGGT TCCGGCAAAA GCACGACGCT GTACGCTGGA TTGCAGGAGC 420

TGAACAACCA CTCGCGTAAC ATTCTCACGG TTGAAGACCC TATCGAATAC ATGATTGAAG 480

GGATCGGTCA GACGCAGGTT AACACCCGCG TCGGCATGAC ATTCGCCCGT GGCCTGCGCG 540

CAATTTTGCG TCAGGACCCG GATGTGGTGA TGGTCGGTGA AATCCGCGAT ACCGAAACCG 600

CAGAAATCGC TGTTCAGGCT TCAACTGGAC CGGACACCTG GGNACTTTCN ACGCTGGNAT 660

ACCAAAAAAA AGGGGTGGGG GGATTATAC 689

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CTCAGCAGAA CCGAGATCTT CCATCAGCTG GCGGGCCTCG GAAGANTCCC GCTGCCAGAC 60

CGCATTCAGC CGCTGTTCAA ATTCGGCCTC GTCGATTTGC CTCAGCGTAA AGGGCGCGTT 120

CAGCCCCCGT TGCAGCTCCT GCAAAACAGA GAGCGACAAC GGATGCACAT GGAGGATCTC 180

CAGCGACGCT TCGCACCATG CCACCAGGCT AAACCGACGG CTGAAACTAT AGGGCAGACG 240

CACGGTGTTA GCGGTGGTTT CCTGTGCTAC AGGCACCATT AACGCGTTCT CCCGGCATTA 300

AGGAACGCAC GAACTTCTGG CGGTAAGGCC TGATTTTGCG CAGGCAATAT CGCTGCGCAG 360

TGTGCGGCAT CAGGCTTAAG CCCTGCTCAT CGCGGTAGAT TTGCTCGGCG CGCATGTAGT 420

TATATTTGCG CTGCGACACA CCGTCTGCCG CCATACCGTC ACGCAGAATG GTCGGGCGGA 480

TAAACACCAT CAGGTTACGT TTTTCTTTTT TATCCGCCGT CGATTTAAAC AGGTTACCAA 540

TCAACGGGAT ATCGCCCAGC AGCGGCACTT CTCGCCACGC TTTCTCCCGC CTGGTCGTCC 600

ATCAGACCGC CAAGCACAAT TAGCTCACCA TCGTTAGCCA ACACGGTGGT TTTCAGTTTG 660

CGCTCACCAA ACACCACGTC GAGGCTGGTC TGTCCTTCCA CCTTCGACAC TTCCTGCTCA 720

ATCACCATCT GTACCGCGTT TCCTTCGTTA ATCTGCGGCG TGACTTTCAG CATGATGCCG 780

ACTTTTTTCC TCTCTACCGT GTTGAAAGGA TTGCTGTTAT TGGAGCCAAC GGTAGATCCA 840

GTTAATACCG GAACGTCCTG GCCCACCATG AAGAAGGCTT CCTGGTTGTC CAGCGTGGTG 900

ATGCTCGGCG TGGAGAGCAC GTTCGAGCTG GAGTCGTTTT TGACCGCCTG TACCAGCGCC 960

ATCCAGTCGC CTTTCAMCAC GCCAACCGCC GTACCGCTAA AGCCAGAAAG AAGCTGAGCA 1020

AGCGTGGAGA GATCGCCGTT AGTATCCGGA TTTATGGTGG TAGCGCCGTT TTCACTGATC 1080

ACCGTGGAGC CTTTCTGCGG TTTTGCYTGA GAAATCGTGC GCCCAGCGTA CCAATAGGGA 1140

TCTGCGTACC GTTAGCAAAC TGCATTAATC CGGCATCTTT CGACGCCCAC TGCACGCCGA 1200

AATTGATAAT TCACCTTCGG CAACTTCCAC GATCAACGCC TCGACATGTA CCTGAGCACG 1260

GCGAATATCC AGTTGTTCAA T 1281

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CAATATTAGC GCACGGCACC AAAGGTGATG AATGAGCAGG CTGRAATATT ATTTTCCCGC 60

GGTGCAGAAA TCCTTGTTCT TGGTTGTACA GAAATTCCGG TTATTCTGGC GCAACGTTAA 120

AGAGCAGCCT TCCCGCTATA TTGACTCACG GCGTCACTCG TTCGTGCCGG AATAAAATGG 180

TACGAAAATC GTGTCGGTAA ACATTATCTT TTAACCCAAT AATCATTTAA ATCGCAGCCA 240

GAAAGTTATT CGCTTTTAAC TGAATTATAT TTATAACGGA GAACATTATG GTTTGGCTGG 300

AAATTATCGT AGTACTTGGT GCAATAKTTT TTGGTATTCG CCAGGGGGGA ATCGGTATTG 360

GTTTATGTGG CGGGCTTGGG CTTGCCATTC TGACTCTGGG ACTTGGTCTG CCTATGGGGG 420

G 421

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GTTAACAATG GCGTAACAAA TTTCAATAAC GTAGAAGATT TGCTGTCAGA AAGGTCAATA 60

TTTCCTTTCA ATGGGTCAAA GACTTGCTTC TGGAATTCAT CCGGTTTTTT CTCCAGACGT 120

NSDOCID <WO 9822575A2 I >

TTTCCTTCTT CATAATAGTC AATATAACTT TTACCACTGA GTGTTTTGKC YCCATTTCTG 180

GTGACACCAG CTAACTCACC TATCAGCGTA TCCCMATGTT GCTGGGTAAT GAGGACTGAT 240

CTTTCAACAG AATACTCTTT ATTATACTGA GATAATATTT TAAAGTTATC TTCTAAAAAT 300

GCAGCATGGC GGGCATCATA TCCCATTTTC AAAGTAATTT TTGCCGTGTT TTTTCTCCCA 360

TTCAGCAATA ACATCGGCCA TTTTACTGGC GACATGTTCA AACATTGCCT GTTTTGAAGC 420

CTCAAGGATG CCTGAAATTA TCCCCGTAAC AGCCCCTACC AGCGCGCTTA CCGGTGCACC 480

AACCAGAGAT GTCGTTGCAG CAGCACTAAT ACCTGAAGAT ACTGAAGCCA GAACAGTGCT 540

TATCGTTGTT AACGATGCAT CAATAGCTCC TGTTTCTTTG TGGAAAGCAG CAAGTAAACT 600

GTCACCATCG TATCCAAGTT TTTTGAATCG TTGTGAATAC TCCTCTATTT TATTGGCACG 660

TTTAAACTTA TCGGCAATGG ACAGGAATGA GAGGGGACTA ATTGCCAGTG TCACAACAGA 720

AGCAATTAAA CCGGCAGCAG CAGCAGATGT AGATAACCCC TGTGCTGCAC GCTGTGCGAY 780

NAATATATTG AGAAATACCT TTTCCAACAT TACCCAGTAC TTTCGTTGTT AATTCAACAC 840

CTGCTGCAGC TTTAGTTCCG GTATCTGCAT CTGCATTGCT CAGAATGAAA CTTGCTGAAA 900

TCGCAGATAA AATACCCGAT ACAGTATCTA ACCCTGCACC GATATTATCA AGGTTAGGTA 960

AATTCTGTAA CTTATTACCA ACACCGTTCN GGNCTGTTGG TATTGGGATA ATACACTT 1018

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGCAATGTTC AAATCGATAT TGTGCAGCAC CTGGGTTGGG CCAAAGTGCT TGGAGACGTT 60

TTTAAATTCA ATCACAGGAT TTTCATCCTT CTTTCCAGAC GACGCAGAAT AAAGCTCAGC 120

ACCAGGGTAA TAATCAGATA GAACACCGCC ACGGCGCTCC AGATCTCAAG GGCGCGGAAG 180

TTACCGGCAA TAATTTCTTG CCCCTGACGG GTCAGTTCCG CCACGCCGAT CACAATAAAC 240

AGCGAGGTGT CTTTAATGCT GATGATCCAC TGGTTACCCA GCGGCGGCAG CATACGACGC 300

GTGCCAGCGG TAAAATGACG TAGCGAATGG TTTCCCMACG TGAAAGACCG AGCGCCAGTC 360

CTGCTTCACG AAAACCTTTG TGGATAGACA GCACCGCACC 400

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

INSDOCID <WO 9822575A2 I_>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CGTGTTCCCC TGGCCNGCTT GGTTTCGCCA TAGACGTTGA GCGGGGAAAT CACATCGGTT 60

TCCACCCAAG GACGTTCACC ACTTCCATCG AAAACATAGT CGGTGGAATA ATGTACTAGC 120

CACGCACCTA ATGCTTCAGC TTCTTTGGCA ATAACCGCCA CACTAGTTGC ATTGAGTAAC 180

TCGGCAAATT CCCGCTCACT CTCCGCTTTG TCGACTGCAG TATGGGCCGC TGCGTTAACA 240

ATCACATCCG GCTTGACGAG ACGTACCGTT TCAGCCACCC CTGCAGAATT GCTAAAATCA 300

CCGCAATAGT CGGTGGAGTC AAAATCAACG GCAGTGATGT GCCCCAGAGG CGCCAATGCA 360

CGCTGCAGCT CCCATCCTAC CTGACCATTT TTGCCAAACA ACAGAATATG CATCAGGTAC 420

GCTCCCTATA GTTTTGTTCA ATCCAGGATT GGTAGGCACC ACTCTTGACG TTGTTAATCC 480

ATTGTTGATT ATCCAGATAC CACTGCACGG TCTTGCGAAT ACCAGACTCA AAAGTCTCCT 540

CTGGCTGCCA ATCCAACGCA GCGCTCATCT TGCAAGCATC AATCGCATAT CGGCGATCGT 600

GTCCGGGGCG ATCCGCCACA TAAGTAATTT GATCGCGATA AGAGCCAGCT TTCGGTACCA 660

TCTCGTCAAG CAGATCACAA ATAGTATGTA CTACATCCAG GTTCTGCTTC TCGTTGTGAC 720

CGCCTATGTT ATAAGTCTCC CCGACCAAGC CAGTGGTCAC TACCTTGTAG AGTGCTCGTG 780

CATGATCTTC CACATACAAC CAGTCACGAA TTTGGTCACC TTTACCATAA ACCGGCAGCG 840

GCTTGCCATC CAGCGCATTG AGGATCACTA GCGGGATCAG CTTCTCGGGA AAGTGGTAAG 900

GGCCATAGTT GTTGGAGCAG TTAGTGACAA TGGTTGGCAG GCCGTACGTA CGGTACCAAG 960

CACGCACCAG ATGATCGCTG GAAGCCTTGG AGGCAGAATA GGGACTGCTA GGAGCGTAGG 1020

AGGTAGTTTC GGTAAAGAGC GGCAATGCCT CACCGGAGGC TACTTCATCC GGATGGGGCA 1080

GATCGCCATA TACTTCATCG GTAGAAATAT GGTGGAAGCG AAAGGCCGCC TTGCTCAACT 1140

CGCCCAGACT GCTCCAATAG GCGCGAGCCG CTTCCAGCAA TGTATAGGTG CCTACGATAT 1200

TGGTTTCGAT AAAGTCGGCT GGCCCTGTGA TAGAACGATC AACATGGCTT TCAGCAGCCA 1260

GATGCATCAC GGCATCTGGC TGGTGCAGAG CAAACACCCG ATCCAACTCA GCACGATTAC 1320

AGATATCAAC TTGTTCAAAC GAATAACGCT CACTTGACGA TACACTGGCC AAAGATTCCA 1380

AATTGCCAGC ATAGGTGAGT TTATCCAGAT TGATAACGGA GTCTCCAGTA TCACTAATGA 1440

TATGACGCAC CACGGCAGAG CCGANAAAAC CAGCACCGCC AGTAACGAGA ATCTTCATAT 1500

ATTTCGCTCT CTTATTTTAC AATTAATAGC TATTAAAAAT AAACTTGTTG ACTCCGATAT 1560

ATTAGAAATA TCGGGATACC GAACTAAATA TTTTTATATG CTTTTGCCAA GCAGACTCTA 1620

TATCCACCCT GTATCACTAT GCTTTCTGGC ATACAATATC CCATCATTGA CACAATGATA 1680

AACATATAAA TAAAGAAAAT TTTAAATCAT ATAACCAAAT TACTTTCATT TATTATCAAT 1740

AAGTATTTTG ATAAGAATAC CTATACCACA GGGAGCCCCC TGAAACATAA TATTAGCGAA 1800

NSDOCID <WO 9822575A2 I_>

GAATGATAAC TGATAGTTAC CATCTTAGAG ATAAAAACTT ATTTGTGTGG CGGGATG 1857

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGCTCTTTCG TGTAAAATAA AATACAGCAT ATCCTATATA GCTTACAATC ATTAAATGAA 60

GTCGCCAATA TTTATATGTT TTATCAATAT CAGCTTGACT CATTGTTATT TCTTTGTCAG 120

GAGACTCTGA AAATATGGAC ATATATAACC TCTTTTATTA TGAAATATTT TCAATAATAA 180

TAATCCGTTA GTAATCCTAT CATAGGGTAA TGTCTCATCA TGTTAAAATG ATCACATTTA 240

TAATCATGTC AAAAAGAACA ACAGAAAAAA TCATATAAAA TCAATTAAAT ATAATTGCCA 300

CATATTGTTG TTATTWAAAC ATTGGTGGTG AATTTAAAGC GAGAACAGTT TGTAACAGTG 360

ACTCCTTGCA GACTAAGTTA GAGTCTCCTT CTAAAATTAG ACGGWKTTCT ATTGATGGAT 420

AATAGTAAGC GCACCGTGAA KGACGTGGGG TAAAAATTAG TTTACAGATT GAGTGACATT 480

CCAGGGCAAC AACTCTTTCA CGCGGTTGGC AGGCCAGGTG TTGATTACAC TGATCACGTG 540

GCGTACATTA CCGGACTCGA TTCCGTTAAG TTTGCAGCTA CCGATCAGGC TGTACATCAC 600

TGCCGCACTC TCGCCTCCAC CATCAGAGCC GAAGAACATG TAGTTACGCC GCCCCAGTGC 660

AATACCCGGA GGCGTTTTCA CACAGGTTAT TGTCGATCTC CACCCAGCCA TTGCGGCAGT 720

ATTCGTTCAG AGCGTCCCAT TGCTTCAGCA GATAGGTGAA CGCTTTCGCT GTATCCGAGT 780

GGCGCGACAG TGCTCATCTG CCCCTGGAGC CACTCATACA ACGACTGCAT TAGCGGTACC 840

GTTCTGGCTT TTCTGACCGC CAGTCGCTCT TCTGCCGGAC TGCCGCGGAT CTCAGCCTCG 900

ATAGCGTACA GTTCACCGAT ACGCTGCAGG GCTTCCGTGG TGATGTCAGG TGGCGCTCTT 960

GCATGCACAT CGTGGATTTT TCTCCGGGCA TGGGCCATAC AAGCCGCTTC GGTTACCTGA 1020

CCGCTTTCGT AAAGAGCATT GTAACCCGCA TATGCATCGG CCTGCAGGAT ACCTCTGTAG 1080

TCCGCCAGAT GTTGCTGTGG GTGGATGCCT TTGCGGTCGG GAGAGTAT 1128

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

3NSDOCID <WO 9822575A2 I >

GTTTGCTTAC GAACCGTGAA ATATGACGGT CCCATATAAC TGCCTGATAC TTGTATATCA 60

TATACTTGTG CATGCATGTC ATCATTAAAA AGTACTTTGT CACCGTCTTT AAGTTGAAGA 120

CGTGTAAAAT CTTTATACGG CAAGTAGACG GAAAACGGGC GCTTTCCCTG TCGCCAATCA 180

CACCGACATG ACTGACTTTT GCGAGAGGAA GTGCATAATT CACCAATTCA GAGCCTAATG 240

CATTGCGCTG GGTAAGCTCA AATCGGAATG GGTTTCGAAC CTTTCCCGCA ACATTGATCA 300

TTGGACCTTG TTGCTCAACT GAAAATCACA TCTTGATCTT TTAATGCCAG CTTCGGGAGT 360

TTCCCATACC GTATGAAATC ATAAAGATCA ATTTGCKGTG NTTACTGCTA TTTTGTGCGT 420

GAACACCTTA ATTTTTGCG 439

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TATTCGTAAT TAGTTATAAA CAGATGATGT AAACACCAGT TGACTAGAGT CAATCTTATA 60

CTGGCAACAT CTATGATTAA TTTGTGTGGT TATAATTTTA AATATCTTAT ATTTATGGGC 120

TATTATTGAT ATCTGTCAGA GTATCAATAA TAGAAGGTAA TTGTTTTACA TACTATCAAC 180

TTTTGGATAA CGTTTTAAAA TGCACCTTGC ACATCGTATT TTATTATTTT CACTAATCTT 240

TTTTATAACG GCCTGCGCAC ATGATCCAAA ACAAGTTGAA GCCTCTCGTC CATTGGTAAC 300

AGCGATTAAT TCTTCTTATT CTCTTATTCC TGAAGATTTG CAGGCACCAT TAAATAACCA 360

AGATCAAGGC ACGACATTCA ACAAAAATGG CGTAATTTAT ACTATTGAGG AAAGGTATAT 420

ATCGGCTTTA GGTTCTCAAT GCATAAAGTT AAGTTATGCG ATGAATAAAA ATTATTCAAA 480

GCGAAGTGTT GTATGTAAAG AGAATAACAA GTGGTATCAA GTACCTCAGT TGGAACAAAC 540

ATCAGTTAGC ACTTTGCTTA TTGAAGAATA AAGTTGAAGG TAGACGGTTA GAAAATAATG 600

AAAATTTCGC AACTTAGCAC TCTTCTCTTT CTTATTTCTG CATCAGCATT CGCCGCAATA 660

GAGCAAAATC AATCTAATGG TTCACATTTA GATTATGATC TTGCTGCCTC GACAGGAGAG 720

TCTCGGAAAA TGCTAGCAGA CATCACTGGA CAGCCTAATA CAACCTCCAC AACAGGAAGC 780

TTCACACAAC AGAATCGTAA TGGGATGTTG CTTCCAGGAG AGTCAGATGT ACGAAAATTA 840

CTGCCGCAAT CTGAAGCAGG CTTACCTCCT CCGTATGGTG CTAATTTATT TGCCGGAGGC 900

TATGAA 906

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGGCCTGAT ATATGCCGTT ATTACAAAAA GAGGATCAAC CACACTGCCT TTTGGACCGT 60

GTTTAAGTCT GGGCGGTATA GCAACACTTT ATCTACAGGC ATTGTTTTAA TGATAACCAC 120

GTCATTATCA AAGTGACATT TTAACTCTTA TTAATAACCT TAGAGATTAT TTACCATGTC 180

GATAAAACAA ATGCCAGGGA GGGTATTAAT ATCGCTATTG TTGAGCGTTA CAGGATTATT 240

AAGTGGCTGT GCCAGCCATA ATGAAAATGC CAGTTTACTG GCGAAAAAAC AGGCGCAAAA 300

TATCAGCCAA AACCTGCCGA TTAAATCTGC GGGATATACC TTAGTGCTGG CGCAAAGTAG 360

TGGCACGACG GTAAAAATGA CCATTATCAG CGAATCGGGT ACTCAGACCA CGCAGACACC 420

TGACGCCTTT TTAACCAGCT ATCAACGACA AATGTGCGCT GACCCAACGG TGAAATTAAT 480

GATCACCGAG GGAATTAATT ACAGCATAAC GATTAATGAT ACACGTACAG GTAACCAGTA 540

TCAGCGGAAA CTGGATCGTA CCACCTGTGG AATAGTCAAA GCATAACGTC GGGTAGATAT 600

AAATTGGCGC GGGTTGTTTT TCGTGACGCA CGAATTTATC TCATTCAATG GCTGACAAAA 660

ATTCGTCACA CTCTTAACCA GAGACAATCT CTTAATACAG ACAAAGAGCA TCTGCGCAAA 720

ATTGCACGCG GGATGTTCTG GCTGATGCTG CTTATTATTT CTGCAAAAGT GGCGCATTCA 780

CTCTGGCGCT ATTTCTCCTT TTCTGCGGAA TATACGGCGG TTTCCCCATC GGCGAATAAA 840

CCGCTCCGTG CGRATGCAAA AGCGTTCGAT AAAAATGACG TGCAATTAAT CAGCCAGCAA 900

AACTGGTTTG GCAAATATCA GCCCGTCGCC ACGCCGGTAA AACAACCCGA ACCTGCACCT 960

GTGGCCGAAA CGCGTCTTRR TGTGGTGTTG CGTGGGATCG CCTTTGGTGC CAGACCCGGC 1020

GCGGTTATTG AAGAAGGTGG TAAACAGCAG GTCTATTTGC AGGGTGAACG CTTGGCTCGC 1080

ACAACGCAGT GATTGAGGAA ATCAACCGCG ACCATGTGAT NTGCGCTATC AGGGAAAAAT 1140

AGAGCGCCTG AGCCTGGCTG AAGAGGAGCG TTCCACCGTT GCCGCGACCA ACAAAAAAGC 1200

TGTCAGTGAC GAAGCAAAGC AAGCTGTTGC TGAACCTGCT GTCAGTGCGC CAGTTGAGAT 1260

CCCNGCTGCC GTGCGTCAGG CACTGGCGAA AGATCCGCAG AAAATTTTTA ACTATATCCA 1320

GCTTACGCCT GTGCGTAAGG AAGGGATTGT CGGTTATGCA GTGAAACCGG GGGCAGATCG 1380

TTCTCTGTTC GATGC 1395

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SNSDOCID <WO 9822575A2 I >

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CACTTGAATA AAACTGACAC CGTTTACCTC CATAATAGTG AGCATAGCCG CCATTGCGGC 60

CTGATCGGCG AACCGGAAAT CGCAACCTGC GAACGACAAC CGAACCGGCA AGCGTGCGGG 120

AAGGACGGAT ACCGGACTCT TTCGCCACTT CAGCAATCAC CGGCAGCGTG GAAAAAACAA 180

TAAACCCAGT ACCGGCCATA ATGGTCATAG ACCAGGTGAT AATCGGCGCG ATTATGTTGA 240

TATATTTCGG GTTACGCCGC ATAAAATTAC CAGCGACGGT ACCAGATAAT CCATTCCCCT 300

GCGGCCTGTA AGGCTGAGGC CGCCACAACA ACGGTCATAA TAATCAGGAT CACGTCGACT 360

GGCGGCGACC CCATAGGCAG 380

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTTTACGGTT TAATAGGGGA ANGCCGACTG GATGNAAAAA TGGAATCTGG AGCCCAGAAT 60

AAATCTGAAT TTAATGTGGA CTGGATATGC TCCAATAACC CCGGCAGGGA GTCATCTGTG 120

CGAAGATATT TGCGTTATGC TGTAATATAA TAATTCAATG TATTTCAGGA ACAGTAATAT 180

ACTACAGTTT CTACTTTCTT GTATTTAATA AATTGTTCCG CATCGCTAAA AGCAGGTCTT 240

TCAGAAGCCA CAAGAATTCT GTGGTCCCAG TATTTTTAGT TATCCTATTT TTATATCTAA 300

CTTGTAATAC TTACAGCATT TTCATTCATC CTAATGGAAG GCTGTAATAA TCTTTGAGCT 360

TAGAAACATC AAAATTATGC ATCTCATTAA TTTTGTCAGT CACACGACCT CTGGTAAAAA 420

TAAAACCCCC AGAAATATGC CATTTCTAGG GGGGGCGTAA GAATCAATAT ATTTTAGTGT 480

TGTTACATTT AGCTCTTAGC TCTTAGCTCT TAGCTCTTAG CTCTTAGCTC TTAGCGTTTG 540

TAGTTTCATC GCAATGAGTA AAAGGACAAC AAGAATAAGT GATAACGTTA AGAGAAGAGC 600

ATAGAAACCA TTCCAGTGGT ATATTTCTAT TATTTTAGAC AATGGATAGC CAGCCGCGGA 660

CGCACCAAGA TATGCGAATA AACTAACAAA ACCAGTAGAA GCACCAGATG CATATTTATG 720

TGAGTTTTCA GCAGCTGCCA TTGCGATCAG AAATTGTGGC CCAAAGATAA AGAAGCCAGT 780

GATGAAAAAT AATAACGAAA AAACATATTT ACTATCAATA GAAACCAACC ATAGACATGC 840

AGAAGCAATG ATTATACCAA TTGTATAAAT AACATTCATT TGAGAGCGAT TGCCCTTAAA 900

CAGAATATCT GATCCCCATC CAGCTACGAT AGCACCAAAA AAGCCTCCAA CCTCAAACAT 960

NSDOCID <WO 9822575A2 I >

CATTACTGTT GCATTTGCTG TTAGCAAGTC ATATT 995

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TAAAAGCGAC TCCATGTGAA ATTTCTGTTT GTCGTTTTTT CCCCGTTGTA GCGGCTCTGC 60

TCCTGGCTTC CCTGATAGTC AGCCCGCAGG CGCCAGGGCC CCAGATTCCC CCCCACAGTC 120

CCGTTATAAC TGAACTGATG AGAGTCTCCT CCCTGATAAT TACGGGAAAC CGTCCCGTTG 180

AGGTTATAAT CCAGCATCAG TCCGGGAATG CCGTCGTCCC AGCGTGAGGG AGGCAGCCAG 240

GTGGCATCAG AATACTCAAG CCAGGCCTGC GGCATATTGA TGCGTAATAC GCCCGCTCCG 300

GTATCAGGAC GAATATCCAC TCCCGGCAAC CCATGAAAAT CCGCACACTG ACCATCATGC 360

CAGTAAACAA CTTTATCCAG AGATTCTGCT GTTAACCCCA TCAGTCTGAC CATATCTGAT 420

GTCAGACAGC TGCGGCAATT TTTTTTCTGC CTTATCTCCT GACAACGCAG GTTCAACAAA 480

TGAMATCTGT AACGATGCGG GAGAAATACT TTGCCCGTTA ACAATCACAT CCAGAAGATA 540

TTGCCCCGGC AGAACATAGC CGGCTTCTGA AAAACGGGTG AAGTCAATAT TTTTCTTGTC 600

CGCTGCGTCA AGTACATCTG TATTAAACTC AACGGCACTG GCTGCGTTAC AAAACAGAGA 660

CAACAATATC ACACAGGTAA TATTGTTGAC TGCAAAAGGT ATTCTGTCTT TCATTCCACG 720

CATCACCAGA TTCACAAAAA AGATAAATAA CCGGACATCT CACCGGAGTG ACTCACTCAT 780

AATCGACCCG GAATCCCAGC ACAGCAAAAT AATTTCC 817

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 709 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTTTTGTCAG AGCGTTCACT CTCTGGCTGG ATGATTTCGG CTCGGGAAAT GCAGGCTTAA 60

TGTGGGGACT GTCGGGGATG TTTGAACGGG TAAAAATAAG TCATGAGTTT TTTCATTATG 120

TCCTGAAAAA CGGGTGTGCA ATGCCACTTC TCCGTGCTGT GGCAGACACT GTTGCCTGTC 180

ACAACAGAGG CGTGATACTC GAAGGTGTTG AAAATGAAGC GTTGTTCCGT ATTGCCAGAG 240

ACATGAATGT CCAGGGCTGT CAGGGATGGC TCTACAGGCG TGTGGGGGTT GATGAATTAT 300

INSDOCID <WO__9822575A2 I >

CCGCGCTTAT TCAGCAGTAT GAATAATCCT TTTTCACAGA CTGGTCAGCT GTCAACATTT 360

ATGTTTTTTT ATCTGCGGGA ATTTATCCGT CTGCCTGTCG GGACTACTCT GTCATACAGA 420

AATCAGGCCA GAATAAATTG TTGTGGAAAG GTGAGATTTA CCGGATGACT GATGTGCTCT 480

TGTGCACAGG TATACAGGCA GTGTGTTTCC AGTATATGGA AAATGATTAA ATGAATAACA 540

CAGACTTATT AGAAAAAATC ATCAGGCATC AACAAAACAA AGATCCTGCA TATCCTTTCC 600

GGGAACATCT TTTGATGCAA CTCTGTATCC GTGTAAACAA AAAAATACAG AACAGTACAT 660

CTGAGTTTTT TGGTGCATAT GGTATAAATC ACTCAGTATA TATGGTTCT 709

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TCATCAAGGG ACGGGGCATA TCTGGATGCG ACAGGGCAAA CCAACCACTG AGAATCCAAC 60

CTGCCAAAGC CTGACCAGGA AGTCCGACGT TAAAGAAACC AGCTCGACTG GCAACGGCAA 120

AACCAAGACC AATCAAGACC AGAGGACCCA TAGCACGGAA GATTTCTCCA ATCCCACGCA 180

GACTGCCAAA GGCTGTATAG AACAATTCTT CGTAGCCCCA AATAGCATCA TAACCGAAGA 240

TCCACATGAC AATGGCTCCG AGTAAAATTC CTAGGAATAC AGAAATCAAG GGAACCGAAA 300

TTTGTTGTAA TTTTTTAGAC ATCACTCTTC TCCTTTCCCA AGTTYCCACC AGCCATCAAG 360

ACACCAAGTT CTTGTTTATT GGTTGTTTCT GGTGATACAA TACCTTGAAT CTTACCATCG 420

TGGATAACGG CAATACGGTC TGAGACGTTT AAAATCTCAT CCAATTCAAA GCTGACNACA 480

AGGAC 485

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

AGCAGAATAG GCAACATCAC CACGCCGACA AACAGCGAGA AGAGAATGAC GCCAGCCGCC 60

AGGAACACCA GCTCATAGCG CGCCGGGAAG ACGTTACCAT CCGGCAAGAG CAGCGGGATA 120

GAGAGCACAC CGGCCAGAGT GATCGCCCCA CGCACCCCGG CGAAAGACGC GATCAGGATT 180

TCTCGTGTGG TCCACGAACC AAACTCCATC GGCTTCTTCT TCAGGAAGCG GTTGCTGAAC 240

TTTTTCATCG TCCACAGCCA GCCGAAACGG ACCAGCATCA GCGCCGCATA TATCAGAATA 300

ATATTGGTAA ACAGCATCCA GATTTCGACG TTAGGGTCGA TTTCTTGCTG GCCATCAGCG 360

GACGTCTTCC AGRATTACCC GGCAGCTGCA GACCTTAACA GCAGGGAACA CCATGGCCGT 420

TTTAAGGACA ATTTCNAGCA TCGGCCCANG TGCTGTTTT 459

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTAATAGCAC TAATACTGTC CTGCTCTATT CCGCTGACAT TTTCAGTCAG CTGCTGTATG 60

GGATGGGTTA CCCAAAACCA GACCAGCATA CCTGACAAGA GACCGCATAT CACTACCAGA 120

AACAGCGACC AGTACAGTGC ATTCCATAGT GCCTTTGTCC AGGCTGTATC AGTAAGAGCA 180

TTAAGTTCCT CTCCCTGTAA AATAATATAC AGATATCCTT TCGGTTCATC ACTCTGGTAA 240

AGCGGTGCGG TACTGAAAAC TTTTTGCTTA TTTACACTTC GGGGATCATC ACCATATACG 300

GGCCAGACAC TGCCGGAGAG AAATTTTTTC AACGGTGCAA TATTGATATA CCGGCGTTTG 360

AGATGACCCG GAGGGCGGCC TCCACAAGCA GTCGCCCTTC CGGTGAAACC ATATACAGCT 420

CCACACTGGG ATTAAGCGTC ATCAGACGCT CAAACAGACT CGTTAATGTC CGGTGTTACC 480

AGACAAAACA AGCATCGCAA GACGCCACAA ACGGTGCGCT TACTTAAATA AGCCGGTTAC 540

AGGTGAAAAA TCACGTCCTG ATATTCAAAT GTTTTTTCAG GTCATATTTT AGCAGGACAC 600

TACCAGCACC TAACAGCAGC ACATCTTTTA TAACAAAACT GTCAACTTTC CCCAGTTGTG 660

GTAACAGGCT GAGCGTGGTT ATTCCTGTAA CAATAACGAT AATATCTCCC AGTACACCAG 720

CAGCAGGCCT GAAGAAACCG ATAATCAATG CCAGAAATGT GATAGTTTCC ACTATGCCGA 780

GGAAATAGCT CCCTCCATGA ATACCAAATA TAATATACAG GATATTCAGC CAGGTGGGAT 840

ATATCAGGGG CTTGAGAGCC ATAACTTCAA AATCAAACCA TTTATAAGTC CCAAAAAGCA 900

TAAATATT 908

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1057 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

BNSDOCID <WO _9822575A2 I >>

CGGGCTAACC CAATATGCTT TATTAACCCG GGATAATTAC CCTGTTGCAT ATTGTAGTTG 60

GGCTAATTTA AGTTTAGAAA ATGAAATNAA ATATCTTAAT GATGTTACTT CATTAGTCGC 120

AGAAGACTGG ACTTCTGGTG ATCGTAAATG GTTCATTGAC TGGATTGCTC CTTTCGGGGA 180

TAACGGTGCC CTGTACAAAT ATATGCGAAA AAAATTCCCT GATGAACTAT TCAGAGCCAT 240

CAGGGTGGAT CCCAAAACTC ATGTTGGTAA AGTATCAGAA TTTCACGGAG GTAAAATTGA 300

TAAACAGTTA GCGAATAAAA TTTTTAAACA ATATCACCAC GAGTTAATAA CTGAAGTAAA 360

AAACAAGTCA GATTTCAATT TTTCATTAAC AGGTTAAGAG GTAATTAAAT GCCAACAATA 420

ACCGCTGCAC AAATTAAAAG CACACTGCAG TCTGCAAAGC AATCCGCTGC AAATAAATTG 480

CACTCAGCAG GACAAAGCAC GAAAGATGCA TTAAAAAAAG CAGCAGAGCA AACCCGCAAT 540

GCGGAAAACA GACTCATTTT ACTTATCCCT AAAGATTATA AAGGGCAGGG TTCAAGCCTT 600

AATGACCTTG TCAGGACGGC AGATGAACTG GGAATTGAAG TCCAGTATGA TGAAAAGAAT 660

GGCACGGCAA TTACTAAACA GGTATTCGGC ACAGCAGAGA AACTCATTGG CCTCACCGAA 720

CGGGGAGTGA CTATCTTTGC ACCACAATTA GACAAATTAC TGCAAAAGTA TCAAAAAGCG 780

GGTAATAAAT TAGGCGGCAG TGCTGAAAAT ATAGGTGATA ACTTAGGAAA GGCAGGCAGT 840

GTACTGTCAA CGTTTCAAAA TTTTCTGGGT ACTGCACTTT CCTCAATGAA AATAGACGAA 900

CTGATAAAGA AACAAAAATC TGGTGGCAAT GTCAGTTCTT CTGAACTGGG CAAAAGCGAG 960

TATTGAGCTA ATCAACCAAC TCGTGGGACA CAGCTGGCCA GCCTTTAATA ATAATGTTNA 1020

ACTCATTTTC TCAACAACTC AATAAGCTGG GGAAGTG 1057

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TACCGGGCCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT TCCTGCAGCC 60

CGGGGGATCC ACTAGTTCTA GAGCGGCCGC CACCGCGGTG GAGCTCCAGC TTTTGTTCCC 120

TTTAGTGAGG GTTAATTTCG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 180

ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT 240

GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 300

AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 360

GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC 420

GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG 480

GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA 540

AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCT GACGAGCATC ACAAAAATCG 600

ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC 660

TGGAAGCTCC CTCGTGCGCT CTCCTGTTTC CGACCCTGCC GCTTTACCGG ATANCTGTNC 720

GGCTTTCTCC CTTCGGGAAG CGTGGCGCTT TC 752

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTTGGGTAAT NGACCTCATA TCCCTCCGCC AAAAAAGGAT CTACATGCGA TTTTGCGAAG 60

CCAGCGTTGA TTGTAGGCGA GAGAATGGTT CTGTTGTTTT GGTACATTTC AGTTGTCATG 120

GATTTCACAA ATGTAGCATG ACCTTTCACC TGTCCAAGAG ACTGCAACAC CATCTGTCCA 180

AAACAATAAA TAGGAATCAA ACAGGCTACC AACATCAACA AGTATCCCAA TAAGGCTCGT 240

AGTTTAGTCC TTGACATGAC GCCCCTCCAA TTGCTTTTCT AGTCCTTTGA CAATCCGTCG 300

ATTACGATAC ACGCGATACA GCAAGAGAAG GATGACCGCC ATCGCTCCTA GTAATAACCA 360

CAACCAGAAT TGCCCACGCT CTCTCACCGC TCGATTCCGC TCTGCAATTG GTGCCGTATA 420

CGGAATCCGC TTCCCACGTA CCAACAGACG ATGACTGTTA ATCCTATACG GTGTACNAGT 480

CAACCA 486

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTACGCNTTC AACCAGGTCT TCTGGTTTAC CAACGCCCAT CAGGTAACGC GGTTTGTCTG 60

CCGGAATTTG CGGGCATACA TGCTCCAGAA TGCGGTGCAT ATCTGCTTTC GGCTCACCCA 120

CAGCCAGACC GCCGACAGCG TACCATCAAA ACCGATATCT ACCAGACCTT TAACAGAAAT 180

ATCACGTAAA TCTTCGTAAA CGCTGCCCTG GATGATACCA AACAGCGCAT TTTTGTTTCC 240

GAGACTGTCA AAACGCTCAC GGCTACGTCG CCCAACGCAG AGACATCTCC ATGGAGCGTT 300

TTGCGTAATC CCA 313

NSDOCID: <WO__9822575A2 I >

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CGGAAATCCC AGTAATTCCA TCCTCANATA TTCCACTCAN CCTCACTGTA ACAAAGTTTC 60

TTCGAATAAT AAAAATCATG CTTTCTGTTA TCAACGGAAA GGTATTTTTA TTCTCTGTGT 120

TTGCTTTATT TGTGAAATTT AGTGAATTTG CTTTTTGTTG GCTTTATNTG ATGTGTGTCA 180

CATTTTGTGT GTTATTTTTC TGTGAAAAGA AAGTCCGTAA AAATGCATTT AGACGATCTT 240

TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA GTGCATTCTT TTTGTTGGTG 300

TTTTATTCTA GTTTGATTTT GTTTTGTGGG TTAAAAGATC GTTTAAATCA ATATTTACAA 360

CATAAAAMMC TAAATTTAAC TTATTGCGTG AAGAGTATTT CCGGGCCGGA AGCATATATC 420

CAGGGGCCCG ACAGAAGGGG GAAACATGGC GCATCATGAA GTCATCAGTC GGTCAGGAAA 480

TGCGTTTTTG CTGAATATAC GCGAGAGCGT ACTGTTGCCC GGCTCTATGT CTGAAATGCA 540

TTTTTTTTTA CTGATAGGTA TTTCTTCTAT TCACAGTGAC AGGGTCATTC TGGCTATGAA 600

GGACTATCTG GTAGGTGGGC ATCCCGTAAG GAGGTCTGCG AGAAATACCA GATGAATAAT 660

GGGTATTTCA GTACAACACT GGGGAGACTT ATACGGCTGA ATGCTCTTGC AGCAAGGCTT 720

GCACCTTATT ATACAGATGA GTCGTCGGCA TTTGACTAAA TTATGGCATT CCGGAGTTTC 780

TGGAAGATAA AAAAAGAAGC CCTTATCAGA AAGCAGACAG GTTATATCAG TATTCTGTCG 840

ATAAATAACC TGCCCTGAAA ATACGAGAAT ATTATTTGTA TTGATCTGGT TATTAAAGGT 900

AATCGGGTCA TTTTAAATTG CCAGATATCT CTGGTGTGTT CAGTAATGAA AAAGAGGTTG 960

TTATTTATGA TTAAGTCGGT TATTGCCGGT GCGGTRCTAT GGCAGTGGTG TCTTTTGGTG 1020

TAAATGCTGC TCCAACTATT CCACAGGGGC AGGGTAAAGT AACTTTTAAC GGAACTGTTG 1080

TTGATGCTCC ATGCAGCATT TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC 1140

TTTCAAAAAG CTTCCTTGAG GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT 1200

TGGTTAATTG TGATATTACT GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA 1260

AGCTGGCTTT TACTGGCCCG ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG 1320

GTACGGGCAC AGCTATCGTA GTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG 1380

AAGTGATGCT AATACCCTGA AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTTAA 1440

GAAGTCGTCA GCCGTTGGTG CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT 1500

CAACCTGACT TATCAGTAAT ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATTCCGCTG 1560

TTTATTTCTC AGGGTATTTA TCATGAGACT GCGATTCTCT GTTCCACTTT TCT 1613

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

NTAGTCCATG GCCCCATGGA GCGAANTCCA AAGTGTGGAT ATTGTCGTTT TAATTCATCC 60

CAAAAGCTGA AATACGCCAA AACCCACGTT CCCTAACATT GGTATCATGC ATAATGACCA 120

CAGCCNTTCA GAAAGCTTTG GCAACCAGCT TTCAAAATCA TGGGTACCGC TTCAAACGTA 180

TGCAAACCAT CAATATGAAG CAGATCAATG CTACCTTGTG AAAAATGCTC TAACGCTTGG 240

TCAAATGTAC TGCGAATGAG AGTAGAAAAA CCTGAATAGT GCTGTTGATT ATATTCTGAT 300

ACTTGCCTGT AAACTTCTTC GCCATACAGC CCCGCATGTT CATCTCCCCC CCAGGTATCA 360

ACGGCAAAGC AGCATGTTTC TAAATCTAGT TTAGAGACTG CTTGGCAAAA TGAGAAATAA 420

GAACTTCCAT AATGAGTTCC CAGCTCAACA ATATTTCTTG GCCGCAGTGT GTCAACTAAC 480

CAGAAAGCAA AAGGAATGTG TTCTAGCCAA GCAGATTGTG CAAGGTATGT AGGACACCAN 540

AAAAGAGATG GTTTGAAAAT GAAATTCAAT TCCCTGCCAA TATCAGTGAT GGGATATAAC 600

TCACGATTCT CTACTAACTG ACTAATTTTT TGACTATCCA TTGAGGAAAA CTCACATGTA 660

TTTATAGAAT TAAATCAAGA AACCTGAAAA TACCTATAGT GCGGTAACTT ATTAACTAAC 720

ATTTAAATAT TAACAATACA CTTGGAAATA TTAGTTAAAA ATAAATCATT ATGATTTCTC 780

ATCAATCCTG GTGCTCACGC AAAGTTGCCA GCCCCATAAT AATAAGACCA TAGAACAAGC 840

AAAGTAATAC ACCCACAGTC GCAAGATTAT AGAATCGCCG TGGATATTCG GCATCTTCCG 900

CTAAAGTTGG TTGGGTAATA ACCAATAGAT 930

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ACGATATCCC CCCTCTGCTT TTGAGAGGCA ATCTGCTTTA ATACATGATT CATCACAACA 60

CCTCTTGCTG CGCTTTGATC TTAATTTTAT ATTTTTGGGT AGGGAAAAGT AATTGCCCCT 120

GATACGGCTC ACCATTTACC AACGTTTCAC AGCTATGTTC CAGAGCTAAA TTAAGACCTG 180

NSDOCID <WO 9822575A2 I >

GTAGAATATC CCAGCAATTC ACCCCTTTGA CATTTTCAAA GCTGTCATAA GCACCGGNNA 240

AGGGGGGGCC AACATGTTAT ACATGGAGCA GCCAATGATA CGATATTCAA AGCCCTCTTC 300

CAGTTGCATC AGATCCTGCT TGGTAASGGA GGAAGAGAGG CCACGAATAC GAGAGCGATG 360

ATGTGTAATC GGCATACCTG TGATATGAAG ATCATTCAAT TCAGGTAAGA AGATGCAGGA 420

CTCTTGATGT TTCCCCTCGG TGTAAATGCT GATACCAATG CCCCACTCTT TGAGCCCAGA 480

GACAAAGTTT TCTGTGCCAT CAATTGGATC TAGAACAATG TAAGAACCTT TGGGATTCCA 540

CTCAATATCT CCTAAAGGGG CTAATTCCTC TGAAATTAGC ACATGCCCTG GTAGATGCTT 600

TCTACAGAGT TCGAAAACTA TATCTTGAAC TTTTAGATCC AGTACTGCGG CCGCGATCC 659

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCGGATATA CATCAGGAGA AATTGGAGCA GCAATTGGAT GCGCCATTAA TGCCTGGTTA 60

GGGATCCCCG CATGTGGGCA CGCAAATGGC TCAGAATATG ATCGACCTTC ACCAGATAAA 120

CCAAATCTGA GCGAACCATT TATCCCAAGA CCCACGTATG ACGCTTCACT TCATTCCTGG 180

CATGGCGGAT ACTGAGTAAA TCATCCTGAA TCATTATGTT CAACATCATC AATTCTCCGG 240

ACTTGTTGTC AGATGTCCGG AGAATATTAA CCTTTTCTTC AGAAACAGAW TGATCAAGAA 300

TCACACTCCT TCTTTAAGAG GATTTTATCC AGAAAACTGA CTTTCTTCTA TCAAAATMAC 360

AGTATCCTGT TTTATCAGGA ATAATCTTTA CCTCCGGTAT CATTCCCATA ATCAGATATC 420

AGAAAAATGT GCCAGTAATT TTTTACTGAT GACTTCAAAC ATTTCACATT CATCACACGT 480

CAGATTACTC CAAAGTTCTT TCAGATATGT GTTCTGCGCC AGAGTGAGTC TCTGAATAAA 540

AAACATACCT TCAGAC 556

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TACCTGTTTG TGGAATTTGA CCCAGAAGTG ATTCATACCA CGACTATCAA CGCGACCCGN 60

GTGTNCAGCC ACTTCGTGCG CTTTGGCGTN CGCAGCGATA GTCCCATCGG CGGTTATTCA 120

TCAGCTATCG GTATATAAAC CGAAAGACAT TGTCGATTCC GGCAACCCCT TATCCGGGTG 180

ATAAGGTGAT TATTACCGAA GCGCGTTCGA AGGCTTTCAG GCCATTTTCA CCGAACCCGA 240

TGGTGAGGCT CGCTCCATGC TATTGCTTAA TCTTATTAAT AAAGAGATTA AGCACAGTGT 300

GAAGAATACC GAGTTCCGCA AACTCTAAAA CGCAATCCCA AACAGTGTTT TGACATTAGC 360

ATCCGTGGTG GCAGCCAGCC ATGCGGCATC TTCTCCACGC CAGTGCGCAA TACGTTGCAA 420

AATATGGGGC AGATGGGCTG GCTCGTTGCG CCGGGATGAN GGCTTTGGCG TGAGATCGCG 480

AGGGAGCAGA TACGGNGCAT CAG 503

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTTAACATCA AAATTACCTG CAGCTGAAAT GATTTTGCTG ATTTCATTAA TTAATGGATT 60

AAGATTACCC TGACTTCCAT AGGCTAATGC ATCATTCCCA TACACATAAC TTGCCTTATT 120

ATTACTCTGT TGATACTNAA GTGCCTTTTT AAGGGAATCT GGTGTGATTA CCCTGCCGTC 180

TTTATCAAAA ATCTGCTCTA TCTGGTGATT AGAGATATCA CCTGACTCTT TTTCAAACCA 240

GTTTTTAAAT GTAATACCAT TTTTGTGGCC AATGGAAAGA ACATTACCTT CAGCTTTATA 300

CATGATGAGG TCATTACCTT CTCGCCTGAA GGCCACATCC CGGAAATCAA TATCAGCCAA 360

ACTGAGTTTA TCGTCTTTCC CCCCATCATC GTCAATAATA TGATGGCCAT ATCCTGAAAG 420

ATAACGATAA ATA 433

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCGCTCTGTT CCCGTTCCTG TTCATCACCA TCGCCTGTGG TGCGGTATCT GGCTTCCACG 60

CGCTGATCTC TTCCGGTACG ACGCCAAAAC TGCTGGCTAA TGAAACCGAC GCGCGTTTCA 120

TCGGCTACGG CGCAATGCTG ATGGAGTCCT TCGTGGCGAT TATGGCGCTG GTTGCTGCGT 180

CCATCATCGA ACCGGGTCTT TACTTCGCGA TGAACACCCC GCCTGCTGGC CTTGGCATCA 240

CCATGCCTAA CCTGCATGAA ATGGGGTGGC GAGAACGCGN CGGATTCATC ATGGCGCANT 300

INSDOCID <WO 9822575A2 I >

GA 302

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTAATAAG CCAAATACTA CATCACGTAA TACTTGCAAA GAAGTGCGTG GAGTTTGACT 60

AATAATGGGT TTGTCCATTA ATACTTACCC AAATAATCGG CTCATTATAG CAACGAGCCT 120

CCGATTAAAA TTTAAAATAC TCAATCATTT AATAGCAACG TTAGCAGCTA CAGCGATTTG 180

ATAAATAATT TGTGTGATAT CTTTAAATGA TTGCATGGTT TTGCTATCAA CCTGAGGTAG 240

AACCAATATC TGATCCCCCG GTTGTACTTT ACCTTGCCCT TTAAATTCTA CAAGACCATT 300

TGCATGTACA ATAGCAATTC GCTTGTCGTT AGCTCGCTCA GTAAAACCTC CGGCCCATGC 360

AACATAATCA TCCAAATTAG CATCGGCATT ATATACTACT GCTTGTGGCA TCAACACTTC 420

ACCCCCCACT TGAATAAGAT CAGTCTTATT TGGAATAACT ATTTGATCGC CTTGTTCTAA 480

TTGGATAWTG GCAATAACAC CTTTATCTGC AACTACTACT TTACCAAGCG GTKGAACTTT 540

ACGAGCCTTT YCAACAAACT GCATCACTAA CTCTGCTTCT TTAGCACGTA TATTCGCCTC 600

ACCATCAGAT CGCGCGGGTG TGGTAAANTT CATACGTTCC AAGCGGTTTA GAGATT 656

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATATGTTATC TGGATCCAGA TAAAGAGCGT TCTTGACCCG CTATATCCAG ACAGGTCAGT 60

TACACCCTGT CCGGAAAAAC TGATCGGAAT AACAACAGTA TATTTTCTAA TACACTGGCA 120

AATGGTGCCG GCGGTGTGGG GATTCAGCTT CTGGATAGCG CTGGTAATGC GGTTGCTGCT 180

GGACAGAAGA AATATCTGGG ACAGGTAGGA CCATCAACAT CTCTCAATAT TGGATTAAGG 240

GCATCTTATG CACTGACCAA TGGACAGACT CCACCTACTC CCGGACGAGT TCAGGCGTTA 300

GTTGATGTTA CCTTCGAGTA TAATTAGGAA TGTCGGGGAT GGGCTATCCC CGATATTATT 360

GCAGGATTAG TCTGTGATAC AGATATACAG CCCATATGAA CAACTGTTTG CATATATAAA 420

AATGATGATA ATTTTA 436

NSDOCID <WO__9822575A2 !_>

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AATAATTAAA TTTGGAGGGA TCAGTTTTCT GATAATGTTC TGTTATTAAA ACATTATCCC 60

ATGGGGCGTA GTTATATCAA TTAGCAGGAT CTTATGAGTT AACTAACATC AGTTTTGAAT 120

TTTTAATGGG GGTAATTTAT CTTTTACTAA AAATATTTTA ACTATTAATA TAGCATCATG 180

GTTGTTACGG TTTGTTTTAA TTCTATTTTA TAATGTGCTA TATATTGTAT TTTTGTGCTT 240

AGATAAATAT GTTTTTTCAT TACTTTAGTG ATGTTAATAT TTTGCGTGTA GTAAAAATCA 300

TTGTTATAAC AAATGTCACT GTTGCTATAC TTTGCTGAAC TGTTTATCGG TCATTTTGAT 360

TCAATCACTG GTTCTATATT TTTTAATAAC CGTTCTGTAG CGATTAATAT ATTGCTCTCC 420

AGAGGATACA CTATATGAAA TATATTAAAA GTCATTAATT TTNATTCAAT GTTGTTTAGA 480

GTTATGTTCA GTGTTTGGNA ATAGGATGTG TTTCTAAACC GTCTTGGGTT CTATAATAAA 540

TTCTATTCTT ANAGGTTTT 559

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CATGTCCCTT CCTGAATACT GGGGAGAAGA GCACGTATGG TGGGACGGCA GGGCTGCTTT 60

TCATGGTGAG GTTGTCAGAC CTGCCTGTAC TCTGGCGATG GAAGACGCCT GGCAGATTAT 120

TGATATGGGG GAAACCCCGG TACGGATTTA CAGAATGGTT TCTCCGGACC TGAAAGAAAA 180

TTCAGCCTCC GGCTCAGGAA TTGTGAATTT AACAGTCAGG GTGGGAACCT TTTCTCTGAT 240

TCCCGGATAA GGGTGACTTT CGATGGCGTC CGGGGTGAAA CGCCGGATAA GTTTAATTTA 300

TCCGGTCAGG CAAAAGGCAT TAATCTGCAG ATAGCTGATG TCAGGGGAAA TATTGCCCGG 360

GCAGGAAAAG TAATGCCTGC AATACCATTG ACGGGTAATG AAGAAGCGCT GGATTACACC 420

CTCAGAATTG TGAGAACGGA AAAAAACTTG AAGCCGGAAA TTATTTTGCT GTCTGGGATT 480

A 481

(2) INFORMATION FOR SEQ ID NO: 122:

INSDOCID <WO_ 9822575A2 I >

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

CCATATAGTG ACTTCATTGA ACAAAATGTA AATGGAATCT TGCTGGAGAA TGACCCACAT 60

ATATGGATAA AAGCTCTTTC ATTACTTGTT AGTGCAGATC ATAAACGTAG CGAGTTGGCG 120

TTCAATGCTA AAAAATATGC TTGTAAAATT GTAGGTGTCG AGTAAAAAGA TATTTTTATT 180

TAATTGGTGC TATTGAATGT TTAAAAATCG AACTGATTGG TGTTTTAATA TTAATCATAG 240

GTTATGATGC AAAAATATAT TAGGCATTGC CTGCTTCAAT TAACTTGAGA GTGTAAGTTG 300

AATTGAAATA TGGTTATATG ATAAAGCAAT ATATGTTAAT ACATATGTCA ACCGAAAATG 360

CCATTATGTG TTTTTTACTT TATCTGTAAC GACACAATAT ATAAAATAAG GCTAATAATC 420

AAAACGCTTT TTAATTTGAT TGTTTTGAAT CAAGTGACTA AGAAATTCTC TTGCTGCAAA 480

TAACTCCCTT AGTGATTTTT TTTGAGTCTA TTTTATTCTC TGGGCATGGT CATGC 535

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CCGGCCCCAT AATGATGGTT TTATTAAGGT TAGCGCCGAC GGTTTCGATG AACGATTTCA 60

GGTCGGTATC TTTAAAATTA GCGGTGAAAG TGGCTTCTTC CGCCCAGACC GGTGAACTGC 120

ATAATGCCGC TGCCAGCACC AGCGGCAGTA AACGCTTTTT TGTTTTGAGG CCAGTTGTCT 180

TCTTACGCCA GACCGACAAC GTCATATCAC GCCAAAACAC GATGAATGAT TCTCCTGGAT 240

TAAATGCGGT TAGCGCAGCG CGATGGAAAT GTCGTGGCGC GCACCCTTGC GTAAAACCGT 300

AAGTTGAATG GAATCCATTG AAGGTAACTG CCGCATCAGA GCAATCATTG CTCGTGGATC 360

AGTGAAATCC TGCTGATTTA GCGCAAATGC GATATCGCCT TCCTTAAAAC CG 412

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

NSDOCID <WO _ 9822575A2 I >

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TAGCCTGTTC AGCGTATATT TGGGATGAGA AGCCAAAGTG GCTTTGGTGG TGTCCCAGCC 60

CAGGTTTTTA TTACTGCTGG TTATTTACCT TTCATGTTTT TCAATAAAGT TGTGACTCAG 120

TTGAAATCTG CTGTCAATGC TAATATGGGA CTTTTTTGTT ATAGACAAGT GACTCCTTTT 180

GCAACTTTTA TAGCACGTTT TATGCTAGAA ACAATGGTGG GCATGATTGT CGGTATAATC 240

CTAGTACTAG GATTATTGTG GTTTGGCTTT GATGCAATAC CTGCGGATCC ATTGCAAGTG 300

ATCCTTGGTT ATTCTCTTCT GATGCTGTTT TCTTTTTCTC TTGGTATTGT ATTTTGTGTT 360

ATTTGTAATT KRGCGARAGA GGCAGATAAA TTTCTTAGCT TGTTAATGAT GCCTTTGATG 420

TTTATCTCTT GTGTTATGTT TCCTCTTGCT ACTATTCCCC CTCAATATCA GCATTGGGTT 480

TTTATGGAAT CCACTTGTGC ATGCTGTAGA ACTAATCCGA AGGGCATGGG ATATCTGGGT 540

TATCGTAGTC CTGATGTAAG TTGGGCGTAT CTGTCG 576

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

TTACCAAGCA GGATCTGATG CAACTGGAAG AAGGCTTTGA ATATCGTATC ATTGGCTGCT 60

CCATGTATAA CATGTTGGCC GCCGTACGCG GTGCCTATGA CAGCTTTGAA AATGTCAAAG 120

GGGTGAATTG CT 132

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GATTAGGGGT CACTCAGGAT TATAAAAAAG CGGCAGAATA CTATAAAAAA GGTGATAAAA 60

ATAATGATAT TACAGCACAA TACCGTCTGG CAAAACTTTA TGAACAAGGT AACGGTGTAA 120

AACGTGATTA TCAACAAGCG ATAAACCTTT ACCTTAAACA TATCAACAGA ATGGATCACA 180

TCACTGCCCC CAGTTTTGTG GCTCTGGGTG ATATCTATTC TCTGGGATTS GGGGTAGAGA 240

AAAACCCACA ACTGGCTGAA AAATGGTATC AAAAAGCGAT AGATGCAGCT AATACACAAC 300

ATAACCAGGA AATAAATCAT TAAACGACAA CACTTAATAC CATATTGTGA AGATGTTCAG 360

ACATGGCGGA ATTCCCCTAT TCTTTGTTGG CGCTTACAAC AGACTATATT CCGCCATATC 420

TGTCTTTATT GTGTATAAAC CATCGATACT GATGTTTGAT AGTGCTAAAT AATCATTGGC 480

GCAATCACAA AGCCTAATGC CACTCCAGCA ATAATTCCCC CCAACCCAGG CAGCATAAAT 540

GG 542

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GAACCACTTA GCGGCAGCTA TCGGGAATCG CCTGCTGAAA GACGGTCAGA CAGTGATTGT 60

GGTTACCGTG GCTGATGTTA TGAGTGCCCT GCACGCCAGC TATGACGATG GGCAGTCAGG 120

CGAAAAATTT TTGCGGGAAC TGTGCGAAGT GGATCTGCTG GTTCTTGATG AAATTGGCAT 180

TCAGCGCGAG ACGAAAAACG AAGCAGGTGG TACTGCACCA GATTGTTGAT CGCCGGACAG 240

CGTCGATGCG CACGTGGGGA TRCTGACAAA CCTGAACTAT GAGGCCATGA AAACATTGCT 300

CGGCGARCGG ATTATGGATC RCATGACCAT GAACGGCGGG CGATGGGTGA ATTTTAACTG 360

GGAGACTGGC GTCCGAATGT CG 382

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGTCCCGCAC CCGGAAATGG TCAGCGAACC AATCAGCAGG GTCATCGCTA GAAATCATCC 60

TTAGCGAAAG CTAAGGATTT TTTTTATCTG AATTCTAGCC AGATCCCCGC TGATTTATGC 120

TGGTTA 126

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

NSDOCID <WO 9822575A2 I_>

ACCCCCAGCC TAGCTGGGGG TTTTCTGTGC ACAAAAAATC CCGGCATAAT GGCCGGGATT 60

TGCGAGCTTT CCCACTATTT CTTGATTCCT AAACGGAACA TATCAGTTGG GAATAAAGGT 120

TGTATTATCA CTTCATCATT ANAAATGAAT AATTTGGGCG ATAAAGCTGT TACGTCATAG 180

ATATTTTCAG CGATTAATCT TAGANTTGAC CTAAAAACTG GAATACTTGC ATCATCTGCA 240

AAGACAAACA TGTCATCG 258

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AACCAGCGGT TCGCATCATC TCATCCCACT GACTCTCCGC TTTTGACAGA TCTGCATATC 60

CTCGGGCCAA CTTATCCAGT ACTCCGTAGT TTGCCGATTT ATTCACCCGC CAGAACACCG 120

CCTCACCTGC ATCGGCAAGC CGGGGGGAAA ACTGATACCC CAGTAGCCAG AACAGACCGA 180

AAATAATATC GCTGCTACCC GCAGTGTCTG TCATGATTTC AACTGGATTC AGCCCTGTCT 240

GCTGCTCAAG AAGTCCTTCC AGTACAAAAA TCGAATCCCG TAATGTACCG GGTACCACAA 300

TGCCATGGAA CCCAGAGTAC TGATCAGATA CGAATTATAC CAGGTGATGC CTCGTCCAGA 360

ACCAAAATAT TTTCTGTTAG ATCCTGAGTT GATGGTCTT 399

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AAATAACATC AACATACATT TGACTCGCGG GGGAAACGTT TACGGAGTCT TCATACTGGC 60

ACTTTTTTAT GCTGCTGACT ACTCTTCGTC ATCGCCATCA ACATGCGCAC GAATCAGCGC 120

CATAAACGGT TTGCCAAAGC GTTCCAGCTT GCGCATCCCA ACGCCGTTAA CGCTGAGCAT 180

TTCGCTGGCG GTGATCGGCA TCTGTTCAGC CATCTCAATC AAGGTTGCGT CGTTAAACAC 240

CACGTACGGC GGGACATTAC TTTCATCGGC TATCGATTTA CGCAGTTTGC GTAATTNGGC 300

GAACAGTTTG CGATCATAGT TGNCGCCGAN CGATNTCTGC ATCGCTTTCG GTTTGAGCGC 360

CACGATACGC GGCACGGCAA TTGCAAAGAG GATTCGCCGC GCAGCACCGG GCGCGCGGCC 420

TCTGTCAGTT GTAGGGCAGA ATGCTGGGCA ATATTTTGCG TCACCAGGCC GAGGTGAATC 480

NSDOCID <WO 9822575A2 I_>

AGCTGGCGGA TCACGCTCAC CCAATGTTCA TGGCTTTTAT CACGGCCCAT GCCATAGACT 540

TTCAGTTTGT CATGACCATA GTCGCGGATA CGCTGGTTAT TAGCACCACG AATCACTTCC 600

ACCACATAAC CCATCCCAAA CCGCTGATTC ACACGACCAA TGGTGGAAAG GGCAATCTGA 660

GCATCGGTTG AACCGTCGTA CTGTTTCGGC GGATCGAGGC AGATATCGCA GTTCNCCGCA 720

CGGCTCCTGA CGCCCTTCGC CAAAA 745

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

AGAATGGCGG CTTCTTGCCC CCCTTTGCCC CGGTCCTGAC TAGCATGGCT GGAGTCCAGT 60

GTCCAGGCCA CGACCATGCT CATCATGGAA GCAGCTTTTG TAGTACANTC GCAGCTTATT 120

TTCCTGGAAC GAAATGTCTG GCATCGTGGT GCATAACATA ACCCCCAATG CCCAGCAGAT 180

GCACAGAAGG TTCTAGAATC GCCCACTGAT ATCCCATACA AAATTTACCA AAACGTGTTC 240

GTATTTCTCG TATAAATAAT GTCTCTATGG TGACGTTCTA GACTTCAAAC CCACTTTTTG 300

AATTTGATGA TGTGCTCCTA ATCTCTTCAG GAATGTAACG CCCTTGGTTT ACAGCTACCA 360

ATACACTGGA GGTATACTTA TCTGCAACTG GATGAACTAG ATGTACTTGA GCAAACATTT 420

CATAAGCTCG ACGACAGTT 439

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CTGGAAAGCG ACGTTGATGG ATTAATGCAG TCGGTAAAAC TGAACGCTGC TCAGGCAAGG 60

CAGCAACTTC CTGATGACGC GACGCTGCGC CACCAANTCA TGGAACGTTT GATCATGGAT 120

CAAMTCATCC TGCAGATGGG GCAGAAAATG GGAGTGAAAA TCTCCGATGA GCAGCTGGAT 180

CAGGCGATTG CTAACATCGC GAAACAGNAC AACATGACGC TGGATCAGAT GCGCACCGTC 240

TGGCTTACGA TGGACTGAAC TACAACACCT ATCGTAACCA GATCCGCAAA GAGATGATTA 300

TCTCTGAAGT GCGTAACAAC GAGGTGCGTC GTCGNATCAC CATCCTGCCG 350

(2) INFORMATION FOR SEQ ID NO: 134:

SDOCID <WO_ 9822575A2 I >

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCCCAAGATT GCTAACAAAT GCGCGTTGTT CATGCCGGAT GCGGCGTGAC CGCCTTATCC 60

GGCCTACGAA ACCGCAAGAA TTCAATATAT TGCAGGAGCG GTGTAGGCCT GATAAGCGTA 120

GCGAWTCAGG CAGTTTTGCG TTTGCCCGCA ACCTTAGGGG ACATTTAGCG ACCCCATTTA 180

TTTCTCACTT TTCCGCCTCA TCATCGCGCG TTAATTTCTT TCATGAATCA CGCTTTACAA 240

TATCCAGCGC GCGCANAACG GTACTGGCAG GGATCTGAAT TTTCCTCCAG CAGCACAATC 300

AAATCGACAG CCAGTTTGAC ATCGTCAAGG GGCATTTTCC CAGTGACATA ATCTCTCCAT 360

TGCTAAGCGG GTTAAAACGC GCTAACCTGT TTCGATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CTATCCTTAT GACCACCCAA CTACNTCATT TACACCCAAA CCAGCGATCT GAATAAAGAA 60

GCGATTGCCC AGTTACGACT GGGCGGAAAA TGCGCGTAAG GATGAAGTAA AGTTTCAGTT 120

GAGCCTGGCA TTTCCCTGTG GCGTGGGATT TTAGGCCCGA ACTCGGTGTT GGGTGCGTCT 180

TATACGCAAA AATCCTGGTG GCAACTGTCC AATAGCGAAG AGTCTTCACC GTTTCGTGAA 240

ACCAACTACG AACCGCAATT GTTCCTCGGT TTTGCCACCG ATTACCGTTT TGCAGGTTGG 300

ACTGCGCGAT GTGGAGATGG GGTATAACCA CGACTCTAAA CGGGCGTTCC GACCCGACCT 360

CCCGCAGCTG GAACCGCCTT TATACTCGCC TGATGGCAGA AAACGGTAAC TGGCTGGTAG 420

AAGTGAAGCC GNGGTATGTG GTGGGTAATA CTGACGATAA CCC 463

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 584 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

INSDOCID <WO_ 9822575A2 I >

TTGGTCAGCC GTACCTGAAT GGGGGCTGAT GCCCGGCTGG TTAATGGCAG GTGGTCTGAT 60

CGCCTGGTTT GTCGGTTGGC GCAAAACACG CTGATTTTTT CATCGCTCAA GGGGGGCCGT 120

GTAACGTATA ATGCGGCTTT GTTTAATCAT CATCTACCAC AGAGGAACAT GTATGGGTGG 180

TATCAGTATT TGGCAGTTAT TGATTATTGC CGTCATCGTT GTACTGCTTT TTGGCACCAA 240

AAAGCTCGGC TCCATCGGTT CCGATCTTGG TGCGTCGATC AAAGGCTTTA AAAAAGCAAT 300

GAGCGATGAT GAACCAAAGC AGGATAAAAC CAGTCAGGAT GCTGATTTTA CTGCGAAAAC 360

TATCGCCGAT AAGCAGGCGG ATACGAATCA GGAACAGGCT AAAACAGAAG ACGCGAAGCC 420

TACGNTAAAG AGCAGGTGTA ATCCGTGTTT GATATCGGTT TTAGCGNACT GCTATTGGTG 480

TTCATCATCG GCCTCGTCGT TCTGGGGGCG CAACGACTGC CTGTGGCGGT AAAAACGGTA 540

GCGGGCTGGA TTCGCGCGTT GCGTTCACTG GCGACAACGG TGCA 584

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GCAGGCAGGA GGAACTGCCC AGTGATACGG TTATTCGTGA TGGCGGAGGG CAGAGCCTTA 60

ACGGACTGGC GTTGAACACC ACGCTGGATA ACAGAGTTGA GCATTGGNTA CACGGGGGAG 120

GGAAAGCAGA CGTTACAATT ATTAACCAGG ATGTTTACCC AGACCATAAA ACATGGCGGA 180

TTGGCAACCG NAACCATCGT CAACACCGTT GCAGAAGKTG GTCCGGAGTC TGAAAATGTG 240

TCCAGCGGTC AGATGGTCGG AGGGACGGCT GAATCCACCA CCATCAACAA AAATGGCCGG 300

CAGTTATCTG GTCTTCGGGG ATGGCACGGG ACACCCTCAT TTGCGCTGGT GGTGACCAGA 360

CGGTACACGG AGAGGCACAT AACACCCGAC TGGAGGGAGG TTAACCAGTA TGTACACAAC 420

GGTGGCACGG CAACAGAGAC GCTGATAAAC CGTGATGGCT GGCAGGTGAT TAAGGAAGGA 480

GGGAACTGCC GGCGCATTAC CACCATCAAN CCNGAAAAGG GAAANCT 527

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GTCAGTCTCT GGGGGAAGTG CGTGTTCCGA CCGGGGAAAT GTGGTGGAGA AAGTTATTGA 60

AGGGGCTTAC GAGGTGGTGG GGGTTTTTGA CCGGATTGAG GAAAAGCGTG ATGCCATGCA 120

GTCGCTGATT CTGCCGCCAC CGGACGCCAG GCGCTGGCAC AGGCGGCACT GACTTACCGT 180

TATGGTGACG AACMTCARCC CGTCACCACC GCCGACATTC TGACACCACG ACGCCGGGAR 240

GATTACGGTA AGGACCTGTG GAGTGCTTAT CAGACCATTC AGGAGAATAT GCTGAAAGGC 300

GGAATTTCCG GTCGCAGTGC CAGAGGAAAA CGTATCCATA CCCGTGCCAT TCACAGCATC 360

GACACCGACA TTAAGCTCAA CCGCGCATTG TGGGTGATGG CTGAAACGCT GCTGGAGAGT 420

ATGCGCTGAT GCCGTTTCCN T 441

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CGAGCGAGAT GAACTTCGAG GGCGGTGTGA GCCAGTCGGC TTACGAGACA CTGGCGGCGC 60

TTAATCTGCC GAAACCGCAG CAAGGGCCGG AAACCATTAA TCAGGTTACC GAGCATAAGA 120

TGTCAGCTGA GTAAGCCTGT ATGCCGGATA AGGCGCTCGC GCCNATTCCG ATGAAATAAG 180

GCGCATCGGG CCTGAAGGAA AGCCGTATGN ATACACCCGC AGCCCGCATC CGGCAAGTTA 240

CAACAAATAA CCTTTAACCA TGCTTTTTGA TGTTTTTCAG CAATACCCCG CGGCGATGCC 300

CATACTGGCA ACCGTCGGGA GGGATTGATC ATCGGCAGTT TTTTGAATGT GGTGATTTGG 360

GCGTTACCCC ATCATGCTGC GCCAACAAAT GGCGGAGT 398

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

GCCGAACAGA CACAGCAATA TGAACCCTGC CAGCGCAGAC GCTTGCTGAT TAATGCTCTG 60

AACAAAAGGC GAAGAATGGC AAATCCTGCG ATCAGCAAAG TCAGCGCACC GACTATCTGT 120

AACATAGTCA CTCCGTGATG AATATCATGT GTATTGTGAA TGCCAGTGAA TGTGGCACTG 180

AAGCGTTTGC ACCTGTCCGG GTCCCGGTCA TGATGACCGS AACAGAGAGA CAATGCCGAA 240

TTATCAGAAG GTCACATTCA GTGTGGCTTG GCCGTTATAA CCTTCAGCGC TGCTGCCGCT 300

GACGCTGTGG GCATAACCGG CCTGAACGCC CAGGGTGATA TTTTCCCGGA CACGGGCTTC 360

3NSDOCID: <WO___9822575A2_I_>

CAGTCCGGCC TGCAGCTCCA GTGACGTGCC ATTCCGGGAC GGTGAGAACG TCATGTTACT 420

GCCGGCTGCG GCTGTACCCA TGCTCATGTC TCCCCGGGAG CTGAAGGTGC GGATAACAGA 480

AGGCTGTACC CACCCGTTCA CCGGCAGTTC ACGCACACTG TGTTTTGCAC TGTCACGCAA 540

GGTGTCACGG GATGAGGTGC CTTCANCAAA AGGTCATATT 580

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGCGGACATC CAGCGTTCCG CCATCATCCA CACGGGTTCT GGTGGCTGTG TGTCCGGTCA 60

GCACATCCAG ACGGCCGCCA TTTTCCAGTA CGACATTATC AGCTTTACCC TCCACAACAG 120

AGAATGCTCC CAGGCGGTTT GTGCCGGTGA CGGTTGCAGC AGTGCTGGTA ACCAGTGCTC 180

CGCCCGTGTT CTGGGTGACA TCAGACGCTT TACCGCCGGC ATTCACCTGC AGCTTTCCTT 240

TCTGGTTGAT GGTGGTATGC GCGGCAGTTC CTCCTTCCTT AATCAMCTGC CAGCCATCAC 300

GGTTTATCAG CGTCTCTGTT GCCGTGCCAA CGTTGTGTAC ATACTGGTTA MCTCCCTCCA 360

GTCGGGTGTT AWGTGSCTCT CCGTGTANCG TCTGGTCANC AACAACGCAA ATGANGGTGT 420

CCCGTGCCAT CCCCGAAGAC CAGTAA 446

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGAATACGTT AAGTCAGCAG ACCGGCGGAG ACAGTCTGAC ACAGACAGCG CTGCAGCAGT 60

ATGAGCCGGT GGTGGTTGGC TCTCCGCAAT GGCACGATGA ACTGGCAGGT GCCCTGAATA 120

ATATTGCCGG AGTTCGCCAC TGACCGGTCA GACCGGTATC AGTGATGACT GGCCACTGCC 180

TTCCGTCAAC AATGGATACC TGGTTCCGTC CACGGACCCG GACAGTCCGT ATCTGATTAC 240

GGTGAACCCG AAACTGGATR GTCTCGGACA GGTGGACAGC CATTTGTTTN CCGGACTGTA 300

TGAGCTTCTT GGAGCGAAAC CGGGTCA 327

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 8

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet [X]

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	97726

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet [ ]

DNA plasmid PAI-1

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
[ ] This sheet was received with the international application	[ ] This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

Form PCT/RO/134 (July 1992)

NSDOCID <WO_9822575A2_I_>

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 8

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet [X]

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	97727

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet [ ]

DNA plasmid PAI-2

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only

[ ] This sheet was received with the international application

Authorized officer

For International Bureau use only

[ ] This sheet was received by the International Bureau on:

Authorized officer

Form PCT/RO/134 (July 1992)

\SDOCID <WO _ 9822575A2 I >

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 14.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	98176

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

Escherichia coli, 596

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

Form PCT/RO/134 (July 1992)

3NSDOCID <WO 9822575A2 I >

What Is Claimed Is:

1. An isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a nucleotide sequence of an open reading frame depicted in one of Tables 1 through 4;

(b) a nucleotide sequence beginning with the first initiation codon encountered reading 5' to 3' in an open reading frame depicted in one of Tables 1 through 4, and ending with the 3' terminal stop codon;

(c) a nucleotide sequence beginning with the first initiation codon encounter reading 5' to 3' in an open reading frame depicted in one of Tables 1 through 4, and ending with the nucleotide preceeding the 3' terminal stop codon;

(d) a nucleotide sequence of (a) excluding codons for amino acids eliminated during processing of the putative protein identified in one of Tables 1 through 4; or

(e) a nucleotide sequence that is complementary to any of the nucleotide sequences in (a), (b), (c), or (d).

2. An isolated nucleic acid molecule of claim 1, wherein said nucleotide sequence is 100% identical to the nucleotide sequence of an open reading frame depicted in Tables 1 through 4, or a complement thereof.

3. An isolated nucleic acid molecule, comprising a polynucleotide that hybridizes under stringent hybridization conditions to a nucleic acid molecule of claim 2.

4. An isolated nucleic acid molecule, comprising a polynucleotide that encodes the amino acid sequence of an epitope-bearing portion of an *E. coli* J96 PAI protein encoded by an open reading frame depicted in one of Tables 1 through 4.

SDOCID <WO__9822575A2 I_>

5. A method of making a recombinant vector, comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.

6. A recombinant vector produced by the method of claim 5.

7. A method of making a recombinant host cell, comprising introducing a recombinant vector of claim 6 into a host cell.

8. A recombinant host cell produced by the method of claim 7.

9. A recombinant method for producing an *E. coli* J96 PAI polypeptide, comprising culturing a recombinant host cell of claim 8 under conditions such that said polypeptide is expressed and recovering said polypeptide.

10. An isolated polypeptide of an *E. coli* J96 PAI IV or PAI V protein encoded by a polynucleotide of claim 1.

11. An isolated polypeptide of an *E. coli* J96 PAI IV or PAI V protein encoded by a polynucleotide of claim 2.

12. An isolated polypeptide comprising an immunogenic epitope of an *E. coli* J96 PAI IV or PAI V protein encoded for by an open reading frame depicted in one of Tables 1, 2, 3 or 4.

13. A vaccine, in dosage form, comprising

(a) a pharmaceutically acceptable diluent, carrier, or excipient, and

(b) an antigen selected from the group consisting of:

(i) a polypeptide having an amino acid sequence at least 95% identical to an amino acid sequence encoded by a uropathogenic *E. coli* J96 PAI IV or PAI V open reading frame depicted in Tables 1, 2, 3 or 4, and

(ii) a polypeptide comprising an immunogenic epitope of an *E. coli* J96 PAI IV or PAI V protein encoded for by an open reading frame depicted in one of Tables 1, 2, 3 or 4;

NSDOCID: <WO 9822575A2 I >

wherein said antigen is present in an amount effective to elicit protective immune responses in an animal to pathogenic *E. coli*.

14. An isolated antibody that binds specifically to a polypeptide of claim 10 or 11.

15. An antibody having binding affinity to a polypeptide according to claim 12.

16. A method of detecting a pathogenic *E. coli* antigen in a sample, comprising:

(a) contacting said sample with an antibody according to claim 14 or 15 under conditions such that immunocomplexes form, and

(b) detecting the presence of said antibody bound to said antigen.

17. A diagnostic kit comprising:

(a) a first container means containing an antibody according to claim 14 or 15 and

(b) second container means containing a conjugate comprising a binding partner of said antibody and a label.

18. A hybridoma which produces an antibody according to claim 14 or 15.

19. A method of detecting the presence of antibodies to pathogenic *E. coli* in a sample, comprising:

(a) contacting said sample with a polypeptide according to one of claims 10, 11 or 12 under conditions such that immunocomplexes form, and

(b) detecting the presence of said antibody bound to said antigen.

20. A kit for detecting the presence of antibodies to pathogenic *E. coli* in a sample comprising at least one container means having disposed therein a polypeptide according to one of claims 10, 11 or 12.

\SDOCID <WO 9822575A2 I_>

21. Computer readable medium having recorded thereon one or more nucleotide sequences depicted in SEQ ID NOs: 1 through 142, or nucleotide sequences at least 99.9% identical thereto.

22. Computer readable medium having recorded thereon a nucleotide sequence of at least one uropathogenic *E. coli* J96 pathogenicity island open reading frame depicted in Tables 1 through 4, or a complement thereof.

23. The computer readable medium of claim 21, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

24. The computer readable medium of claim 22, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

25. A computer-based system for identifying fragments of uropathogenic *E. coli* J96 pathogenicity islands PAI IV and PAI V that are homologous to target nucleotide sequences, comprising:

a) a data storage means comprising a nucleotide sequence of SEQ ID NOs: 1 through 142, or a nucleotide sequence at least 99.9% identical thereto;

b) a search means for comparing a target sequence to said nucleotide sequence of said data storage means of step (a) to identify a homologous sequence, and

c) a retrieval means for obtaining said homologous sequence of step (b).

3NSDOCID <WO 9822575A2 1 >

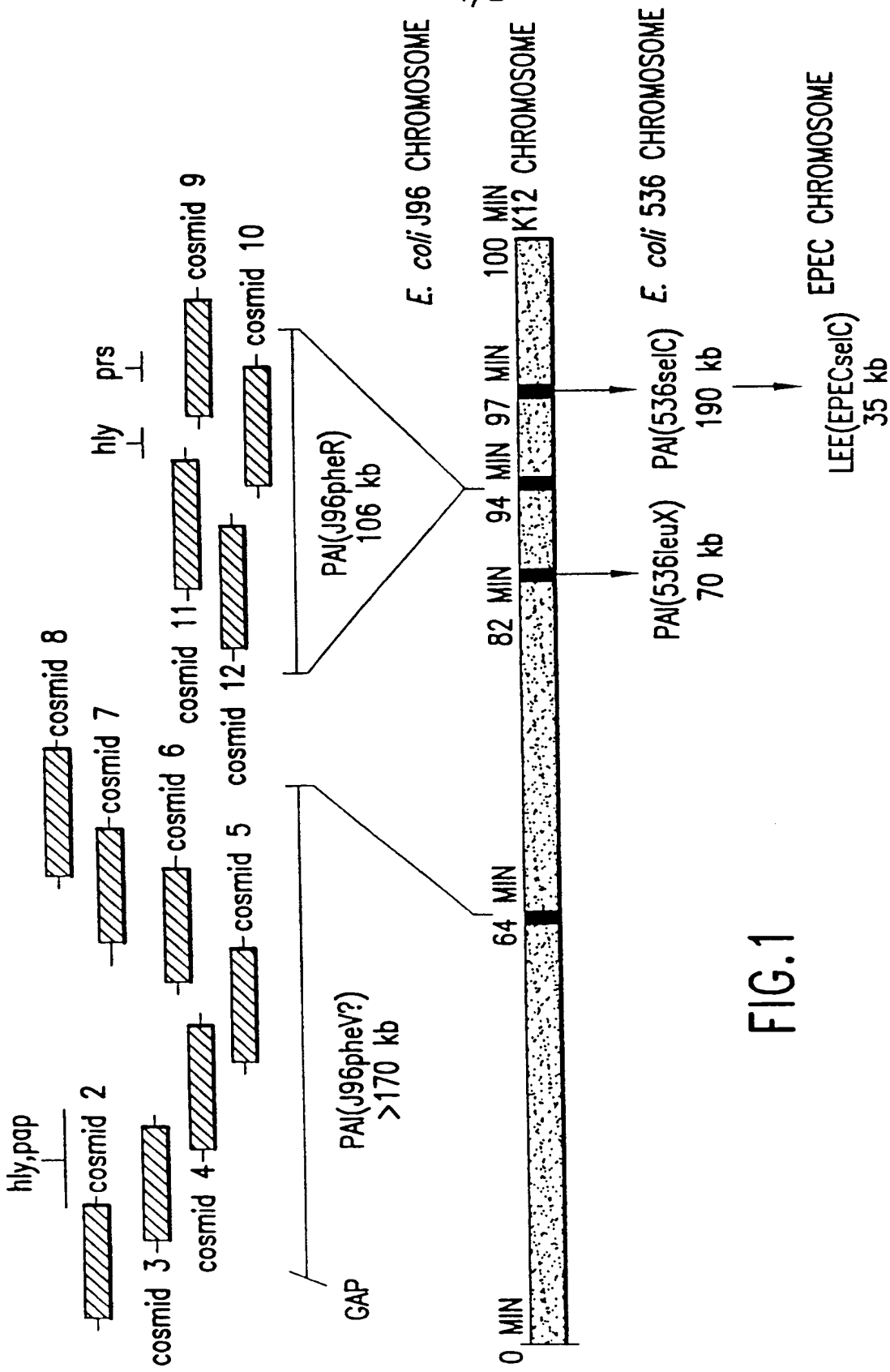


FIG.1

ISDOCID <WO 9822575A2 I >

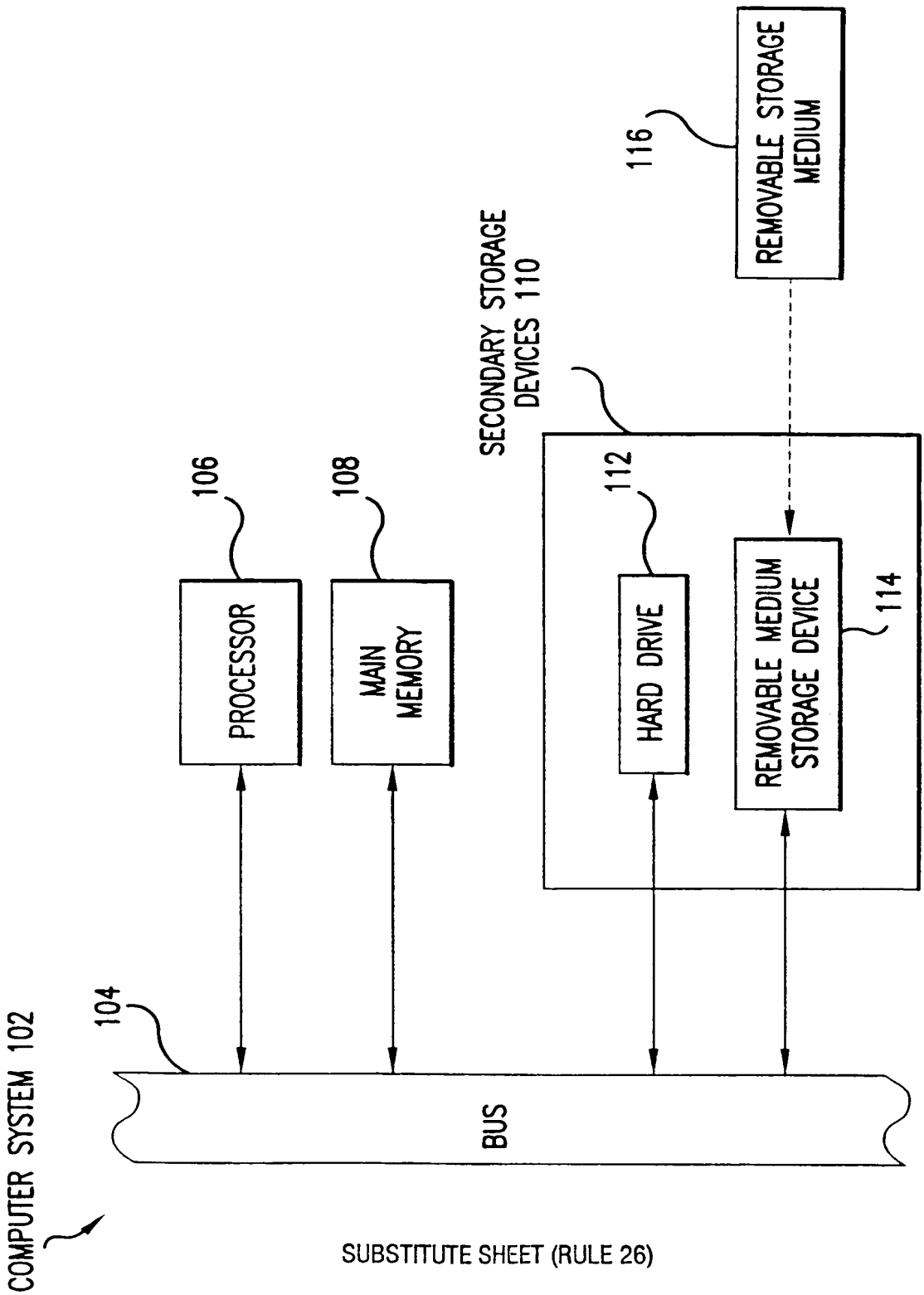


FIG.2

3NSDOCID: <WO_ 9822575A2 I_>

Applicant's or agent's file reference number 1488.074PC02	International application No. PCT/US97/21347

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page ___5___, line ____8_____.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	97726

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA plasmid PAI-1

The applicants hereby request that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents .

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the international Bureau later *(specify the general nature of the indications, e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

ISDOCID <WO_ 9822575A2 I >

Applicant's or agent's file reference number 1488.074PC02	International application No. PCT/US97/21347

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page ___5___, line ____8_____.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	97727

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA plasmid PAI-2

The applicants hereby request that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents .

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the international Bureau later *(specify the general nature of the indications, e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

3NSDOCID <WO_ 9822575A2 I_>

Applicant's or agent's file reference number 1488.074PC02	International application No. PCT/US97/21347

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page ___5___, line ____14_____.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	98176

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

Escherichia coli, 596

The applicants hereby request that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents .

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the international Bureau later *(specify the general nature of the indications, e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

NSDOCID <WO . 9822575A2 I >

CORRECTED VERSION*

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 15/31, 5/16, C07K 14/245, 16/12, A61K 39/108, G01N 33/68, G06F 17/30

A2

(11) International Publication Number: WO 98/22575

(43) International Publication Date: 28 May 1998 (28.05.98)

(21) International Application Number: PCT/US97/21347

(22) International Filing Date: 21 November 1997 (21.11.97)

(30) Priority Data:

60/031,626	22 November 1996 (22.11.96)	US
60/061,953	14 October 1997 (14.10.97)	US

(71) Applicants *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). UNIVERSITY OF WISCONSIN [US/US]; 1300 University Avenue, Madison, WI 53706 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: DILLON, Patrick, J. [US/US]; 7508 Boxberry Terrace, Gaithersburg, MD 20879 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). WELCH, Rodney, A. [US/US]; 410 Ridge Street, Madison, WI 53705 (US).

(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005-3934 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

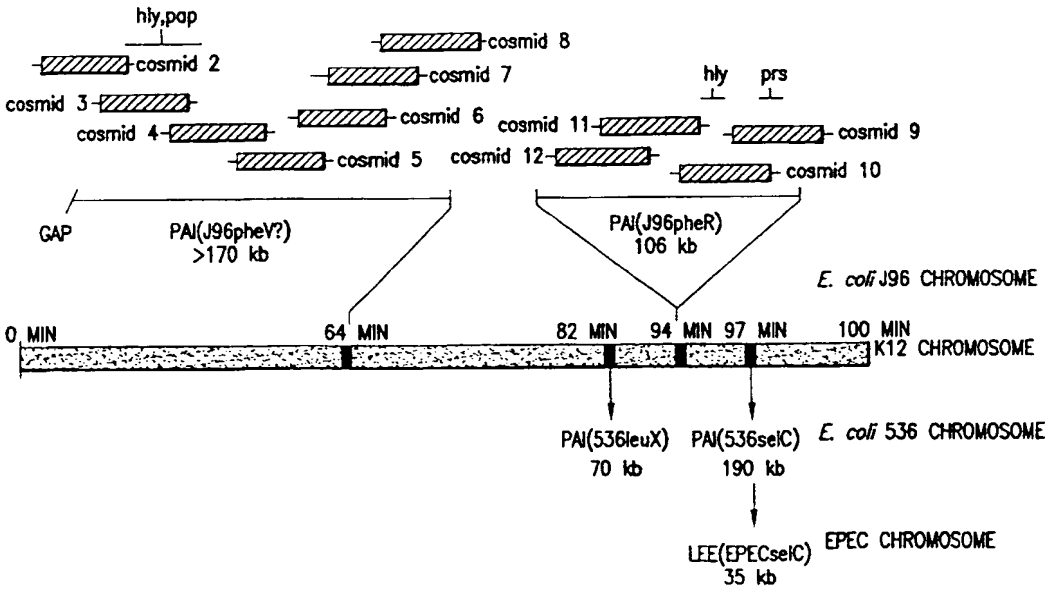
Published

Without international search report and to be republished upon receipt of that report.

With an indication in relation to a deposited microorganism furnished under Rule 13bis separately from the description.

Date of receipt by the International Bureau:
20 March 1998 (20.03.1998)

(54) Title: NUCLEOTIDE SEQUENCE OF *ESCHERICHIA COLI* PATHOGENICITY ISLANDS



(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.

*(Referred to in PCT Gazette No. 44/1998, Section II)

ISDOCID: <WO_ 9822575A2_IA>

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	**ES**	Spain	**LS**	Lesotho	**SI**	Slovenia
AM	Armenia	**FI**	Finland	**LT**	Lithuania	**SK**	Slovakia
AT	Austria	**FR**	France	**LU**	Luxembourg	**SN**	Senegal
AU	Australia	**GA**	Gabon	**LV**	Latvia	**SZ**	Swaziland
AZ	Azerbaijan	**GB**	United Kingdom	**MC**	Monaco	**TD**	Chad
BA	Bosnia and Herzegovina	**GE**	Georgia	**MD**	Republic of Moldova	**TG**	Togo
BB	Barbados	**GH**	Ghana	**MG**	Madagascar	**TJ**	Tajikistan
BE	Belgium	**GN**	Guinea	**MK**	The former Yugoslav Republic of Macedonia	**TM**	Turkmenistan
BF	Burkina Faso	**GR**	Greece			**TR**	Turkey
BG	Bulgaria	**HU**	Hungary	**ML**	Mali	**TT**	Trinidad and Tobago
BJ	Benin	**IE**	Ireland	**MN**	Mongolia	**UA**	Ukraine
BR	Brazil	**IL**	Israel	**MR**	Mauritania	**UG**	Uganda
BY	Belarus	**IS**	Iceland	**MW**	Malawi	**US**	United States of America
CA	Canada	**IT**	Italy	**MX**	Mexico	**UZ**	Uzbekistan
CF	Central African Republic	**JP**	Japan	**NE**	Niger	**VN**	Viet Nam
CG	Congo	**KE**	Kenya	**NL**	Netherlands	**YU**	Yugoslavia
CH	Switzerland	**KG**	Kyrgyzstan	**NO**	Norway	**ZW**	Zimbabwe
CI	Côte d'Ivoire	**KP**	Democratic People's Republic of Korea	**NZ**	New Zealand		
CM	Cameroon			**PL**	Poland		
CN	China	**KR**	Republic of Korea	**PT**	Portugal		
CU	Cuba	**KZ**	Kazakstan	**RO**	Romania		
CZ	Czech Republic	**LC**	Saint Lucia	**RU**	Russian Federation		
DE	Germany	**LI**	Liechtenstein	**SD**	Sudan		
DK	Denmark	**LK**	Sri Lanka	**SE**	Sweden		
EE	Estonia	**LR**	Liberia	**SG**	Singapore		

3NSDOCID <WO 9822575A2 IA>

CORRECTED VERSION*

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/11, 15/63, C07K 16/12, G01N 33/569, G06F 17/30, G11B 7/00

A3

(11) International Publication Number: WO 98/22575

(43) International Publication Date: 28 May 1998 (28.05.98)

(21) International Application Number: PCT/US97/21347

(22) International Filing Date: 21 November 1997 (21.11.97)

(30) Priority Data:

60/031,626	22 November 1996 (22.11.96)	US
60/061,953	14 October 1997 (14.10.97)	US

(71) Applicants *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). UNIVERSITY OF WISCONSIN [US/US]; 1300 University Avenue, Madison, WI 53706 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: DILLON, Patrick, J. [US/US]; 7508 Boxberry Terrace, Gaithersburg, MD 20879 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). WELCH, Rodney, A. [US/US]; 410 Ridge Street, Madison, WI 53705 (US).

(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005-3934 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

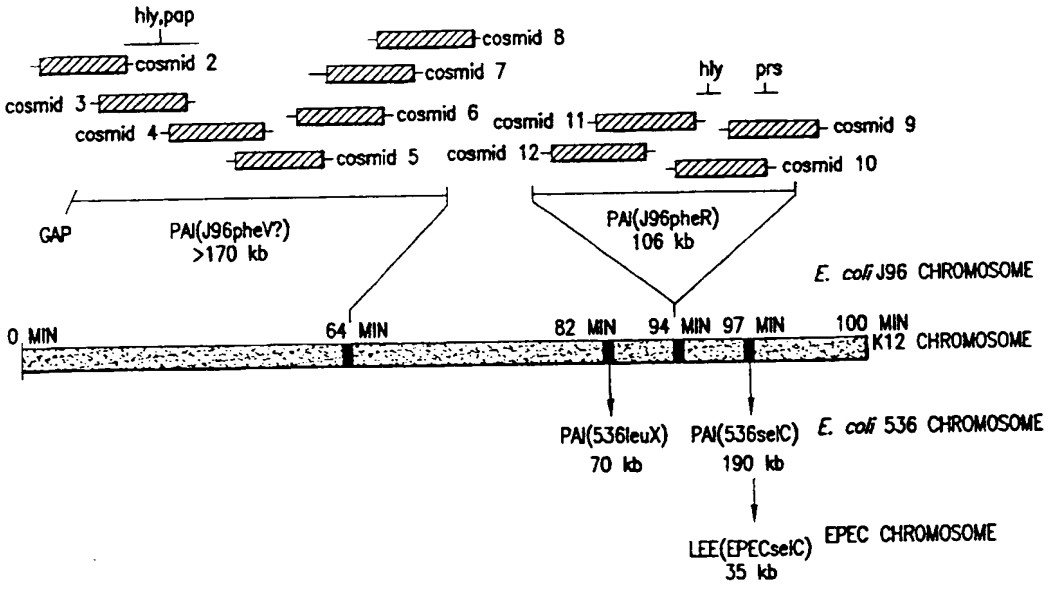
With international search report.

With an indication in relation to a deposited microorganism furnished under Rule 13[bis] separately from the description.

Date of receipt by the International Bureau:
20 March 1998 (20.03.98)

(88) Date of publication of the international search report:
10 December 1998 (10.12.98)

(54) Title: NUCLEOTIDE SEQUENCE OF *ESCHERICHIA COLI* PATHOGENICITY ISLANDS



(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.

*(Referred to in PCT Gazette No. 44/1998, Section II)

INSDOCID <WO 9822575A3 I >

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	**ES**	Spain	**LS**	Lesotho	**SI**	Slovenia
AM	Armenia	**FI**	Finland	**LT**	Lithuania	**SK**	Slovakia
AT	Austria	**FR**	France	**LU**	Luxembourg	**SN**	Senegal
AU	Australia	**GA**	Gabon	**LV**	Latvia	**SZ**	Swaziland
AZ	Azerbaijan	**GB**	United Kingdom	**MC**	Monaco	**TD**	Chad
BA	Bosnia and Herzegovina	**GE**	Georgia	**MD**	Republic of Moldova	**TG**	Togo
BB	Barbados	**GH**	Ghana	**MG**	Madagascar	**TJ**	Tajikistan
BE	Belgium	**GN**	Guinea	**MK**	The former Yugoslav Republic of Macedonia	**TM**	Turkmenistan
BF	Burkina Faso	**GR**	Greece			**TR**	Turkey
BG	Bulgaria	**HU**	Hungary	**ML**	Mali	**TT**	Trinidad and Tobago
BJ	Benin	**IE**	Ireland	**MN**	Mongolia	**UA**	Ukraine
BR	Brazil	**IL**	Israel	**MR**	Mauritania	**UG**	Uganda
BY	Belarus	**IS**	Iceland	**MW**	Malawi	**US**	United States of America
CA	Canada	**IT**	Italy	**MX**	Mexico	**UZ**	Uzbekistan
CF	Central African Republic	**JP**	Japan	**NE**	Niger	**VN**	Viet Nam
CG	Congo	**KE**	Kenya	**NL**	Netherlands	**YU**	Yugoslavia
CH	Switzerland	**KG**	Kyrgyzstan	**NO**	Norway	**ZW**	Zimbabwe
CI	Côte d'Ivoire	**KP**	Democratic People's Republic of Korea	**NZ**	New Zealand		
CM	Cameroon			**PL**	Poland		
CN	China	**KR**	Republic of Korea	**PT**	Portugal		
CU	Cuba	**KZ**	Kazakstan	**RO**	Romania		
CZ	Czech Republic	**LC**	Saint Lucia	**RU**	Russian Federation		
DE	Germany	**LI**	Liechtenstein	**SD**	Sudan		
DK	Denmark	**LK**	Sri Lanka	**SE**	Sweden		
EE	Estonia	**LR**	Liberia	**SG**	Singapore		

NSDOCID <WO__ 9822575A3 I >

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/21347

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/11 C12N15/63 C07K16/12 G01N33/569 G06F17/30
G11B7/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SWENSON D.L.: "Two pathogenicity islands in Escherichia coli J96: cosmid cloning and sample sequencing" INFECTION AND IMMUNITY, vol. 64, no. 9, September 1996, pages 3736-3743, XP002069149 WASHINGTON US cited in the application see the whole document ---	1-12, 14-17
X	Database EMBL, Heidelberg, DE AC: u59875 12-NOV-1996 Yersinia pestis pesticin plasmid putative insertion sequence IS100 XP002069557 & MCDONOUGH K.A. ET AL.: J.BACTERIOL., vol. 179, 1997, pages 2081-2085, --- -/--	1-12

[X] Further documents are listed in the continuation of box C. [ ] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
29 June 1998	08. 10. 98

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Panzica, G

3

Form PCT/ISA/210 (second sheet) (July 1992)

NSDOCID <WO 9822575A3 I >

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/21347

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EMBL, Heidelberg, DE AC z32853 05-MAY-1994 Yersinia pestis insertion sequence IS100 XP002069152 see abstract & PODLACHIKOVA O. ET AL.: FEMS MICROBIOL. LETT., vol. 121, 1994, pages 269-274, ---	1-12
A	BURLAND V. ET AL.: "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes" NUCLEIC ACID RESEARCH, vol. 23, 1995, pages 2105-2119, XP000612159 OXFORD, GB -----	

3

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

3NSDOCID <WO 9822575A3 I >

INTERNATIONAL SEARCH REPORT

Inter ·ional application No.
PCT/US 97/21347

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

NSDOCID <WO 9822575A3 I >

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ US 97/21347

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-20 (partially)

   Invention 1.

   An isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence consisting of the sequence of the ORF ID 2 (Contig Id.No.65 Start: nt1902 Stop: nt1042) and uses thereof.

2. Claims: 1-20 (partially)

   Inventions 2 to 175:

   same as invention 1, but according to each single ORF ID as set forth in Tables 1 through 4, starting from the second of the list (2: Contig ID 65, ORF ID 3, start: nt2096 stop: nt1821; 3: Contig ID 63, ORF ID 11, start: nt7856 stop: nt9238; ... 175: Contig ID 24, ORF ID 1, start: nt492, stop: nt4)

3. Claims: 21-24

   Invention 176.

   A computer readable medium having recorded thereon nucleotide sequences depicted in SEQ.ID.NOs.1 through 142 or sequences at least 99.9% identical thereto, or a complementary thereof.
   Said computer readable medium selected from floppy disc, hard disc, RAM, ROM, CD-ROM.

4. Claim : 25

   Invention 177.

   A computer-based system for identifying fragments of uropathogenic E.coli J96 pathogenicity islands PAI IV and PAI V that are homlogous to target nucleotide sequences, comprising:

   a) A data storage means comprising nucleotide sequences out of SEQ.ID.NOs:1 through 142 or a nucleotide sequence at least 99.9% identical thereto,

   b) A search means for comparing a target sequence to said nucleotide sequence of said data storage means of step a) to identify a homologous sequence,

   c) A retrieval means for obtaining said homologous sequence of step b).

INSDOCID <WO 9822575A3 I >

CORRECTED VERSION*

CORRECTED VERSION**

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 15/11, 15/63, C07K 16/12, G01N 33/569, G06F 17/30, G11B 7/00

A3

(11) International Publication Number: **WO 98/22575**

(43) International Publication Date: 28 May 1998 (28.05.98)

(21) International Application Number: PCT/US97/21347

(22) International Filing Date: 21 November 1997 (21.11.97)

(30) Priority Data:

60/031,626	22 November 1996 (22.11.96)	US
60/061,953	14 October 1997 (14.10.97)	US

(71) Applicants *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). UNIVERSITY OF WISCONSIN [US/US]; 1300 University Avenue, Madison, WI 53706 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: DILLON, Patrick, J. [US/US]; 7508 Boxberry Terrace, Gaithersburg, MD 20879 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). WELCH, Rodney, A. [US/US]; 410 Ridge Street, Madison, WI 53705 (US).

(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005–3934 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

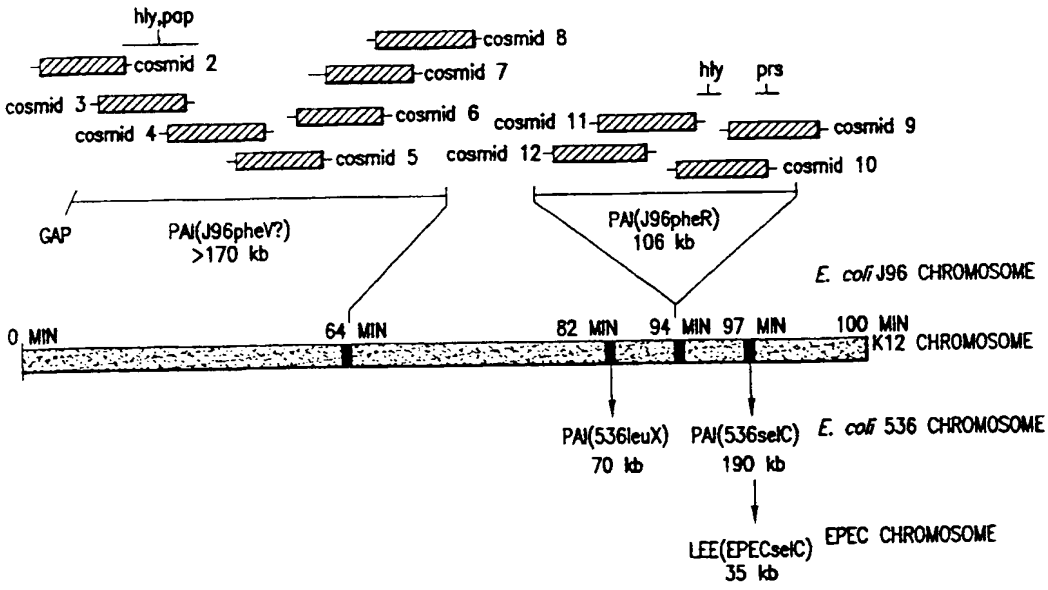
With international search report.

With an indication in relation to a deposited microorganism furnished under Rule 13bis separately from the description.

Date of receipt by the International Bureau:
20 March 1998 (20.03.98)

(88) Date of publication of the international search report:
10 December 1998 (10.12.98)

(54) Title: NUCLEOTIDE SEQUENCE OF *ESCHERICHIA COLI* PATHOGENICITY ISLANDS



(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein–coding open reading frames within the sequenced fragments.

*(Referred to in PCT Gazette No. 44/1998, Section II) **(Referred to in PCT Gazette No 1/1999, Section II)

NSDOCID <WO 9822575A3 IA>

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	**ES**	Spain	**LS**	Lesotho	**SI**	Slovenia
AM	Armenia	**FI**	Finland	**LT**	Lithuania	**SK**	Slovakia
AT	Austria	**FR**	France	**LU**	Luxembourg	**SN**	Senegal
AU	Australia	**GA**	Gabon	**LV**	Latvia	**SZ**	Swaziland
AZ	Azerbaijan	**GB**	United Kingdom	**MC**	Monaco	**TD**	Chad
BA	Bosnia and Herzegovina	**GE**	Georgia	**MD**	Republic of Moldova	**TG**	Togo
BB	Barbados	**GH**	Ghana	**MG**	Madagascar	**TJ**	Tajikistan
BE	Belgium	**GN**	Guinea	**MK**	The former Yugoslav Republic of Macedonia	**TM**	Turkmenistan
BF	Burkina Faso	**GR**	Greece			**TR**	Turkey
BG	Bulgaria	**HU**	Hungary	**ML**	Mali	**TT**	Trinidad and Tobago
BJ	Benin	**IE**	Ireland	**MN**	Mongolia	**UA**	Ukraine
BR	Brazil	**IL**	Israel	**MR**	Mauritania	**UG**	Uganda
BY	Belarus	**IS**	Iceland	**MW**	Malawi	**US**	United States of America
CA	Canada	**IT**	Italy	**MX**	Mexico	**UZ**	Uzbekistan
CF	Central African Republic	**JP**	Japan	**NE**	Niger	**VN**	Viet Nam
CG	Congo	**KE**	Kenya	**NL**	Netherlands	**YU**	Yugoslavia
CH	Switzerland	**KG**	Kyrgyzstan	**NO**	Norway	**ZW**	Zimbabwe
CI	Côte d'Ivoire	**KP**	Democratic People's Republic of Korea	**NZ**	New Zealand		
CM	Cameroon			**PL**	Poland		
CN	China	**KR**	Republic of Korea	**PT**	Portugal		
CU	Cuba	**KZ**	Kazakstan	**RO**	Romania		
CZ	Czech Republic	**LC**	Saint Lucia	**RU**	Russian Federation		
DE	Germany	**LI**	Liechtenstein	**SD**	Sudan		
DK	Denmark	**LK**	Sri Lanka	**SE**	Sweden		
EE	Estonia	**LR**	Liberia	**SG**	Singapore		

INSDOCID <WO__9822575A3 IA>

Nucleotide Sequence of *Escherichia coli* Pathogenicity Islands

Background of the Invention

Field of the Invention

The present invention relates to novel genes located in two chromosomal regions within *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs).

Related Background Art

Escherichia coli (*E. coli*) is a normal inhabitant of the intestine of humans and various animals. Pathogenic *E. coli* strains are able to cause infections of the intestine (intestinal *E. coli* strains) and of other organs such as the urinary tract (uropathogenic *E. coli*) or the brain (extraintestinal *E. coli*). Intestinal pathogenic *E. coli* are a well established and leading cause of severe infantile diarrhea in the developing world. Additionally, cases of newborn meningitis and sepsis have been attributed to *E. coli* pathogens.

In contrast to non-pathogenic isolates, pathogenic *E. coli* produce pathogenicity factors which contribute to the ability of strains to cause infectious diseases (Mühldorfer, I. and Hacker, J., *Microb. Pathogen.* 16:171-181 1994). Adhesions facilitate binding of pathogenic bacteria to host tissues. Pathogenic *E. coli* strains also express toxins including haemolysins, which are involved in the destruction of host cells, and surface structures such as O-antigens, capsules or membrane proteins, which protect the bacteria from the action of phagocytes or the complement system (Ritter, *et al.*, *Mol. Microbiol.* 17:109-212 1995).

The genes coding for pathogenicity factors of intestinal *E. coli* are located on large plasmids, phage genomes or on the chromosome. In contrast to intestinal *E. coli*, pathogenicity determinants of uropathogenic and other extraintestinal *E. coli* are, in most cases, located on the chromosome. *Id.*

NSDOCID <WO 9822575A3 IA>

Large chromosomal regions in pathogenic bacteria that encode adjacently located virulence genes have been termed *pathogenicity islands* ("PAIs"). PAIs are indicative of large fragments of DNA which comprise a group of virulence genes behaving as a distinct molecular and functional unit much like an island within the bacterial chromosome. For example, intact PAIs appear to transfer between organisms and confer complex virulence properties to the recipient bacteria.

Chromosomal PAIs in bacterial cells have been described in increasing detail over recent years. For example, J. Hacker and co-workers described two large, unstable regions in the chromosome of uropathogenic *Escherichia coli* strain 536 as PAI-I and PAI-II (Hacker J., *et al.*, *Microbiol. Pathog.* 8:213-25 1990). Hacker found that PAI-I and PAI-II containing virulence regions can be lost by spontaneous deletion due to recombination events. Both of these PAIs were found to encode multiple virulence genes, and their loss resulted in reduced hemolytic activity, serum resistance, mannose-resistant hemagglutination, uroepithelial cell binding, and mouse virulence of the *E. coli.* (Knapp, S *et al.*, *J. Bacteriol.* 168:22-30 1986). Therefore, pathogenicity islands are characterized by their ability to confer complex virulence phenotypes to bacterial cells.

In addition to *E. coli,* specific deletion of large virulence regions has been observed in other bacteria such as *Yersinia pestis*. For example, Fetherston and co-workers found that a 102-kb region of the *Y. pestis* chromosome lost by spontaneous deletion resulted in the loss of many *Y. pestis* virulence phenotypes. (Fetherston, J.D. and Perry, R.D., *Mol. Microbiol.* 13:697-708 1994, Fetherston, *et al.*, *Mol. Microbiol.* 6:2693-704 1992). In this instance, the deletion appeared to be due to recombination within 2.2-kb repetitive elements at both ends of the 102-kb region.

It is possible that deletion of PAIs may benefit the organism by modulating bacterial virulence or genome size during infection. PAIs may also represent foreign DNA segments that were acquired during bacterial evolution that conferred important pathogenic properties to the bacteria. Observed flanking

INSDOCID <WO_ 9822575A3 IA>

repeats, as observed in *Y. pestis* for example, may suggest a common mechanism by which these virulence genes were integrated into the bacterial chromosomes.

Integration of the virulence genes into bacterial chromosomes was further elucidated by the discovery and characterization of a locus of enterocyte effacement (the LEE locus) in enteropathogenic *E. coli* (McDaniel, *et al.*, *Proc. Natl Acad. Sci.* (USA) 92:1664-8 1995). The LEE locus comprises 35-kb and encodes many genes required for these bacteria to "invade" and degrade the apical structure of enerocytes causing diarrhea. Although the LEE and PAI-I loci encode different virulence genes, these elements are located at the exact same site in the *E. coli* genome and contain the same DNA sequence within their right-hand ends, thus suggesting a common mechanism for their insertion.

Besides being found in enteropathogenic *E. coli*, the LEE element is also present in rabbit diarrheal *E. coli*, *Hafnia alvei*, and *Citrobacter freundii* biotype 4280, all of which induce attaching and effacing lesions on the apical face of enterocytes. The LEE locus appears to be inserted in the bacterial chromosome as a discrete molecular and functional virulence unit in the same fashion as PAI-I, PAI-II, and *Yersinia* PAI.

Along these same lines, a 40-kb *Salmonella typhimurium* PAI was characterized on the bacterial chromosome which encodes genes required for *Salmonella* entry into nonphagocytic epithelial cells of the intestine (Mills, D.M., *et al.*, *Mol. Microbiol.* 15:749-59 1995). Like the LEE element, this PAI confers to *Salmonella* the ability to invade intestinal cells, and hence may likewise be characterized as an "invasion" PAI.

The pathogenicity islands described above all possess the common feature of conferring complex virulence properties to the recipient bacteria. However, they may be separated into two types by their respective contributions to virulence. PAI-I, PAI-II, and the *Y. pestis* PAI confer multiple virulence phenotypes, while the LEE and the *S. typhimurium* "invasion" PAI encode many genes specifying a single, complex virulence process.

It is advantageous to characterize closely-related bacteria that contain or do not contain the PAI by the isolation of a discrete molecular and functional unit

SDOCID <WO 9822575A3 IA>

on the bacterial chromosome. Since the presence versus the absence of essential virulence genes can often distinguish closely-related virulent versus avirulent bacterial strains or species, experiments have been conducted to identify virulence loci and potential PAIs by isolating DNA sequences that are unique to virulent bacteria (Bloch, C.A., *et al.*, *J Bacteriol.* 176:7121-5 1994, Groisman, E.A., *EMBO J.* 12:3779-87 1993).

At least two PAIs are present in *E. coli* J96. These PAIs, PAI IV and PAI V are linked to tRNA loci but at sites different from those occupied by other known *E. coli* PAIs. Swenson *et al., Infect. and Immun. 64*:3736-3743 (1996).

The era of true comparative genomics has been ushered in by high through-put genomic sequencing and analysis. The first two complete bacterial genome sequences, those of *Haemophilus influenzae* and *Mycoplasma genitalium* were recently described (Fleischmann, R.D., *et al.*, *Science 269*:496 (1995); Fraser, C.M., *et al.*, *Science 270*:397 (1995)). Large scale DNA sequencing efforts also have produced an extensive collection of sequence data from eukaryotes, including *Homo sapiens* (Adams, M.D., *et al.*, *Nature* 377:3 (1995)) and *Saccharomyces cerevisiae* (Levy, J., *Yeast 10*:1689 (1994)).

The need continues to exist for the application of high through-put sequencing and analysis to study genomes and subgenomes of infectious organisms. Further, a need exists for genetic markers that can be employed to distinguish closely-related virulent and avirulent strains of a given bacteria.

Summary of the Invention

The present invention is based on the high through-put, random sequencing of cosmid clones covering two pathogenic islands (PAIs) of uropathogenic *Escherichia coli* strain J96 (O4:K6; *E. coli* J96). PAIs are large fragments of DNA which comprise pathogenicity determinants. PAI IV is located approximately at 64 min (near *pheV*) on the *E. coli* chromosome and is greater than 170 kilobases in size. PAI V is located at approximately 94 min (at *pheR*) on the *E. coli* chromosome and is approximately 106 kb in size. These PAIs

3NSDOCID <WO 9822575A3 IA>

differ in location from the PAIs described by Hacker and colleagues for uropathogenic strain 536 (PAI I, 82 minutes {*sel*C} and PAI II, 97 minutes {*leu*X}).

The location of the PAIs relative to one another and the cosmid clones covering the J96 PAIs is shown in Figure 1. The present invention relates to the nucleotide sequences of 142 fragments of DNA (contigs) covering the PAI IV and PAI V regions of the *E. coli* J96 chromosome. The nucleotide sequences shown in SEQ ID NOs: 1 through 142 were obtained by shotgun sequencing eleven *E. coli* J96 subclones, which were deposited in two pools on September 23, 1996 at the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, and given accession numbers 97726 (includes 7 cosmid clones covering PAI (IV) and 97727 (includes 4 cosmid clones covering PAI V). The deposited sets or "pools" of clones are more fully described in Example 1. In addition, *E. coli* strain J96 was also deposited at the American Type Culture Collection on September 23, 1996, and given accession number 98176.

Three hundred fifty-one open reading frames have been thus far identified in the 142 contigs described by SEQ ID NOs: 1 through 142. Thus, the present invention is directed to isolated nucleic acid molecules comprising open reading frames (ORFs) encoding *E. coli* J96 PAI proteins, and fragments of said nucleic acid molecules.

The present invention also relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of *E. coli* J96 PAI proteins. Further embodiments include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an *E. coli* J96 PAI ORF described herein, and fragments of said nucleic acid molecules.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention and fragments thereof, host cells containing the recombinant vectors, as well as methods for

VSDOCID <WO 9822575A3 IA>

making such vectors and host cells for *E. coli* J96 PAI protein production by recombinant techniques.

The invention further provides isolated polypeptides encoded by the *E. coli* J96 PAI ORFs or fragments of said ORFs. It will be recognized that some amino acid sequences of the polypeptides described herein can be varied without significant effect on the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope-bearing portion is an immunogenic or antigenic epitope useful for raising antibodies.

The invention further provides a vaccine comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*, such as strain J96.

The invention also provides a method of eliciting a protective immune response in an animal comprising administering to the animal the above-described vaccine.

The invention further provides a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for one or more of:

(a) polynucleic acids encoding an open reading frame listed in Tables 1-4 or a fragment of said polynucleic acid;

(b) full length or mature polypeptides encoded for by an open reading frame listed in Tables 1-4; or

INSDOCID: <WO_ 9822575A3 IA>

(c) antibodies specific to polypeptides encoded for by an open reading frame listed in Tables 1-4.

The invention further provides a nucleic acid probe for the detection of the presence of one or more *E. coli* PAI nucleic acids (nucleic acids encoding one or more ORFs as listed in Tables 1-4) in a sample from an individual comprising one or more nucleic acid molecules sufficient to specifically detect under stringent hybridization conditions the presence of the above-described molecule in the sample.

The invention also provides a method of detecting *E. coli* PAI nucleic acids in a sample comprising:

a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and

b) detecting the presence of the probe bound to an *E. coli* PAI nucleic acid.

The invention further provides a kit for detecting the presence of one or more *E. coli* PAI nucleic acids in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

The invention also provides a diagnostic kit for detecting the presence of pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antibodies.

The invention also provides a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antigens.

Brief Description of the Figures

Figure 1 is a schematic diagram of cosmid clones derived from *E. coli* J96 pathogenicity island and map positions of known *E. coli* PAIs (not drawn to scale). The gray bar represents the *E. coli* K-12 chromosome with minute demarcations of PAI junction points located above the bar. *E. coli* J96 overlapping cosmid clones are represented by hatched bars (overlap not drawn to

JSDOCID <WO_ 9822575A3 IA>

scale) with positions of *hly*, *pap*, and *prs* operons indicated above bar. The PAIs and estimated sizes are shown above and below the K-12 chromosome map.

Figure 2 is a block diagram of a computer system 102 that can be used to implement the computer-based systems of present invention.

Detailed Description of the Invention

The present invention is based on high through-put, random sequencing of a uropathogenic strain of *Escherichia coli*. The DNA sequences of contiguous DNA fragments covering the pathogenicity islands, PAI IV (also referred to as $PAI_{J96(pheV)}$) and PAI V (also referred to as $PAI_{J96(pheU)}$) from the chromosome of the *E. coli* uropathogenic strain, J96 (04:K6) were determined. The sequences were used for DNA and protein sequence similarity searches of the database.

The primary nucleotide sequences generated by shotgun sequencing cosmid clones of the PAI IV and PAI V regions of the *E. coli* chromosome are provided in SEQ ID NOs:1 through 142. These sequences represent contiguous fragments of the PAI DNA. As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system. The present invention provides the nucleotide sequences of SEQ ID NOs:1 through 142, or representative fragments thereof, in a form that can be readily used, analyzed, and interpreted by a skilled artisan. Within these 142 sequences, there have been thus far identified 351 open reading frames (ORFs) that are described in greater detail below.

As used herein, a "representative fragment" refers to *E. coli* J96 PAI protein-encoding regions (also referred to herein as open reading frames or ORFs), expression modulating fragments, and fragments that can be used to diagnose the presence of *E. coli* in a sample. A non-limiting identification of such representative fragments is provided in Tables 1 through 6, preferably in Tables 1 through 4. As described in detail below, representative fragments of the present invention further include nucleic acid molecules having a nucleotide sequence at least 95% identical, preferably at least 96%, 97%, 98%, or 99%

INSDOCID <WO 9822575A3 IA>

identical, to an ORF identified in Tables 1 through 6, or more preferably Tables 1 through 4.

As indicated above, the nucleotide sequence information provided in SEQ ID NOs:1 through 142 was obtained by sequencing cosmid clones covering the PAIs located on the chromosome of *E. coli* J96 using a megabase shotgun sequencing method. The sequences provided in SEQ ID NOs:1 through 142 are highly accurate, although not necessarily a 100% perfect, representation of the nucleotide sequences of contiguous stretches of DNA (contigs) which include the ORFs located on the two pathogenicity islands of *E. coli* J96. As discussed in detail below, using the information provided in SEQ ID NOs:1 through 142 and in Tables 1 through 6 together with routine cloning and sequencing methods, one of ordinary skill in the art would be able to clone and sequence all "representative fragments" of interest including open reading frames (ORFs) encoding a large variety of *E. coli* J96 PAI proteins. In rare instances, this may reveal a nucleotide sequence error present in the nucleotide sequences disclosed in SEQ ID NOs: 1 through 142. Thus, once the present invention is made available (i.e., once the information in SEQ ID NOs: 1 through 142 and in Tables 1 through 6 is made available), resolving a rare sequencing error would be well within the skill of the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler™ can be used as an aid during visual inspection of nucleotide sequences.

Even if all of the rare sequencing errors were corrected, it is predicted that the resulting nucleotide sequences would still be at least about 99.9% identical to the reference nucleotide sequences in SEQ ID NOs: 1 through 142. Thus, the present invention further provides nucleotide sequences that are at least 99.9% identical to the nucleotide sequence of SEQ ID NOs: 1 through 142 in a form which can be readily used, analyzed and interpreted by the skilled artisan. Methods for determining whether a nucleotide sequence is at least 99.9% identical to a reference nucleotide sequence of the present invention are described below.

SDOCID <WO 9822575A3 IA>

Nucleic Acid Molecules

The present invention is directed to isolated nucleic acid fragments of the PAIs of *E. coli* J96. Such fragments include, but are not limited to, nucleic acid molecules encoding polypeptides, nucleic acid molecules that modulate the expression of an operably linked ORF (hereinafter expression modulating fragments (EMFs)), and nucleic acid molecules that can be used to diagnose the presence of *E. coli* in a sample (hereinafter diagnostic fragments (DFs)).

By "isolated nucleic acid molecule(s)" is intended a nucleic acid molecule, DNA or RNA, that has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells, purified (partially or substantially) DNA molecules in solution, and nucleic acid molecules produced synthetically. Isolated RNA molecules include *in vitro* RNA transcripts of the DNA molecules of the present invention.

In one embodiment, *E. coli* J96 PAI DNA can be mechanically sheared to produce fragments about 15-20 kb in length, which can be used to generate an *E. coli* J96 PAI DNA library by insertion into lambda clones as described in Example 1 below. Primers flanking an ORF described in Tables 1 through 6 can then be generated using the nucleotide sequence information provided in SEQ ID NOs: 1 through 142. The polymerase chain reaction (PCR) is then used to amplify and isolate the ORF from the lambda DNA library. PCR cloning is well known in the art. Thus, given SEQ ID NOs: 1 through 142, and Tables 1 through 6, it would be routine to isolate any ORF or other representative fragment of the *E. coli* J96 PAI subgenomes. Isolated nucleic acid molecules of the present invention include, but are not limited to, single stranded and double stranded DNA, and single stranded RNA, and complements thereof.

Tables 1 through 6 herein describe ORFs in the *E. coli* J96 PAI cosmid clone library.

BNSDOCID <WO__9822575A3 IA>

Tables 1 and 3 list, for PAI IV and PAI V, respectively, a number of ORFs that putatively encode a recited protein based on homology matching with protein sequences from an organism listed in the Table. Tables 1 and 3 indicate the location of ORFs (i.e., the position) by reference to its position within the one of the 142 *E. coli* J96 contigs described in SEQ ID NOs: 1 through 142. Column 1 of Tables 1 and 3 provides the Sequence ID Number (SEQ ID NO) of the contig in which a particular open reading frame is located. Column 2 numerically identifies a particular ORF on a particular contig (SEQ ID NO) since many contigs comprise a plurality of ORFs. Columns 3 and 4 indicate an ORF's position in the nucleotide sequence (contig) provided in SEQ ID NOs: 1 through 142 by referring to start and stop positions in the contig sequence.

One of ordinary skill in the art will appreciate that the ORFs may be oriented in opposite directions in the *E. coli* chromosome. This is reflected in columns 3 and 4. For these ORFs, the sense strand is complementary to the actual sequence given. The corresponding sense-strand of the ORF must be read as the 5'-3' complement of the antisense strand actually shown in the Sequence Listing, wherein the location is specified 3'-5'.

Column 5 provides a database accession number to a homologous protein identified by a similarity search of public sequence databases (*see*, infra). Column 6 describes the matching protein sequence and the source organism is identified in brackets. Column 7 of Tables 1 and 3 indicates the percent similarity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 of Tables 1 and 3 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. The concepts of percent identity and percent similarity of two polypeptide sequences are well understood in the art and are described in more detail below. Identified genes can frequently be assigned a putative cellular role category adapted from Riley (*see*, Riley, M., *Microbiol. Rev. 57*:862 (1993)). Column 9 of Tables 1 and 3 provides the nucleotide length of the open reading frame.

ISDOCID <WO. 9822575A3 IA>

Tables 2 and 4, below, provide ORFs of *E. coli* J96 PAI IV and PAI V, respectively, that did not elicit a homology match with a known sequence from either *E. coli* or another organism. As above, the first column in Tables 2 and 4 provides the contig in which the ORF is located and the second column numerically identifies a particular ORF in a particular contig. Columns 3 and 4 identify an ORF's position in one of SEQ ID NOs: 1 through 142 by reference to start and stop nucleotides.

Tables 5 and 6, below, provide the *E. coli* J96 PAI IV ORFs and PAI V ORFs, respectively, identified by the present inventors that provided a significant match to a previously published *E. coli* protein. Columns 1-6 correspond to columns 1-6 appearing in Tables 1 and 3. Column 7 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 indicates the length of the high-scoring segment pair (HSP). Column 9 provides the nucleotide length of the open reading frame.

As used herein, "open reading frame" or "ORF" refers to the nucleotide sequences as described in Tables 1 through 6. In Tables 1 through 6, each ORF is designated by a nucleotide sequence start position and stop position according to numbering of contig nucleotides in the Sequence Listing provided (Contig ID = SEQ ID NO).

In a first embodiment, the invention comprises a nucleotide sequence described in Tables 1 through 4 which begins with the nucleotide following the last nucleotide of an upstream stop codon (first nucleotide of the "ORF"), an initiation codon, in-frame putative polypeptide-encoding sequence, and nucleotides of an in-frame stop codon.

In a second embodiment, the invention comprises a nucleotide sequence of Tables 1 through 4 which contains an initiation codon (*e.g.* a methionine or valine codon) on their 5' end and a stop codon on their 3' end. The sequences of this embodiment are present within the nucleotide sequence described in Tables 1 through 4 by start and stop position as numbered in the Sequence Listing. To

3NSDOCID <WO__9822575A3 IA>

determine the 5' start position of this embodiment, one simply reads 5' to 3' from the designated 5' end position until an initiation codon is found.

In a third embodiment, the invention comprises a nucleotide sequence of the second embodiment, except that the 3' stop codon is not present.

In a fourth embodiment, the invention comprises a nucleotide sequence encoding a putative protein which is a sequence of Tables 1 through 4 excluding sequence encoding amino acids subject to removal by post-translational processing and sequences 3' of the last codon coding for an amino acid present in the putative polypeptide (*e.g.*, sequences not containing the stop codon and encoding the mature form of the polypeptide).

Certain embodiments of the invention may therefore either include or exclude initiation codons for methionine or valine and either include or exclude the stop codon.

Further details concerning the algorithms and criteria used for homology searches are provided in the Examples below. A skilled artisan can readily identify ORFs in the *Escherichia coli* J96 cosmid library other than those listed in Tables 1 through 6, such as ORFs that are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

Isolated nucleic acid molecules of the present invention include DNA molecules having a nucleotide sequence substantially different than the nucleotide sequence of an ORF described in Tables 1 through 4, but which, due to the degeneracy of the genetic code, still encode a *E. coli* J96 PAI protein. The genetic code is well known in the art. Thus, it would be routine to generate such degenerate variants.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of an *E. coli* protein encoded by an ORF described in Table 1 through 4. Non-naturally occurring variants may be produced using art-known mutagenesis techniques and include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more

NSDOCID <WO 9822575A3 IA>

nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *E. coli* protein or portions thereof. Also especially preferred in this regard are conservative substitutions.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an ORF described in Tables 1 through 6, preferably 1 through 4. By a polynucleotide having a nucleotide sequence at least, for example, 95% identical to the reference *E. coli* ORF nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the ORF sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference ORF nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5′ or 3′ terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleotide sequence of an *E. coli* J96 PAI ORF can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). Bestfit uses the local homology algorithm of Smith and Waterman, *Advances in Applied Mathematics 2*: 482-489 (1981),

to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

Preferred are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence of an *E. coli* J96 PAI ORF that encode a functional polypeptide. By a "functional polypeptide" is intended a polypeptide exhibiting activity similar, but not necessarily identical, to an activity of the protein encoded by the *E. coli* J96 PAI ORF. For example, the *E. coli* ORF [Contig ID 84, ORF ID 3 (84/3)] encodes a hemolysin. Thus, a "functional polypeptide" encoded by a nucleic acid molecule having a nucleotide sequence, for example, 95% identical to the nucleotide sequence of 84/3, will also possess hemolytic activity. As the skilled artisan will appreciate, assays for determining whether a particular polypeptide is "functional" will depend on which ORF is used as the reference sequence. Depending on the reference ORF, the assay chosen for measuring polypeptide activity will be readily apparent in light of the role categories provided in Tables 1, 3, 5 and 6.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of a reference ORF will encode a functional polypeptide. In fact, since degenerate variants all encode the same amino acid sequence, this will be clear to the skilled artisan even without performing a comparison assay for protein activity. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a functional polypeptide. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not

SDOCID <WO_ 9822575A3 IA>

likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid).

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science 247*:1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie, J.U. *et al., supra,* and the references cited therein.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated nucleic acid molecule having the nucleotide sequence of an *E. coli* J96 PAI ORF is intended fragments at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length that are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-500 nt in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequence of an *E. coli* J96 PAI ORF. By a fragment at least 20 nt in length, for example, is intended fragments that include 20 or more contiguous bases from the nucleotide sequence of an *E. coli* J96 PAI ORF. Since *E. coli* ORFs are listed in Tables 1 through 6 and the sequences of the ORFs have been provided within the contig sequences of SEQ ID NOs: 1 through 142, generating

3NSDOCID <WO _9822575A3 IA>

such DNA fragments would be routine to the skilled artisan. For example, restriction endonuclease cleavage or shearing by sonication could easily be used to generate fragments of various sizes from the PAI DNA that is incorporated into the deposited pools of cosmid clones. Alternatively, such fragments could be generated synthetically.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of an *E. coli* J96 PAI protein. Methods for determining such epitope-bearing portions are described in detail below.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide that hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, an ORF described in Tables 1 through 6, preferably an ORF described in Tables 1, 2, 3 or 4. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5 x SSC (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 x SSC at about 65°C.

By a polynucleotide that hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide (e.g., a *E. coli* ORF), for instance, a portion 50-500 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of an *E. coli* J96 PAI ORF.

ISDOCID <WO 9822575A3 IA>

By "expression modulating fragment" (EMF), is intended a series of nucleotides that modulate the expression of an operably linked, putative polypeptide-encoding region (encoding region). A sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments that induce the expression of an operably linked encoding region in response to a specific regulatory factor or physiological event. EMF sequences can be identified within the *E. coli* genome by their proximity to the encoding regions within ORFs described in Tables 1 through 6. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken 5′ from any one of the encoding regions of ORFs of Tables 1 through 6 will modulate the expression of an operably linked 3′ encoding region in a fashion similar to that found within the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to the fragments of the *E. coli* J96 PAI subgenome that are between two encoding regions herein described. Alternatively, EMFs can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site 5′ to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence that is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed

host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

By a "diagnostic fragment" (DF), is intended a series of nucleotides that selectively hybridize to *E. coli* sequences. DFs can be readily identified by identifying unique sequences within the *E. coli* J96 PAI subgenome, or by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format for amplification or hybridization selectivity.

Each of the ORFs of the *E. coli* J96 PAI subgenome disclosed in Tables 1 through 4, and EMFs found 5′ to the encoding regions of the ORFs, can be used in numerous ways as polynucleotide reagents. The sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of uropathogenic *E. coli* in a sample. This is especially the case with the fragments or ORFs of Table 2 and 4 which will be highly selective for uropathogenic *E. coli* J96, and perhaps other uropathogenic or extraintestinal strains that include one or more PAIs.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56*:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the

ISDOCID: <WO__9822575A3 IA>

sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

Vectors and Host Cells

The present invention further provides recombinant constructs comprising one or more fragments of the *E. coli* J96 PAIs. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which, for example, an *E. coli* J96 PAI ORF is inserted. The vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the encoding region of an ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments (preferably an ORF) of the *E. coli* J96 PAIs described herein. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a

IOCID <WO 9822575A3 IA>

lower eukaryotic host cell, such as a yeast cell, or the host cell can be a procaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)). Host cells containing, for example, an *E. coli* J96 PAI ORF can be used conventionally to produce the encoded protein.

Polypeptides and Fragments

The invention further provides isolated polypeptides having the amino acid sequence encoded by an *E coli* PAI ORF described in Tables 1 through 6, preferably Tables 1 through 4, or a peptide or polypeptide comprising a portion of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least two amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

It will be recognized in the art that some amino acid sequences of *E. coli* polypeptides can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

Thus, the invention further includes variations of polypeptides encoded for by ORFs listed in Tables 1 through 6 which show substantial pathogenic activity or which include regions of particular *E. coli* PAI proteins such as the protein portions discussed below. Such mutants include deletions, insertions,

SDOCID <WO _9822575A3 IA>

inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" amino acid substitutions will generally have little effect on activity.

Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

As indicated in detail above, further guidance concerning which amino acid changes are likely to be phenotypically silent (i.e., are not likely to have a significant deleterious effect on a function) can be found in Bowie, J.U., *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science 247*:1306-1310 (1990).

Thus, the fragment, derivative or analog of a polypeptide encoded by an ORF described in one of Tables 1 through 6, may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Of particular interest are substitutions of charged amino acids with another charged amino acid and with neutral or negatively charged amino acids. The latter results in proteins with reduced positive charge to improve the

characteristics of said proteins. The prevention of aggregation is highly desirable. Aggregation of proteins not only results in a loss of activity but can also be problematic when preparing pharmaceutical formulations, because they can be immunogenic. (Pinckard *et al., Clin Exp. Immunol. 2*:331-340 (1967); Robbins *et al., Diabetes 36*:838-845 (1987); Cleland *et al. Crit. Rev. Therapeutic Drug Carrier Systems 10*:307-377 (1993)).

The replacement of amino acids can also change the selectivity of binding to cell surface receptors. Ostade *et al., Nature 361*:266-268 (1993) describes certain mutations resulting in selective binding of TNF-α to only one of the two known types of TNF receptors. Thus, proteins encoded for by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6, and that bind to a cell surface receptor, may include one or more amino acid substitutions, deletions or additions, either from natural mutations or human manipulation.

As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 7).

TABLE 7. Conservative Amino Acid Substitutions

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

\SDOCID: <WO___9822575A3_IA>

Amino acids in the proteins encoded by ORFs of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, *Science 244*:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as receptor binding or *in vitro*, or *in vitro* proliferative activity. Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al., J. Mol. Biol. 224*:899-904 (1992) and de Vos *et al. Science 255*:306-312 (1992)).

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the polypeptides can be substantially purified by the one-step method described in Smith and Johnson, *Gene 67*:31-40 (1988).

The polypeptides of the present invention include the polypeptide encoded by the ORFs listed in Tables 1-6, preferably Tables 1-4, as well as polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above, and also include portions of such polypeptides with at least 30 amino acids and more preferably at least 50 amino acids.

By "% similarity" for two polypeptides is intended a similarity score produced by comparing the amino acid sequences of the two polypeptides using the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) and the default settings for determining similarity. Bestfit uses the local homology algorithm of Smith and Waterman *(Advances in Applied Mathematics 2*:482-489, 1981) to find the best segment of similarity between two sequences.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a reference amino acid sequence of a polypeptide is intended

NSDOCID <WO 9822575A3 IA>

that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of said polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence encoded by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6 can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The polypeptide of the present invention could be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art.

As described in detail below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting pathogenic protein expression as described below or as

NSDOCID <WO 9822575A3 IA>

agonists and antagonists capable of enhancing or inhibiting protein function of important proteins encoded by the ORFs of the present invention. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" protein binding proteins which are also candidate agonist and antagonist according to the present invention. The yeast two hybrid system is described in Fields and Song, *Nature 340*:245-246 (1989).

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen *et al., Proc. Natl. Acad. Sci. USA 81*:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R.A. (1983) Antibodies that react with predetermined sites on proteins. *Science 219*:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. Sutcliffe *et al.*,

NSDOCID <WO 9822575A3_IA>

supra, at 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. Sutcliffe *et al.*, *supra*, at 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (e.g., about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. See, for instance, Wilson *et al.*, *Cell 37*:767-778 (1984) at 777. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods well known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are

WSDOCID <WO 9822575A3 IA>

considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks. Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides: specificity of antigen-antibody interaction at the level of individual amino acids. *Proc. Natl. Acad. Sci. USA 82*:5131-5135. This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten *et al.* (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously. Houghten *et al.*, *supra*, at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe *et al.*, *supra*; Wilson *et al.*, *supra*; Chow, M. *et al.*, *Proc. Natl. Acad. Sci. USA 82*:910-914; and Bittle, F. J. *et al.*, *J. Gen. Virol. 66*:2347-2354 (1985).

NSDOCID: <WO__9822575A3 IA>

Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 μg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an enzyme-linked immunosorbent assay. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction

NSDOCID <WO 9822575A3 IA>

with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) on Peralkylated Oligopeptide Mixtures discloses linear C_1-C_7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

The entire disclosure of each document cited in this section on "Polypeptides and Peptides" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, *E. coli* PAI polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, e.g., for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins (EP A 394,827; Traunecker *et al., Nature 331*:84-86 (1988)). Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other

3NSDOCID <WO 9822575A3 IA>

molecules than the monomeric *E. coli* J96 PAI proteins or protein fragments alone (Fountoulakis *et al., J. Biochem 270*:3958-3964 (1995)).

Vaccines

In another embodiment, the present invention relates to a vaccine, preferably in unit dosage form, comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit a protective immune response in an animal to pathogenic *E. coli*. Antigens of *E. coli* J96 PAI IV and V may be obtained from polypeptides encoded for by the ORFs listed in Tables 1-6, particularly Tables 1-4, using methods well known in the art.

In a preferred embodiment, the antigens are *E. coli* J96 PAI IV or PAI V proteins that are present on the surface of pathogenic *E. coli*. In another preferred embodiment, the pathogenic *E. coli* J96 PAI IV or PAI V protein-antigen is conjugated to an *E. coli* capsular polysaccharide (CP), particularly to capsular polypeptides that are more prevalent in pathogenic strains, to produce a double vaccine. CPs, in general, may be prepared or synthesized as described in Schneerson *et al. J. Exp. Med. 152*:361-376 (1980); Marburg *et al. J. Am. Chem. Soc.* 108:5282 (1986); Jennings *et al., J. Immunol. 127*:1011-1018 (1981); and Beuvery *et al., Infect. Immunol. 40*:39-45 (1983). In a further preferred embodiment, the present invention relates to a method of preparing a polysaccharide conjugate comprising: obtaining the above-described *E. coli* J96 PAI antigen; obtaining a CP or fragment from pathogenic *E. coli*; and conjugating the antigen to the CP or CP fragment.

In a preferred embodiment, the animal to be protected is selected from the group consisting of humans, horses, deer, cattle, pigs, sheep, dogs, and chickens. In a more preferred embodiment, the animal is a human or a dog.

In a further embodiment, the present invention relates to a prophylactic method whereby the incidence of pathogenic *E. coli*-induced symptoms are

ISDOCID <WO_9822575A3 IA>

decreased in an animal, comprising administering to the animal the above-described vaccine, wherein the vaccine is administered in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*. This vaccination method is contemplated to be useful in protecting against severe diarrhea (pathogenic intestinal *E. coli* strains), urinary tract infections (uropathogenic *E. coli*) and infections of the brain (extraintestinal *E. coli*). The vaccine of the invention is used in an effective amount depending on the route of administration. Although intra-nasal, subcutaneous or intramuscular routes of administration are preferred, the vaccine of the present invention can also be administered by an oral, intraperitoneal or intravenous route. One skilled in the art will appreciate that the amounts to be administered for any particular treatment protocol can be readily determined without undue experimentation. Suitable amounts are within the range of 2 micrograms of the protein per kg body weight to 100 micrograms per kg body weight.

The vaccine can be delivered through a vector such as BCG. The vaccine can also be delivered as naked DNA coding for target antigens.

The vaccine of the present invention may be employed in such dosage forms as capsules, liquid solutions, suspensions or elixirs for oral administration, or sterile liquid forms such as solutions or suspensions. Any inert carrier is preferably used, such as saline, phosphate-buffered saline, or any such carrier in which the vaccine has suitable solubility properties. The vaccines may be in the form of single dose preparations or in multi-dose flasks which can be used for mass vaccination programs. Reference is made to Remington's *Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, Osol (ed.) (1980); and *New Trends and Developments in Vaccines*, Voller *et al.* (eds.), University Park Press, Baltimore, MD (1978), for methods of preparing and using vaccines.

The vaccines of the present invention may further comprise adjuvants which enhance production of antibodies and immune cells. Such adjuvants include, but are not limited to, various oil formulations such as Freund's complete adjuvant (CFA), the dipeptide known as MDP, saponins (ex. *Quillajasaponin* fraction QA-21, U.S. Patent No. 5,047,540), aluminum hydroxide, or lymphatic

3NSDOCID <WO_ _9822575A3 IA>

cytokines. Freund's adjuvant is an emulsion of mineral oil and water which is mixed with the immunogenic substance. Although Freund's adjuvant is powerful, it is usually not administered to humans. Instead, the adjuvant alum (aluminum hydroxide) may be used for administration to a human. Vaccine may be absorbed onto the aluminum hydroxide from which it is slowly released after injection. The vaccine may also be encapsulated within liposomes according to Fullerton, U.S. Patent No. 4,235,877.

Protein Function

Each ORF described in Tables 1 and 3 possesses a biological role similar to the role associated with the identified homologous protein. This allows the skilled artisan to determine a function for each identified coding sequence. For example, a partial list of the *E. coli* protein functions provided in Tables 1 and 3 includes many of the functions associated with virulence of pathogenic bacterial strains. These include, but are not limited to adhesins, excretion pathway proteins, O-antigen/carbohydrate modification, cytotoxins and regulators. A more detailed description of several of these functions is provided in Example 1 below.

Diagnostic Assays

In another preferred embodiment, the present invention relates to a method of detecting pathogenic *E. coli* nucleic acid in a sample comprising:

a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and

b) detecting the presence of the probe bound to pathogenic *E. coli* nucleic acid.

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* nucleic acid in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

WSDOCID <WO...9822575A3 IA>

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antibodies.

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antigens.

The present invention provides methods to identify the expression of an ORF of the present invention, or homolog thereof, in a test sample, using one of the antibodies of the present invention. Such methods involve incubating a test sample with one or more of the antibodies of the present invention and assaying for binding of the antibodies to components within the test sample.

In a further embodiment, the present invention relates to a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for a nucleic acid, protein, polypeptide-antigen or antibody specific to one of the ORFs described in Tables 1-4 herein from *E. coli* J96 PAI IV or V. Analysis of nucleic acid specific to pathogenic *E. coli* can be by PCR techniques or hybridization techniques (cf. *Molecular Cloning: A Laboratory Manual, second edition*, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989; Eremeeva *et al., J. Clin. Microbiol. 32*:803-810 (1994) which describes differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA).

Proteins or antibodies specific to pathogenic *E. coli* may be identified as described in *Molecular Cloning: A Laboratory Manual, second edition*, Sambrook *et al.*, eds., Cold Spring Harbor Laboratory (1989). More specifically, antibodies may be raised to *E. coli* J96 PAI proteins as generally described in *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988). *E. coli* J96 PAI-specific antibodies can also be obtained from infected animals (Mather, T. *et al.*, *JAMA 205*:186-188 (1994)).

NSDOCID <WO 9822575A3 IA>

In another embodiment, the present invention relates to an antibody having binding affinity specifically to an *E. coli* J96 PAI antigen as described above. The *E. coli* J96 PAI antigens of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, a peptide can be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well as fragments of these antibodies. The invention further includes single chain antibodies. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques, for example, such fragments include but are not limited to: the $F(ab')_2$ fragment; the Fab' fragments, Fab fragments, and Fv fragments.

Of special interest to the present invention are antibodies to pathogenic *E. coli* antigens which are produced in humans, or are "humanized" (i.e. non-immunogenic in a human) by recombinant or other technology. Humanized antibodies may be produced, for example by replacing an immunogenic portion of an antibody with a corresponding, but non-immunogenic portion (i.e. chimeric antibodies) (Robinson, R.R. *et al.*, International Patent Publication PCT/US86/02269; Akira, K. *et al.*, European Patent Application 184,187; Taniguchi, M., European Patent Application 171,496; Morrison, S.L. *et al.*, European Patent Application 173,494; Neuberger, M.S. et al., PCT Application WO 86/01533; Cabilly, S. *et al.*, European Patent Application 125,023; Better, M. *et al., Science 240*:1041-1043 (1988); Liu, A.Y. *et al., Proc. Natl. Acad. Sci. USA 84*:3439-3443 (1987); Liu, A.Y. *et al., J. Immunol. 139*:3521-3526 (1987); Sun, L.K. *et al., Proc. Natl. Acad. Sci. USA 84*:214-218 (1987); Nishimura, Y. *et al., Canc. Res. 47*:999-1005 (1987); Wood, C.R. *et al., Nature 314*:446-449 (1985)); Shaw *et al., J. Natl. Cancer Inst. 80*:1553-1559 (1988). General reviews of "humanized" chimeric antibodies are provided by Morrison, S.L. (*Science, 229*:1202-1207 (1985)) and by Oi, V.T. *et al., BioTechniques 4*:214 (1986)). Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones, P.T. *et al., Nature 321*:552-525 (1986); Verhoeyan *et al.*,

Science 239:1534 (1988); Beidler, C.B. *et al., J. Immunol. 141*:4053-4060 (1988)).

In another embodiment, the present invention relates to a hybridoma which produces the above-described monoclonal antibody. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "*Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*," Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al., J. Immunol. Methods 35*:1-21 (1980)).

In another embodiment, the present invention relates to a method of detecting a pathogenic *E. coli* antigen in a sample, comprising: a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and b) detecting the presence of said antibody bound to the antigen. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard, *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock *et al., Techniques in Immunocytochemistry,* Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology,* Elsevier Science Publishers, Amsterdam, The Netherlands

3NSDOCID: <WO _ 9822575A3_IA>

(1985); and *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is capable with the system utilized.

In another embodiment, the present invention relates to a method of detecting the presence of antibodies to pathogenic *E. coli* in a sample, comprising: a) contacting the sample with an above-described antigen, under conditions such that immunocomplexes form, and b) detecting the presence of said antigen bound to the antibody. In detail, the methods comprise incubating a test sample with one or more of the antigens of the present invention and assaying whether the antigen binds to the test sample.

In another embodiment of the present invention, a kit is provided which contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: i) a first container means containing an above-described antibody, and ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies. Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits.

VSDOCID <WO 9822575A3 IA>

One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

Screening Assay for Binding Agents

Using the isolated proteins described herein, the present invention further provides methods of obtaining and identifying agents that bind to a protein encoded by an *E. coli* J96 PAI ORF or to a fragment thereof.

The method involves:

(a) contacting an agent with an isolated protein encoded by a *E. coli* J96 PAI ORF, or an isolated fragment thereof; and

(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques. For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by an ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide ligands, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides, In *Synthetic Peptides, A User's Guide*, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry 28*:9230-8 (1989).

3NSDOCID <WO 9822575A3 IA>

In addition to the foregoing, one class of agents of the present invention, can be used to control gene expression through binding to one of the ORF encoding regions or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed and selected. Targeting the encoding region or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF encoding region or multiple encoding regions that rely on the same EMF for expression control.

One class of DNA binding agents are those that contain nucleotide base residues that hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives having base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*: 1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56*:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Computer Related Embodiments

The nucleotide sequence provided in SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to the sequences provided in SEQ ID NOs: 1 through 142, can be "provided" in

\SDOCID <WO___9822575A3 IA>

a variety of media to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, that contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NOs: 1 through 142, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NOs: 1 through 142. Such a manufacture provides the *E. coli* J96 PAI subgenomes or a subset thereof (e.g., one or more *E. coli* J96 PAI open reading frame (ORF)) in a form that allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *E. coli* J96 PAI subgenome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, one or more nucleotide sequences of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on

3NSDOCID <WO 9822575A3 IA>

computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of dataprocessor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to SEQ ID NOs: 1 through 142, in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem. 17*:203-207 (1993)) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the *E. coli* J96 PAI subgenome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the *E. coli* J96 PAI subgenome and are useful in producing commercially important proteins such as enzymes used in modifying surface O-antigens of bacteria. A comprehensive list of ORFs encoding commercially important *E. coli* J96 PAI proteins is provided in Tables 1 through 6.

The present invention provides a DNA sequence - gene database of pathogenicity islands (PAIs) for *E. coli* involved in infectious diseases. This database is useful for identifying and characterizing the basic functions of new virulence genes for *E. coli* involved in uropathogenic and extraintestinal diseases. The database provides a number of novel open reading frames that can be selected for further study as described herein.

Selectable insertion mutations in plasmid subclones encoding PAI genes with potentially significant phenotypes for *E. coli* uropathogenesis and sepsis can

ISDOCID <WO 9822575A3 IA>

be isolated. The mutations are then crossed back into wild type, uropathogenic *E. coli* by homologous recombination to create wild-type strains specifically altered in the targeted gene. The significance of the genes to *E. coli* pathogenesis is assessed by *in vitro* assays and *in vivo* murine models of sepsis/peritonitis and ascending urinary tract infection.

New virulence genes and PAI sites in uropathogenic *E. coli* may be identified by the transposon signature-tagged mutagenesis system and negative selection of *E. coli* mutants avirulent in murine models of ascending urinary tract infection or peritonitis.

Epidemiological investigations of new virulence genes and PAIs may be used to test for their occurrence in the genomes of other pathogenic and opportunistic members of the Enterobacteriaceae.

One can choose from the ORFs included in SEQ ID NOs: 1 through 142, using Tables 1 through 6 as a useful guidepost for selecting, as candidates for targeted mutagenesis, a limited number of candidate genes within the PAIs based on their homology to virulence, export or regulation genes in other pathogens. For the large number of apparent genes within the PAIs that do not share sequence similarity to any entries in the database, the transposon signature-tagged mutagenesis method developed by David Holden's laboratory can be employed as an independent means of virulence gene identification.

Allelic knock-outs are constructed using different *pir*-dependent suicide vectors (Swihart, K.A. and R.A. Welch, *Infect. Immun. 58*:1853-1869 (1990)). In addition, two different animal model systems can be employed for assessment of pathogenic determinants. The initial identification of *E. coli* hemolysin as a virulence factor came from the construction of isogenic *E. coli* strains that were tested in a rat model of intra-abdominal sepsis (Welch, R.A. *et al., Nature (London) 294*:665-667 (1981)). The ascending UTI (Urinary Tract Infection) mouse model was also successfully performed with allelic knock-outs of the *hpmA* hemolysin of *Proteus mirabilis* (Swihart, K.A. and R.A. Welch, *Infect. Immun. 58*:1853-1869 (1990)).

INSDOCID <WO 9822575A3 IA>

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *E. coli* J96 PAI subgenome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *E. coli* genome that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

NSDOCID <WO 9822575A3 IA>

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the *E. coli* J96 PAI subgenome, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequence and the homologous *E. coli* J96 PAI sequence identified using a search means as described above, and an output means for outputting the identified homologous *E. coli* J96 PAI sequence. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *E. coli* J96 PAI subgenome possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the

3NSDOCID: <WO__ 9822575A3_IA>

E. coli J96 PAI subgenomes. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) can be used to identify open reading frames within the *E. coli* J96 PAI subgenome A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

One application of this embodiment is provided in Figure 2. Figure 2 provides a block diagram of a computer system 102 that can be used to implement the present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114 once inserted in the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. Software for accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108 during execution.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

JSDOCID <WO_ _9822575A3 IA>

Experimental

Example 1: High Through-put Sequencing of Cosmid Clones Covering PAI IV and PAI V in E. coli J96

The complete DNA sequence of the pathogenicity islands, PAI IV and PAI V (respectively >170 kb and ~110 kb), from uropathogenic *E. coli* strain, J96 (04:K6) was determined using a strategy, cloning and sequencing method, data collection and assembly software essentially identical to those used by the TIGR group for determining the sequence of the *Haemophilus influenzae* genome (Fleischmann, R.D., *et al.*, *Science 269*:496 (1995)). The sequences were then used for DNA and protein sequence similarity searches of the databases as described in Fleischmann, *Id.*

The analysis of the genetic information found within the PAIs of *E. coli* J96 was facilitated by the use of overlapping cosmid clones possessing these unique segments of DNA. These cosmid clones were previously constructed and mapped (as further described below) as an overlapping set in the laboratory of Dr. Doug Berg (Washington University). A gap exists between the left portion of cosmid 2 and the end of the PAI IV that would represent the *phe*V junction to the *E. coli* K-12 genome.

Uropathogenic strain *E. coli* J96 (O4:K6) was used as a source of chromosomal DNA for construction of a cosmid library. *E. coli* K-12 DH5α and DH12 (Gibco/BRL, Gaithersburg, Md.) were used as hosts for maintaining cosmid and plasmid clones. The cosmid library of *E coli* J96 DNA was constructed essentially as described by Bukanow & Berg (*Mol. Microbiol 11*:509-523 (1994)). DNA was digested with *Sau*3AI under conditions that generated fragments with an average size of 40 to 50 kb and electrophoresed through 1% agarose gels. Fragments of 35 to 50 kb were isolated and cloned into Lorist 6 vector that had been linearized with *Bam*III and treated with bacterial alkaline phosphatase to block self-ligation. (Lorist 6 is a 5.2-kb moderate-copy-number cosmid vector with T7 and SP6 promoters close to the cloning site.) Cloned

3NSDOCID: <WO__9822575A3 IA>

DNA was packaged in lambda phage particles *in vitro* by using a commercial kit (Amersham, Arlington Heights, IL) and cosmid-containing phage particles were used to transduce *E. coli* DH5α. Transductant colonies were transferred to 150 μL of Luria-Bertani broth supplemented with kanamycin in 96-well microtiter plates and grown overnight at 37°C with shaking. Two sets of clones, one for each PAI were ultimately assembled, as previously described (Swenson *et al.*, *Infection and Immunity 64*:3736-3743 (1996)), fully incorporated by reference herein).

The two sets of clones contain eleven sub-clones that were employed in the sequencing method described below. One set of four overlapping cosmid clones covers the *prs*-containing PAI V, ATCC Deposit No. 97727, deposited September 23, 1996. A second set of seven subclones covers much of the *pap*-containing PAI V, ATCC Deposit No. 97726, deposited September 23, 1996. See Figure 1.

A high through-put, random sequencing method (Fleischmann *et al.*, *Science 269*:496 (1995); Fraser *et al.*, *Science 270*:397 (1995)) was used to obtain the sequences for 142 (contigs) fragments of *E. coli* J96 PAIs. All clones were sequenced from both ends to aid in the eventual ordering of contigs during the sequence assembly process. Briefly, random libraries of ~ 2 kb clones covering the two J96 PAIs were constructed, ~ 2,800 clones were subjected to automated sequencing (~ 450 nt/clone) and preliminary assemblies of the sequences accomplished which result in 142 contigs for each of the two PAIs that total 95 and 135 kb respectively. The estimated sizes of the PAI IV and PAI V based on the overlapping cosmid clones are 1.7×10^5 and 1.1×10^5 bp respectively. The 142 sequences were assembled by means of the TIGR Assembler (Fleischmann *et al.*; Fraser *et al.*); Sutton *et al.*, *Genome Sci. Tech. 1*:9 (1995)). Sequence and physical gaps were closed using a combination of strategies (Fleischmann *et al.*; Fraser *et al.*). Presently the average depth of sequencing for each base assembled in the contigs is 6-fold. The tentative identity of many genes based on sequence homology is covered in Tables 1, 3, 5 and 6.

JSDOCID <WO _ 9822575A3 IA>

Open reading frames (ORFs) and predicted protein-coding regions were identified as described (Fleischmann *et al.*; Fraser *et al.*) with some modification. In particular, the statistical prediction of uropathogenic *E. coli* J96 pathogenicity island genes was performed with GeneMark (Borodovsky, M. & McIninch, *J. Comput. Chem. 17*:123 (1993)). Regular GeneMark uses nonhomogeneous Markov models derived from a training set of coding sequences and ordinary Markov models derived from a training set of noncoding sequences. The ORFs in Tables 1-6 were identified by GeneMark using a second-order Markov model trained from known *E. coli* coding regions and known *E. coli* non-coding regions.

Among the important genes that are implicated in the virulence of *E. coli* J96 PAIs are adhesins, excretion pathway proteins, proteins that participate in alterations of the O-antigen in the PAIs, cytotoxins, and two-component (membrane sensor/DNA binding) proteins.

I. Adhesins. It is believed that the principal adhesin determinants involved in uropathogenicity that are present within PAIs of uropathogenic *E. coli* are the pili encoded by the *pap*-related operons (Hultgren *et al.*, *Infect. Immun. 50*:370-377 (1993), Stromberg *et al.*, *EMBO J 9*:2001-2010 (1990), High *et al.*, *Infect. Immun. 56*:513-517 (1988)) and the distantly related afimbrial adhesins (Labigne-Roussel *et al.*, *Infect. Immun. 46*:251-259 (1988)). The presence of two of these (*pap*, and *prs*) has been confirmed. In addition potential genes for five other adhesins including *sla* (described above), AIDA-I (diffuse adherence-DEAC), *hra* (heat resistant hemagglutinin-ETEC), *fha* (filamentous hemagglutinin- *Bordetella pertussis*) and the arg-gingipain proteinase of *Porphyromonas gingivalis* have been found.

II. Type II exoprotein secretion pathway. Highly significant statistics support the presence of multiple genes involved in the type II exoprotein pathway. Curiously, perhaps two different determinants appear to be present in PAI IV where one set of genes has the highest sequence similarity to *eps*-like genes (*Vibrio cholerae* Ctx export) and the other has greatest similarity to *exe* genes (*Aeromonas hydophilia* aerolysin and protease export). At present, the assembly of contigs involving these potential genes is incomplete. Thus, it is

3NSDOCID <WO 9822575A3 IA>

uncertain if two separate and complete determinants are present. However, it is clear that these genes are newly discovered and novel to pathogenic *E. coli* because the derived sequences do not have either the *bfp* or *hop* genes as the highest matches. The gene products that are the target of the type II export pathway are not evident at this time.

Within PAI IV there are sequences which suggest genes very similar to *secD* and *secF*. These two linked genes encode homologous products that are localized to the inner membrane and are hypothesized to play a late role in the translocation of leader-peptide containing proteins across the inner membrane of gram-negative bacteria. In addition, in each PAI, sequences are found that are reminiscent of the heat-shock htrA/degA gene that encodes a piroplasmic protease. They may perform endochaperone-like function as Pugsley *et al.* have hypothesized for different exoprotein pathways.

III. O-antigen/capsule/carbohydrate modification (Nod genes). J96 has the O4. The O-antigen portion of lipopolysaccharide is encoded by *rfb* genes that are located at 45 min. on the *E. coli* chromosome. We have found in both PAIs a cumulative total of five possible *rfb*-like genes which could participate alterations of the O-antigen in the PAIs. Overall these data suggest that PAIs provide the genetic potential for greater change of the cell surface for uropathogenic *E. coli* strains than what was previously known.

The apparent capsule type for strain J96 is a non-sialic acid K6-type. Sequence similarity "hits" were made in PAI IV region to two region-1 capsule genes, *kpsS* and *kpsE* involved in the stabilization of polysaccharide synthesis and polysaccharide export across the inner membrane. This is not altogether surprising based on the genetic mapping of the *kps* locus to *serA* at 63 minutes on the genome of the K1 capsular type of *E. coli*. This suggests that these *kps*-like genes either are participating in the K6-biosynthesis or perhaps are involved in complex carbohydrate export for other purposes.

An intriguing discovery are the hits made on genes involved in bacteria-plant interactions by *Rhizobium, Bradyrhizobium* and *Agrobacterium*. Four potential genes identified thus far share significant sequence similarity to genes

SDOCID: <WO 9822575A3 IA>

encoding products that modify lipo-oligosaccharides that influence nodule morphogenesis on legume roots. These are: ORF140, carbamyl phosphate synthetase; nodulation protein 1265; phosphate-regulatory protein; and an ORF at a plant-inducible locus in *Agrobacterium*. To date there are no descriptions in the literature of such gene products being utilized by human or animal bacterial pathogens for the purposes of modification or secretion of extracellular carbohydrate. However, the sequence similarity to the capsular region-2 genes and to lipooligosaccharide biosynthetic genes in *Rhizobium* spp has been recently noted by Petit (1995).

IV. Cytotoxins. Besides the previously known hemolysin and CNF toxins in the PAIs, in each PAI sequences similar to the *shlBA* operon (cosmid 5 and 12) were found for a cytolytic toxin from *Serratia marcescens* and *Proteus mirabilis*. Ironically, the *P. mirabilis* hemolysin (HpmA) member of this family of toxins was discovered by Uphoff and Welch (1990), but not thought to exist in other members of the Enterobacteriaceae (Swihart (1990)). A *shlB*-like transporter does also appear to be involved in the export of the filamentous hemagglutinin of *Bordetella pertussis* which was described above and a cell surface adhesin of *Haemophilus influenzae*. It has been demonstrated that cosmid #5 of *E. coli* J96 encodes an extracellular protein that is ~180 kDa and cross-reactive to polyclonal antisera to the *P. mirabilis* HpmA hemolysin. Thus, there is evidence suggesting there is new member of this family of proteins in extraintestinal *E. coli* isolates. In addition, there is also a hit on the FhaC hemolysin-like gene within the PAI V although its statistical significance for the sequence thus far available is only 0.0043.

V. Regulators. A common regulatory motif in bacteria are the two-component (membrane sensor/DNA binding) proteins. In numerous instances in pathogenic bacteria, external signals in the environment cause membrane-bound protein kinases to phosphorylate a cytoplasmic protein which in turn acts as either a negative or positive effector of transcription of large sets of operons. On cosmid 11 representing PAI V were found, in two different *PstI* clones, sequences

NSDOCID <WO 9822575A3 IA>

for two-component regulators (similar probabilities for OmpR/ AIGB and separately RcsC, probabilities at the 10^{-22} level).

In addition, the phosphoglycerate transport system (*pgtA*, *pgtC*, and *pgtP*) including the *pgtB* regulator is present in PAI IV. This transport system which was originally described in *S. typhimurium* is not appreciated as a component of any pathogenic *E. coli* genome. The operon had been previously mapped at 49 minutes, near or within one of the *S. typhimurium* chromosome specific-loops not present in the K-12 genome. It should be noted that the *E. coli* K-12 glpT gene product is similar to pgtP gene product (37% identity), but the *E. coli* J96 genes are clearly homologs to the *pgt* genes and their linkage within the middle of PAI IV element (cosmid #4) is suspicious.

VI. Mobile genetic elements. There are numerous sequences that share similarity to genes found on insertion elements, plasmids and phages. The temperate bacteriophage P4 inserts within tRNA loci in the *E. coli* chromosome. The hypothesis was made that PAIs are the result of bacteriophage P4-virulence gene recombination events (Blum *et al., Infect. Immun. 62*:606-614 (1994). Data supporting this hypothesis was found during our sequencing with the identification of P4-like sequences in each of the PAIs (cosmids 7 and 9). This is a very important preliminary result which supports the hypothesis that PAIs can be identified by common sequence or genetic elements. However, there are indications that multiple mobile genetic elements involved in the evolution of the J96 PAIs. Conjugal plasmid-related sequences may also be present at two different locations (F factor and Rl plasmid). Sequences for multiple transposable elements are present that are likely to have originated from different bacterial genera (Tnl000, IS630, IS911, IS100, IS21, IS 1203, IS5376 (*B. stearothermophflus*) and RHS). Of particular interest is IS100, which was originally identified in *Yersinia pestis* (Fetherston *et al., Mol. Microbiol. 6*:2693-2704 (1992)). The presence of IS100 is significant because it has been associated with the termini of a large chromosomal element encoding pigmentation and some aspect of virulence in *Y. pestis*. This element undergoes spontaneous deletions similar to the PAIs from *E. coli* 536 (Fetherston *et al., Mol. Microbiol.*

ISDOCID <WO_ 9822575A3 IA>

6:2693-2704 (1992)) and appears to participate in plasmid-chromosome rearrangements. This element was not previously known to be in genera outside of *Yersinia*.

The discovery of the apparent *att* site for bacteriophage P2 in the PAIs is interesting. P2 acts as a helper phage for the P4 satellite phage. The P2 *att* site is at 44 min in the K-12 genome. The significance of this hit is unknown at present, but may be explained as either a cloning artifact (some K-12 fragments in the *Pst* I library of cosmid 5) or evidence of some curious chromosomal-P4/P2 phage history. It may indicate that the J96 PAIs are composites of multiple smaller PAIs.

Example 2: Preparation of PCR Primers and Amplification of DNA

Various fragments of the sequenced *E. coli* J96 PAIs, such as those disclosed in Tables 1 through 6 can be used, in accordance with the present invention, to prepare PCR primers. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers are useful during PCR cloning of the ORFs described herein.

Example 3: Gene expression from DNA Sequences Corresponding to ORFs

A fragment of an *E. coli* J96 PAI (preferably, a protein-encoding sequence provided in Tables 1 through 6) is introduced into an expression vector using conventional technology (techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art). Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper

NSDOCID <WO 9822575A3 IA>

protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Pat. No. 5,082,767, which is hereby incorporated by reference.

The following is provided as one exemplary method to generate polypeptide(s) from a cloned ORF of an *E. coli* J96 PAI whose sequence is provided in SEQ ID NOs: 1 through 142. A poly A sequence can be added to the construct by, for example, splicing out the poly A sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *E. coli* J96 PAI DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *E. coli* J96 PAI DNA and containing restriction endonuclease sequences for PstI incorporated into the 5′ primer and BglII at the 5′ end of the corresponding *E. coli* J96 PAI DNA 3′ primer, taking care to ensure that the *E. coli* J96 PAI DNA is positioned such that its followed with the poly A sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface.

Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *E. coli* J96 PAI DNA

NSDOCID <WO 9822575A3 IA>

sequence are injected into mice to generate antibody to the polypeptide encoded by the *E. coli* J96 PAI DNA.

If antibody production is not possible, the *E. coli* J96 PAI DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as a chimeric with, for example, ß-globin. Antibody to ß-globin is used to purify the chimeric. Corresponding protease cleavage sites engineered between the ß-globin gene and the *E. coli* J96 PAI DNA are then used to separate the two polypeptide fragments from one another after translation. One useful expression vector for generating ß-globin chimerics is pSG5 (Stratagene). This vector encodes rabbit ß-globin. Intron II of the rabbit ß-globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides may additionally be produced from either construct using *in vitro* translation systems such as In vitro Express™ Translation Kit (Stratagene).

Example 4

E. coli Expression of an E. coli J96 PAI ORF and protein purification

An *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified using PCR oligonucleotide primers designed from the nucleotide sequences flanking the selected ORF and/or from portions of the ORF's NH_2- or COOH-terminus. Additional nucleotides containing restriction sites to facilitate cloning are added to the 5′ and 3′ sequences, respectively.

The restriction sites are selected to be convenient to restriction sites in the bacterial expression vector pQE60. The bacterial expression vector pQE60 is used for bacterial expression in this example. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible

3NSDOCID <WO 9822575A3 IA>

promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin sold by QIAGEN, Inc., *supra,* and suitable single restriction enzyme cleavage sites. These elements are arranged such that a DNA fragment encoding a polypeptide may be inserted in such as way as to produce that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of an *E. coli* J96 PAI is amplified from the deposited cDNA clone using PCR oligonucleotide primers which anneal to the amino terminal sequences of the desired portion of the *E. coli* protein and to sequences in the deposited construct 3' to the cDNA coding sequence. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

The amplified *E. coli* J96 PAI DNA fragments and the vector pQE60 are digested with one or more appropriate restriction enzymes, such as SalI and XbaI, and the digested DNAs are then ligated together. Insertion of the *E. coli* J96 PAI DNA into the restricted pQE60 vector places the *E. coli* J96 PAI protein coding region, including its associated stop codon, downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described in Sambrook *et al., Molecular Cloning: a Laboratory Manual, 2nd Ed.;* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989). *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing an *E. coli* J96 PAI protein, is available commercially from QIAGEN, Inc., *supra.* Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from

SDOCID <WO 9822575A3 IA>

resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the laci repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH8. The cell debris is removed by centrifugation, and the supernatant containing the *E. coli* J96 PAI protein is dialyzed against 50 mM Na-acetate buffer pH6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. coli* J96 PAI protein. The purified protein is stored at 4°C or frozen at -80°C.

Example 5

Cloning and Expression of an E. coli J96 PAI protein in a Baculovirus Expression System

A *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified as above. The plasmid is digested with appropriate restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1%

agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.). This vector DNA is designated herein "V1".

Fragment F1 and the dephosphorylated plasmid V1 are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria are identified that contain the plasmid with the *E. coli* J96 PAI gene by digesting DNA from individual colonies using appropriate restriction enzymes and then analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing. This plasmid is designated herein pBac *E. coli J96*.

Five μg of the plasmid pBac *E. coli* J96 is co-transfected with 1.0 μg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA.), using the lipofection method described by Felgner *et al., Proc. Natl. Acad. Sci. USA 84*:7413-7417 (1987). 1 μg of BaculoGold™ virus DNA and 5 μg of the plasmid pBac *E. coli* J96 are mixed in a sterile well of a microliter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27°C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation is continued at 27°C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc.) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies

NSDOCID <WO 9822575A3 IA>

Inc., page 9-10). After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4 °C. The recombinant virus is called V-*E. coli* J96.

To verify the expression of the *E. coli* gene Sf9 cells are grown in Grace's medium supplemented with 10% heat inactivated FBS. The cells are infected with the recombinant baculovirus V-*E. coli* J96 at a multiplicity of infection ("MOI") of about 2. Six hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc.). If radiolabeled proteins are desired, 42 hours later, 5 µCi of ^{35}S-methionine and 5 µCi ^{35}S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then they are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled). Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the mature protein and thus the cleavage point and length of the secretary signal peptide.

Example 6

Cloning and Expression in Mammalian Cells

Most of the vectors used for the transient expression of an *E. coli* J96 PAI gene in mammalian cells should carry the SV40 origin of replication. This allows the replication of the vector to high copy numbers in cells (e.g., COS cells) which express the T antigen required for the initiation of viral DNA synthesis. Any other mammalian cell line can also be utilized for this purpose.

A typical mammalian expression vector contains the promoter element, which mediates the initiation of transcription of mRNA, the protein coding

3NSDOCID <WO 9822575A3_IA>

sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription can be achieved with the early and late promoters from SV40, the long terminal repeats (LTRS) from Retroviruses, e.g., RSV, 1HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter). Suitable expression vectors for use in practicing the present invention include, for example, vectors such as PSVL and PMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146) and pBC12MI (ATCC 67109). Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV I, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the gene can be expressed in stable cell lines that contain the gene integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful to develop cell lines that carry several hundred or even several thousand copies of the gene of interest. Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy *et al., Biochem J. 227*:277-279 (199 1); Bebbington *et al., Bio/Technology 10:*169-175 (1992)). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

The expression vectors pC1 and pC4 contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen *et al.,* Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart *et al., Cell 41*:521-530 (1985)). Multiple cloning sites, e.g., with the restriction enzyme

SDOCID <WO 9822575A3_IA>

cleavage sites BamHI, Xbal and Asp718, facilitate the cloning of the gene of interest. The vectors contain in addition the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene.

Example 6(a): Cloning and Expression in COS Cells

The expression plasmid, p *E. coli* J96HA, is made by cloning a cDNA encoding *E. coli* J96 PAI protein into the expression vector pcDNAI/Amp or pcDNAIII (which can be obtained from Invitrogen, Inc.).

The expression vector pcDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a cDNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson *et al., Cell 37:*767 (1984). The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pcDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding the *E. coli* J96 PAI protein is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The *E. coli* cDNA of the deposited clone is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *E. coli* J96 PAI protein in *E. coli.*

The PCR amplified DNA fragment and the vector, pcDNAI/Amp, are digested with appropriate restriction enzymes for the chosen primer sequences

NSDOCID <WO 9822575A3 IA>

and then ligated. The ligation mixture is transformed into *E. coli* strain SURE (available from Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the *E. coli* J96 PAI protein-encoding fragment.

For expression of recombinant *E. coli* J96 PAI protein, COS cells are transfected with an expression vector, as described above, using DEAE-DEXTRAN, as described, for instance, in Sambrook *et al., Molecular Cloning: a Laboratory Manual,* Cold Spring Laboratory Press, Cold Spring Harbor, New York (1989). Cells are incubated under conditions for expression of *E. coli* J96 PAI protein by the vector.

Expression of the *E. coli* J96 PAI - HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow *et al., Antibodies: A Laboratory Manual, 2nd Ed.;* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988). To this end, two days after transfection, the cells are labeled by incubation in media containing ^{35}S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson *et al.* cited above. Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 6(b): Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of an *E. coli* J96 PAI protein. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Acc. No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early

VSDOCID <WO 9822575A3 IA>

promoter. Chinese hamster ovary- or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies, Inc.) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented (see, e.g., Alt, F. W. *et al.*, 1978, *J. Biol. Chem. 253*:1357-1370, Hamlin, J. L. and Ma, C. 1990, *Biochim. et Biophys. Acta, 1097*:107-143, Page, M. J. and Sydenham, M.A. 1991, *Biotechnology 9*:64-68). Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains for expressing the gene of interest the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus (Cullen, *et al., Molecular and Cellular Biology,* March 1985:438-447) plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV) (Boshart *et al., Cell 41*:521-530 (1985)). Downstream of the promoter is BamHI restriction enzyme site that allows the integration of the gene. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β-actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLVI. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. coli* protein in a regulated way in mammalian cells (Gossen, M., & Bujard, H. 1992, *Proc. Natl. Acad. Sci. USA 89*: 5547-5551). For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the

NSDOCID <WO 9822575A3 IA>

chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

The DNA sequence encoding the complete *E. coli* J96 PAI protein including its leader sequence is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene.

The amplified fragment is digested with appropriate endonucleases for the chosen primers and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. 5 μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using lipofectin (Felgner *et al., supra).* The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methothrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nm, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM, 2 μM, 5 μM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μM. Expression

NSDOCID <WO_ 9822575A3 IA>

of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 7

Production of an Antibody to an E. coli J96 Pathogenicity Island Protein

Substantially pure *E. coli* J96 PAI protein or polypeptide is isolated from the transfected or transformed cells described above using an art-known method. The protein can also be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler and Milstein, *Nature 256*:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol. 70*:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis,

3NSDOCID <WO 9822575A3 IA>

L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than other molecules and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab. 33*:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall (*See* Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973)). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2nd ed., Rose and Friedman, (eds.), Amer. Soc. For Microbio., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample.

NSDOCID <WO 9822575A3 IA>

Table 1 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
65	2	1902	1042	gi|1655838	ORFB; putative transposase [Yersinia pestis]	100	100	861
65	3	2096	1821	gi|467612	ORF1 [Yersinia pestis]	100	100	276
63	11	7856	9238	gi|154262	transporter protein pgtP [Salmonella typhimurium]	98	93	1383
65	4	2889	1915	gi|1655837	ORFA; putative transposase [Yersinia pestis]	97	96	975
138	1	2	172	gi|1208992	unknown [Escherichia coli]	97	78	171
64	6	4075	4338	gi|1143207	Description: IS630 insertion element; ORF5 protein; Method: conceptual translation supplied by author [Shigella sonnei]	92	92	264
67	1	1	273	gi|809648	ExeF gene product [Aeromonas hydrophila]	92	71	273
73	4	3029	2511	gi|799234	glucose-1-phosphate thymidylyltransferase [Escherichia coli]	92	86	519
73	5	3139	2996	gi|454900	rfbC gene product [Shigella flexneri]	92	92	144
64	5	3741	4088	gi|47542	ORF (343 AA) [Shigella sonnei]	91	85	348
73	3	2613	2242	gi|46985	glucose-1-phosphate thymidylyltransferase [Salmonella enterica]	91	82	372
90	1	1	366	gi|38826	ExeE gene product [Aeromonas hydrophila]	91	77	366
91	2	604	248	gi|609625	putative [Vibrio cholerae]	91	67	357
63	9	6301	5234	gi|858753	regulatory protein pgtB [Salmonella typhimurium]	89	84	1068
73	2	2179	1811	gi|294899	dTDP-6-deoxy-L-mannose-dehydrogenase [Shigella flexneri]	89	84	369
90	2	201	689	gi|38826	ExeE gene product [Aeromonas hydrophila]	89	80	489
95	2	1519	413	gi|581654	dTDP-glucose 4,6-dehydratase [Salmonella enterica]	88	81	1107
96	1	729	457	pir|S43483|S434	Orf104 homolog - Escherichia coli	88	72	273
63	6	4281	3019	gi|154255	phosphoglycerate transport system activator protein [Salmonella typhimurium]	87	79	1263
67	2	251	745	gi|609628	putative [Vibrio cholerae]	87	72	495
82	12	5254	4406	gi|1208992	unknown [Escherichia coli]	87	74	849
60	1	693	4	gi|609625	putative [Vibrio cholerae]	86	57	690
95	1	428	3	gi|508238	dTDP-6-deoxy-L-mannose-dehydrogenase [Escherichia coli]	85	74	426
64	7	4336	4731	gi|47542	ORF (343 AA) [Shigella sonnei]	84	81	396
80	8	2800	2582	gi|38832	ExeK gene product [Aeromonas hydrophila]	84	53	219
82	10	4380	3829	gi|1033137	ORF_o152 [Escherichia coli]	84	72	552

SUBSTITUTE SHEET (RULE 26)

Table 1 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
63	8	5399	4830	sp|P37433|PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-).	83	75	570
63	10	7572	6259	gi|154258	regulatory protein pgtC [Salmonella typhimurium]	83	78	1314
65	7	3351	3100	gi|1196999	unknown protein [Transposon Tn3411]	82	80	252
100	1	337	2	gi|41004	URF 2 [Escherichia coli]	82	64	336
138	2	109	429	gi|1033128	ORF_o273 [Escherichia coli]	80	62	321
74	4	1331	831	gi|38826	ExeE gene product [Aeromonas hydrophila]	79	62	501
63	7	4873	4256	sp|P37433|PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-).	78	72	618
70	13	5759	5529	gi|1773143	Hha protein [Escherichia coli]	78	58	231
91	3	1154	534	gi|609625	putative [Vibrio cholerae]	77	65	621
75	5	3524	3255	gi|463911	heat resistant agglutinin 1 [Escherichia coli]	76	62	270
63	1	2	667	gi|1574313	H. influenzae predicted coding region HI1472 [Haemophilus influenzae]	75	56	666
104	2	485	315	gi|530438	arabinose transport protein [Mycoplasma capricolum]	72	41	171
63	3	2180	1629	gi|622948	transposase [Escherichia coli]	71	60	552
63	12	9688	10005	sp|P39213|YI91_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN	71	57	318
61	3	1283	876	gi|581535	ORF140 gene product [Rhizobium sp.]	70	54	408
84	3	2361	3437	gi|1772623	HecA [Erwinia chrysanthemi]	70	60	1077
91	1	300	4	gi|295430	epsE [Vibrio cholerae]	70	49	297
74	1	541	2	gi|609627	putative [Vibrio cholerae]	69	54	540
67	4	1297	1581	gi|151469	PilD-dependent protein [Pseudomonas aeruginosa]	68	50	285
84	1	578	1741	gi|1772622	HecB [Erwinia chrysanthemi]	68	54	1164
84	2	1698	2363	gi|1772622	HecB [Erwinia chrysanthemi]	67	48	666
63	2	1734	1393	gi|1323798	transposase [Plasmid pRL1063a]	65	46	342
71	1	1134	4	gi|397405	kpsE gene product [Escherichia coli]	65	36	1131
64	2	2828	1839	gi|310632	hydrophobic membrane protein [Streptococcus gordonii]	64	38	990
74	2	861	355	gi|148436	secretory component [Erwinia chrysanthemi]	64	54	507
66	1	556	2	gi|1235662	RfbC [Myxococcus xanthus]	62	39	555
70	6	3017	2814	gi|1657478	similar to *E. coli* ORF_o208 [Escherichia coli]	62	41	204

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26) <WO 9822575A3 IA>

Table 1 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
85	1	278	66	pir|A45253|A452	activator 1 37K chain - human	62	56	213
126	1	3	323	gi|1778562	hypothetical protein [Escherichia coli]	62	45	321
73	1	773	3	pir|S32879|S328	lipA protein - Neisseria meningitidis	61	46	771
96	2	796	644	gn1|PID|e276217	T03F6.f [Caenorhabditis elegans]	61	46	153
67	3	743	1312	gi|609629	putative [Vibrio cholerae]	60	43	570
70	10	4666	4292	gi|1657478	similar to *E. coli* ORF_o208 [Escherichia coli]	60	45	375
81	1	1	1179	gi|1591717	spore coat polysaccharide biosynthesis protein E [Methanococcus jannaschii]	60	44	1179
80	5	2563	1790	gi|609632	putative [Vibrio cholerae]	59	41	774
137	1	73	528	gi|1736670	Adhesin AIDA-I precursor. [Escherichia coli]	59	45	456
61	1	773	3	gi|1196968	unknown protein [Insertion sequence IS66]	58	41	771
63	5	2831	2178	gi|622948	transposase [Escherichia coli]	58	41	654
64	3	3568	2690	gi|1335913	unknown [Erysipelothrix rhusiopathiae]	57	36	879
64	1	1819	917	gi|153826	adhesin B [Streptococcus sanguis]	55	30	903
64	9	7008	6685	gi|152259	lcrB gene product [Rhizobium sp.]	55	42	324
70	14	6481	6753	pir|G42465|G424	hypothetical protein 88 - phage phi-R73	53	30	273
85	5	9317	1530	gi|144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	7788
64	8	5063	4806	gnl|PID|e264304	F53C11.6 [Caenorhabditis elegans]	51	27	258
80	9	3411	2761	gi|149309	pulJ [Klebsiella pneumoniae]	50	40	651
88	1	98	388	gi|156087	[Brugia malayi myosin heavy chain gene, complete cds.], gene product [Brugia malayi]	50	32	291
96	3	1127	687	gi|1196964	unknown protein [Plasmid Ti]	50	38	441
89	1	981	4	gi|57633	neuronal myosin heavy chain [Rattus rattus]	48	22	978
113	1	657	199	gi|147899	extragenic suppressor [Escherichia coli]	48	25	459
118	1	654	145	pir|S27564|S275	polysaccharide translocation-related protein - Escherichia coli	48	25	510
58	2	2101	4245	gi|1235662	RfbC [Myxococcus xanthus]	47	35	2145
87	1	595	134	gi|1235662	RfbC [Myxococcus xanthus]	42	28	462
85	2	1018	515	bbs|117606	glycine-rich protein, atGRP (clone atGRP-1) (Arabidopsis thaliana, C24, Peptide Partial, 210 aa) [Arabidopsis thaliana]	36	36	504
85	3	1779	973	bbs|157676	silk fibroin heavy chain (C-terminal) [Bombyx mori=silkworms, Peptide Partial, 633 aa] [Bombyx mori]	34	29	807

SUBSTITUTE SHEET (RULE 26)

NSDOCID <WO 9822575A3 IA>

Table 2 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
58	1	1176	2120
61	2	54	560
63	4	1875	2639
64	4	3911	3627
65	6	3009	3239
65	12	6027	6683
66	2	1289	978
70	2	1418	861
70	3	1886	1476
70	4	2124	1900
70	5	2795	2220
70	7	3645	3259
70	8	4078	3680
70	9	4220	4513
70	11	4950	4498
70	12	4594	4866
70	15	6805	7449
70	16	9520	10806

Contig ID	ORF ID	Start (nt)	Stop (nt)
73	7	3247	3666
74	3	720	1301
75	1	1	165
79	1	719	354
80	6	2108	2575
80	7	2831	2469
80	10	3223	3387
80	11	3541	3362
82	8	3313	4260
82	11	4340	5218
82	13	6090	5614
84	4	3487	3281
85	4	1485	2285
85	6	8373	9320
104	1	358	2
112	1	677	105
142	1	3	143
142	2	119	328

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

<NSDOCID <WO 9822575A3 IA>

Table 3 (PAI V)

Putative coding regions of novel *E. coli* PAI V proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
14	3	2826	3686	gi|1655838	ORFB; putative transposase [Yersinia pestis]	100	100	861
14	2	1837	2907	gi|1655837	ORFA; putative transposase [Yersinia pestis]	99	99	1071
3	9	7927	7595	gi|1657499	putative transposase for insertion sequence IS3 [Escherichia coli]	89	85	333
20	6	3462	4304	gi|1208992	unknown [Escherichia coli]	87	73	843
6	6	3541	3263	pir|S43483|S434	Orf104 homolog - Escherichia coli	81	62	279
20	3	1616	2332	gi|1033129	ORF_o233 [Escherichia coli]	80	61	717
9	1	1	681	gi|537112	ORF_o396 [Escherichia coli]	77	55	681
15	3	1899	1672	pir|S43483|S434	Orf104 homolog - Escherichia coli	75	55	228
20	9	4302	4880	gi|1552816	similar to *E. coli* ORF_o152 [Escherichia coli]	74	60	579
14	13	12972	15359	gi|1772623	HecA [Erwinia chrysanthemi]	70	60	2388
5	3	1112	1570	gi|1001717	regulatory components of sensory transduction system [Synechocystis sp.]	68	45	459
3	1	2572	1373	gi|849022	Lactate oxidase [Aerococcus viridans]	66	46	1200
3	8	6869	6498	gi|581535	ORF140 gene product [Rhizobium sp.]	66	45	372
6	5	3265	2951	gi|642184	F19C6.1 [Caenorhabditis elegans]	66	44	315
14	12	11775	12974	gi|1772622	HecB [Erwinia chrysanthemi]	66	50	1200
20	1	545	1450	gi|1033127	ORF_o289 [Escherichia coli]	66	45	906
57	1	696	124	gi|1772622	HecB [Erwinia chrysanthemi]	66	47	573
3	3	3320	3700	gi|431950	similar to a B. subtilis gene (GB: BACHEMEHY_5) [Clostridium pasteurianum]	65	34	381
5	7	4565	4239	sp|P39213|YI91_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN.	65	38	327
22	2	1651	557	gi|290430	adhesin [Escherichia coli]	64	48	1095
5	4	1455	1841	gi|1575577	DNA-binding response regulator [Thermotoga maritima]	61	47	387
14	11	11161	11937	gi|1772622	HecB [Erwinia chrysanthemi]	60	39	777
14	1	930	1700	gi|1657478	similar to *E. coli* ORF_o208 [Escherichia coli]	58	47	771
5	6	3834	3391	gi|155032	ORF B [Plasmid pEa34]	56	36	444
3	5	6500	5982	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma- associated herpes-like virus]	54	25	519
14	7	8429	8809	gi|1196729	unknown protein [Bacteriophage P4]	54	41	381

Table 3 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
14	14	15191	21793	gi|144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	6603
14	16	21427	22671	bbs|117613	glycine-rich protein, atGRP (clone atGRP-4) [Arabidopsis thaliana, C24, Peptide Partial, 112 aa] [Arabidopsis thaliana]	52	39	1245
5	2	1004	381	gi|48518	HydC [Wolinella succinogenes]	51	34	624
5	5	1941	3311	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	51	21	1371
14	4	3968	5431	gi|1033120	ORF_o469 [Escherichia coli]	51	29	1464
32	1	481	227	gi|1673731	(AE000010) Mycoplasma pneumoniae, fructose-permease IIBC component; similar to Swiss-Prot Accession Number P20966, from *E. coli* [Mycoplasma pneumoniae]	50	41	255
20	17	7039	7284	gi|1123054	coded for by C. elegans cDNA CEESN53F; similar to protein kinases including CDC15 in yeast [Caenorhabditis elegans]	48	28	246

SUBSTITUTE SHEET (RULE 26)

ISDOCID <WO 9822575A3 IA>

Table 4 (PAI V)

Putative coding regions of novel *E. coli* PAI V proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	1	809	1165
3	2	3275	2640
3	6	6006	6425
3	7	6423	6833
4	1	3	455
5	1	501	4
6	1	2168	1749
6	2	2527	2114
6	3	2648	2331
6	4	3099	2626
14	5	7112	7699
14	6	7800	8507
14	8	9040	9624
14	10	10586	10846
14	15	21721	20921
15	1	575	826
15	2	850	1365
20	2	904	605
20	4	2330	3157
20	5	3139	3396
20	7	3812	3492
20	8	4373	3828
20	18	7282	7950
22	1	356	3
24	1	492	4

NSDOCID <WO _ 9822575A3_IA>

SUBSTITUTE SHEET (RULE 26)

SDOCID <WO 9822575A3 I>

Table 5 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
59	1	968	54	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	99	790	915
59	2	1551	805	emb|Y00529|ECPA	*E. coli* papC gene involved in formation of pap pili	99	518	747
59	3	1742	1494	emb|Y00529|ECPA	*E. coli* papC gene involved in formation of pap pili	99	182	249
61	4	1975	1220	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	100	69	756
63	13	10097	10480	gb|AE000133|	Escherichia coli from bases 263572 to 274477 (section 23 of 400) of the complete genome	91	216	384
65	1	886	671	gb|U06468|	Escherichia coli 0111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	93	164	216
65	5	3218	2868	gb|U06468|	Escherichia coli 0111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	85	285	351
65	8	4064	3216	gb|U06468|	Escherichia coli 0111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	86	145	849
65	9	4939	4337	emb|Y00976|ECHN	*E. coli* hns gene for DNA-binding protein H-NS (5'-region)	96	53	603
65	10	4919	5266	emb|Y00976|ECHN	*E. coli* hns gene for DNA-binding protein H-NS (5'-region)	98	310	348
65	11	5206	5781	gb|AE000133|	Escherichia coli from bases 263572 to 274477 (section 23 of 400) of the complete genome	89	431	576
68	1	1575	1315	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	100	186	261
	2	2468	1848	emb|X51704|ECPA	Eschericia coli papJ gene for PapJ protein	99	621	621
68	3	2232	2594	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	99	363	363
68	4	3212	2466	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	100	747	747
69	1	300	4	gb|M14040|	*E. coli* apt gene encoding adenine phosphoribosyl-transferase (APRT), completed cds	98	225	297
69	2	383	117	gb|M14040|	*E. coli* apt gene encoding adenine phosphoribosyl-transferase (APRT), complete cds	95	162	267
70	1	832	149	gb|U09857|	Escherichia coli 4787 o115:v165:f165 fimbrial regulatory f1652I, f1652B and f1652 A genes, complete cds	89	225	684
70	17	10799	11767	gb|AE000291|	Escherichia coli, asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	95	553	969
70	18	11809	11045	gb|AE000291|	Escherichia coli, asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	94	595	765
70	19	12022	15222	dbj|D90838|D908	*E. coli* genomic DNA, Kohara clone #348 (44.5-44.9 min.)	89	2667	3201

SUBSTITUTE SHEET (RULE 26)

SDOCID <WO 9822575A3 IA>

Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
70	20	15316	16836	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	1488	1521
70	21	16722	17711	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	82	990
70	22	17426	16776	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	63	651
72	1	12	1061	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1024	1050
72	2	947	1285	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	96	261	339
73	6	4437	3205	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	392	1233
73	8	6177	4555	gb|U28377|	Escherichia coli K-12 genome; approximately 65 to 68 minutes	90	1133	1623
73	9	6835	6128	gb|AE000380|	Escherichia coli, glcB, glcG, glcD genes from bases 3112500 to 3126189 (section 270 of 400) of the complete genome	93	703	708
75	2	1553	1059	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	90	385	495
75	3	2579	1566	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	464	1014
75	4	3297	2743	gb|U07174|	Escherichia coli 09:H10:K99 heat resistant agglutinin 1 gene, complete cds	81	283	555
76	1	698	3	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	693	696
78	1	382	59	gb|AE000360|	Eschrichia coli from bases 2885166 to 2897277 (section 250 of 400) of the complete genome	99	315	324
79	2	2620	1529	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1084	1092
79	3	2925	2587	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	97	322	339
79	4	3576	2923	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C,A, B and D	99	654	654
80	1	376	83	gb|U05251|	Escherichia coli polysialic acid gene cluster region 3, promoter region	93	210	294
80	2	638	210	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	347	429
80	3	1246	710	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	96	388	537

Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
80	4	1796	1182	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	397	615
82	1	1	567	emb|X74567|ECKP	*E. coli* K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	87	551	567
82	2	549	1157	emb|X74567|ECKP	*E. coli* K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	88	554	609
82	3	1500	1180	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	90	62	321
82	4	2163	1519	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	143	645
82	5	2594	2139	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	97	456	456
82	6	3000	2605	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	98	396	396
82	7	3463	3047	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	283	417
82	9	3831	3337	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	495
83	1	3	311	gb|AE000151|	Escherichia coli, ybaE, cof, mdlA, mdlB, glnK, amtB, tesB, ffs genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	99	207	309
83	2	176	433	gb|AE000151|	Escherichia coli, ybaE, cof, mdlA, mdlB, glnK, amtB, tesB, ffs genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	100	223	258
86	1	529	2	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	93	398	528
93	1	440	3	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	95	351	438
94	1	368	72	emb|X14180|ECGL	Escherichia coli glutamine permease glnHPQ operon	100	229	297
99	1	161	586	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	98	426	426
99	2	643	476	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	168	168
99	3	532	1092	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	537	561
99	4	1094	1396	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	274	303

SUBSTITUTE SHEET (RULE 26)

VSDOCID <WO 9822575A3 IA>

SUBSTITUTE SHEET (RULE 26)

NSDOCID <WO 9822575A3 IA>

Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
102	1	527	3	emb|Y00529|ECPA	*E. coli* papC gene involved in formation of pap pili	100	427	525
102	2	762	373	emb|Y00529|ECPA	*E. coli* papC gene involved in formation of pap pili	99	333	390
105	1	377	3	gb|AE000480|	Escherichia coli from bases 4277211 to 4288813 (section 370 of 400) of the complete genome	100	343	375
107	1	2	397	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	390	396
107	2	406	966	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	549	561
110	1	148	2	emb|X56175|ECSE	Escherichia coli secD and secF genes for membrane proteins involved in protein export	99	143	147
110	2	312	40	gb|M63939|	*E. coli* tRNA-guanine-transglycosylase (tgt) gene, complete cds	100	125	273
115	1	501	325	gb|AE000459|	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	98	177	177
117	1	3	302	gb|AE000506|	Escherichia coli from bases 4584059 to 4594314 (section 396 of 400) of the complete genome	100	263	300
121	1	2	250	gb|M16202|	*E. coli* papH gene encoding a pilin-like protein	98	148	249
123	1	361	2	gb|AE000379|	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	113	360
127	1	2	229	gb|AE000233|	Escherichia coli, racC, ydaD, sieB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	100	200	228
127	2	227	382	gb|AE000233|	Escherichia coli, racC, ydaD, sieB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	97	113	156
130	1	337	2	emb|X60200|ECTN	*E. coli* transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	335	336
131	1	510	79	gb|M30198|	*E. coli* recQ gene complete cds, and pldA gene, 3' end	98	304	432
131	2	743	270	gb|M30198|	*E. coli* recQ gene complete cds, and pldA gene, 3' end	99	314	474
133	1	1	258	gb|AE000115|	Escherichia coli, yabF, kefC, folA, apaH, apaG, ksgA, pdxA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	98	237	258
133	2	192	350	gb|AE000115|	Escherichia coli, yabF, kefC, folA, apaH, apaG, ksgA, pdxA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	99	115	159
135	1	103	327	emb|X02143|ECPL	Escherichia coli K-12 pldA gene for DR-phospholipase A	97	178	225
135	2	152	409	emb|X02143|ECPL	Escherichia coli K-12 pldA gene for DR-phospholipase A	98	157	258

Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
136	1	122	532	gb|AE000459|	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	97	237	411
140	1	576	244	gb|AE000291|	Escherichia coli, asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	89	329	333
141	1	445	2	gb|AE000291|	Escherichia coli, asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	77	432	444

SUBSTITUTE SHEET (RULE 26)

SDOCID: <WO 9822575A3 IA>

SUBSTITUTE SHEET (RULE 26)

BNSDOCID <WO 9822575A3 IA>

Table 6 (PAI V)

Putative coding regions of novel *E. coli* PAI V containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3	4	6150	4855	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	91	129	1296
3	10	8214	7723	emb|X02311|ECIS	*E. coli* insertion sequence IS3	76	274	492
3	11	7867	8319	emb|Z11606|ECIS	*E. coli* DNA for insertion sequence IS3	80	378	453
3	12	8462	8157	emb|Z11606|ECIS	*E. coli* DNA for insertion sequence IS3	90	267	306
3	13	8487	8663	gb|L19084|	Escherichia coli RhsD genetic element; core protein (rhsD) gene, complete cds; complete ORF-D2; complete ORF-D3	96	112	177
4	2	1441	815	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	91	577	627
4	3	923	1372	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	448	450
4	4	2343	1324	gb|AE000498|	Escherichia coli from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	244	1020
7	1	3	743	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	100	741	741
7	2	977	615	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	99	363	363
7	3	741	1214	emb|X51704|ECPA	Eschericia coli papJ gene for PapJ protein	98	459	474
8	1	438	4	emb|X60200|ECTN	*E. coli* transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	435	435
10	1	1932	2426	emb|X61238|ECPR	*E. coli* prsEFG genes for F13 pili tip proteins	97	462	495
11	1	903	1550	gb|M10133|	*E. coli* (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	452	648
12	1	2559	1531	gb|U82598|	Escherichia coli genomic sequence of minutes 9 to 12	100	1029	1029
12	2	1594	1860	emb|X13668|ECIS	*E. coli* insertion element 5 (IS5) DNA	100	267	267
12	3	1858	2235	gb|U95365|	Escherichia coli transposon IS5, transposase (is5B) gene, complete cds	99	354	378
13	1	93	1424	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	99	885	1332
14	9	9832	10515	gb|U09857|	Escherichia coli 4787 o115:v165:f165 fimbrial regulatory f1652I, f1652B and f1652 A genes, complete cds	92	225	684
16	1	1	375	gb|U07174|	Escherichia coli 09:H10:K99 heat resistant agglutinin 1 gene, complete cds	94	320	375
16	2	263	616	gb|U07174|	Escherichia coli 09:H10:K99 heat resistant agglutinin 1 gene, complete cds	98	283	354
17	1	282	4	emb|Y00529|ECPA	*E. coli* papC gene involved in formation of pap pili	98	240	279
17	2	410	174	emb|Y00529|ECPA	*E. coli* papC gene involved in formation of pap pili	100	168	237

SUBSTITUTE SHEET (RULE 26)

SDOCID: <WO 9822575A3 I>

Table 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
19	1	1	369	gb|AE000418|	Escherichia coli from bases 3550279 to 3561054 (section 308 of 400) of the complete genome	99	347	369
20	10	5401	4829	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	468	573
20	11	4874	5371	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	498
20	12	5245	5679	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	235	435
20	13	5732	6139	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	93	329	408
20	14	6316	5822	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	95	239	495
20	15	6048	6590	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	406	543
20	16	6569	7075	gb|AE000292|	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	136	507
20	19	8686	9915	gb|M67452|	Escherichia coli lysine decarboxylase (cadB, and cadC, complete cds, and cadA, 5′ end) genes	98	1205	1230
20	20	10604	11938	gb|U14003|	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	1308	1335
20	21	11940	12368	gb|M76411|	*E. coli* cadA gene, 5′ cds and cadB and cadC genes, complete cds	100	363	429
21	1	369	4	emb|X03391|ECPA	*E. coli* major pilu subunit genes genes papI, papB, papA and papH 5′-region	98	201	366
23	1	1	879	gb|U14003|	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	879	879
23	2	900	16	gb|U14003|	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	885	885
23	3	953	1186	emb|X77707|ECCY	*E. coli* ORF112, DIPZ and ORF191 genes	99	225	234
23	4	1223	2677	emb|X77707|ECCY	*E. coli* ORF112, DIPZ and ORF191 genes	97	1454	1455
25	1	536	171	emb|X60200|ECTN	*E. coli* transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	164	366
25	2	1128	562	emb|X60200|ECTN	*E. coli* transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	459	567
27	1	708	436	emb|X61239|ECPA	*E. coli* papABCDEFGHIJK genes for F13 P-pili proteins	100	252	273
28	1	309	4	emb|X77707|ECCY	*E. coli* ORF112, DIPZ and ORF191 genes	98	278	306
28	2	431	213	emb|X77707|ECCY	*E. coli* ORF112, DIPZ and ORF191 genes	96	150	219

SUBSTITUTE SHEET (RULE 26)

INSDOCID: <WO 9822575A3 IA>

Table 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
30	1	399	4	gb|M26893|	*E. coli* amidophosphoribosyltransferase (purF) gene, complete cds	98	295	396
31	1	706	170	emb|X56780|ECRR	*E. coli* terminator sequence of RNA G operon gene	99	513	537
37	1	2	400	gb|M63703|	*E. coli* pyruvate kinase type II (pykA) gene, complete cds	98	399	399
38	1	463	2	emb|X13463|ECGU	Escherichia coli gutM gene and gutR gene for activator and repressor proteins	99	363	462
42	1	413	3	gb|M64367|	Escherichia coli DNA recombinase (recG) gene, complete cds, spoU gene, 3′ end, and gltS gene, 3′ end	97	316	411
42	2	115	591	gb|M64367|	Escherichia coli DNA recombinase (recG) gene, complete cds, spoU gene, 3′ end, and gltS gene, 3′end	98	266	477
46	1	2	277	emb|X77707|ECCY	*E. coli* ORF112, DIPZ and ORF191 genes	98	187	276
48	1	1	171	gb|AE000491|	Escherichia coli from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	162	171
48	2	105	464	gb|AE000491|	Escherichia coli from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	144	360
49	1	2	172	gb|U00800|	Escherichia coli cloning vector Pk184, complete sequence, kanamycin phosphotransferase (kan) and (lacZalpha) genes, complete cds	98	167	171
50	1	414	4	gb|AE000341|	Escherichia coli, glyA, hmpA, glnB, yfhA, yfhG genes from bases 2677406 to 2687636 (section 231 of 400) of the complete genome	99	411	411
52	1	2	307	emb|X60200|ECTN	*E. coli* transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	284	306
53	1	280	41	gb|M36536|	*E. coli* htrA gene, complete cds	100	131	240
53	2	558	214	gb|M36536|	*E. coli* htrA gene, complete cds	99	315	345
54	1	9	263	gb|AE000381|	Escherichia coli from bases 3125914 to 3136425 (section 271 of 400) of the complete genome	94	111	255
55	1	1	675	gb|AE000179|	Escherichia coli, modA, modB, modC, ybhA, ybhE, ybhD genes from bases 794199 to 805132 (section 69 of 400) of the complete genome	98	332	675

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications recited herein are hereby incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Human Genome Sciences, Inc.
9410 Key West Avenue
Rockville, Maryland 20850
United States of America

University of Wisconsin
1300 University Avenue
Madison, Wisconsin 53706
United States of America

APPLICANTS/INVENTORS: Dillon, Patrick J.
Choi, Gil H.
Welch, Rodney A.

(ii) TITLE OF INVENTION: Nucleotide Sequence of *Escherichia coli* Pathogenicity Islands

(iii) NUMBER OF SEQUENCES: 142

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Ave., N.W., Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
(B) FILING DATE: 22-NOV-1996 AND 14-OCT-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.074PC02/EKS/CBM

(vi) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

NSDOCID <WO_9822575A3_IA>

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CNTANATTAG GCCTGCTNAA TGTATTTATA TCTAAAAAAA TTCGCATCCA AAAGGAATCC 60

AATCTGTACT GTTTTTTCTT GTGCTGACAT CTTCTTTTCC CTGGCTGGTA TGGCAAGTGA 120

CGGAGACAAG AGAAACGTTT TAAGCTCAGT TATCTCCGCC ATCACTTTCC ACGAATGACA 180

AGTAATTTTG CCTATTTTAA AACCATGCAA AAGGCAGGGT AAAAGGAGAA AATTCGATCG 240

AATCGATCGA CAAAATCGAT CATACATGAT GAAGATTTCT TATCGAATCC ATAAAAATAG 300

TGACAGCTAA CCGGCGTTGC AGGAACAGTC AGAAATGGGC GTTTGGGAAA GAGCCATAGC 360

ATACGTCGTC GCTGACATAG AGGAACTGTG CTTTGTTGAT AAGATCCTTT ATACGGCAAC 420

CAATCCACTG GACAAAAGAT GAACTACGTA ATCACCGGGT TCTCACTGAC GAAATACAGA 480

AGTTAATGAC ACAACTGTGC CATGCACCTT GTACAACAGC GGTGGAAAGC TCTCAGAACA 540

ATGGAATTGC AGAAAGGTGT TAAAACGATG AAAGCCTTCA TACCCAAATC GAATGTAAGA 600

ACGGCAGTAA AGACTGAATT GCGTAACCTT GCAGTAGCTC GAGTATTACA CTGCATAGTG 660

TGCAGGGTTA TCTCCCATCG AGAAAATATC GGCGCCAGCG AATAACGTCA CCTTAGATGT 720

AGCAGTTGCC AAATAGTGAC TCAAGGGCGG GCTTACCGCA TACACTGACA CTTAGCGGAT 780

CGACAGAATA TTATTAGCAG ATCATCACTG AACGCTACGT AATTATCGTA ATAAAGGCTT 840

TTTCTGGCTA CCAGGAAGAC CTGACATGGC TCTGCTCTGG AACCAGGCCG CAGGAAGCAT 900

CAATCTGGAG TTTATCAGCT ACTGGAATTC CGGTGTATTG GCAGCCCCTG ATAATCACCT 960

GACCCACGAA GAGCGCTCTG CTTTGCAGAA ACTCTGGGGC GGTTTGGAGA CAGGAGATGT 1020

AACGATTATA GGACGTTCTG ATGAAGTCCA TGATTTTACC TCCGCCTTAA TTAACTGTTT 1080

TCTTTCTGAA GAAGAAATTG TCTGGTGGCA ATCAGGTGGC ATTTTCCCGG ATCCTTGGCC 1140

CGCTAATATA TCCCGGCTGA ACTGACGATT AACGCGAT 1178

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCCTATTCA TTTTGCCATG ACGGGCGAAC TCCAGATAAA GGTTTTGAAA GTAATGAGAA 60

ATTATTAATT CATCCATGTT ACTGGCTTGG TTTGAATCTA AATCGTAATG CACTTGCTCC 120

AGAGGAAGCA GAGGAGATAA ATGACGAATA TGATATTAAT ATTATTTCAG ATAATTCAGC 180

CATTAGAAAT AAAACAATAG GTCAAATAAC TACTCATCTA GATCAGATAC CGATAGGAAA 240

TGAAGGTGCC ACTGAATTTG AACAATGGTG TTTAGACGCA CTAAGAATAG TATTTGCATC 300

CCACCTAACA GACATCAAGT CCCATCCAAA TGGTAACGCA GTTCAGAGAC GAGATATTAT 360

AGGCACCAAT GGTGGCAAAT CTGAWTTTTG GRAACGAGTA TTGGAGGACT ATAA 414

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGGATCTG GTACANTCCA CCCAGCGGCA TTATCCNGAA GGCAATATTT TTAAGGATTA 60

TTCGTCCACA AAATCAGTAC TGGAACCAGG CTCAAAAAAG GCTTTAACGT GACCTGCTNC 120

CATCTACAGT AGATGTACAA CCTGTTAAGT TAATTGAAAA TGGTGTTAAT CCGGTTGTTT 180

CTCCAGGGGT AGCAAGGGCC TTATTCGATA CAGTGGGTAA TGTTACTGTA AAATTACCAT 240

CATTCCCTGT GGTCACATTG CAGGTCTGAG CTACAACTTT GCCTGTAAAC GTAATTGTTC 300

CGTCATAGGC CATAGCTGAA CCAACAAACA CAGCAGAAAC AAATGTAGCC AATGCTATAA 360

CTTTTATTTT CATAAAATGA ATTCCTGTTT AATTCCGGTA TTGATCATTT GTTCAGCAAT 420

CATCCCCAAC AAAACAATCA TTTTCAAAAT GTTTTTACCG ATCGATAACC AGCACATGAT 480

AGATTGCACC TATCATGATT GCTAAAACGA TCGGGAAAAG CGATCAAAAA CCATATTTAT 540

TGTGTTGGTA ATGACAAAAG ATATGCTTTA CCCTGAAATG AGCGACCTAT TCATGAAAAT 600

ATGTAGGTCT GTATTTGATT ACTATCATTG CTATATTTCC ACTATCCAAT TTATATTTCA 660

TGATTAAAAT ATACCTTTTT ACACTATTAT TTATTTGTTG CAGCTTGCCT GGCTTTATCT 720

TATTCCGACT ATTTTATGGT AGATACAGAA TACAATTAAT TAAACTTATT TAAAGATTTT 780

ATAAATACCA TATTGGAGTT GACCGATAGA TACCTACTAA CAAGAGCAAT CACCACCACC 840

CCATGAGGTG TTTAGGAATA CAATCAATAA ACAACATCCA TGCCCGGCGA CGTACATACC 900

TGTTTGCTAT GATATCTGTT ACGCTACGCT TGCTAATTTA CTGAAACTCA GCATCTGTCG 960

ACGGAGATTC GTCCGGGCCC TGATACAACA AGGGCAAGAA AACCACCCGA AATACAGATA 1020

TTCTTATAAA AATGGATCAT ATTTCCATGT GCAAGTTCAG CTGGCATCGT CCAGAATGCG 1080

TGTCCAAGAA ATGAAGCAAA CACGGTATAC AGGCACAGAA TAATGCTCAC TGGCCGGGTG 1140

AAAAAGCCRA AAACAATCAT TAATGCTCCA ACGATTTCGA CAAGGACCAC TATTGCTGCA 1200

GTAATCGCCG GAAATATAAG CCCAAGAGAG GCCATTTTAT CGATAGTGCC AGTGAATGAT 1260

AGCAGCTTGG GAACGCCGGA TATCATATAA AGGCATGCCA GCATCAGACG GGCAAGGAGC 1320

WSDOCID: <WO 9822575A3 IA>

AACAATGCCG ACGTGTAATT TCCCATATTA AAATACCTGA TTTTATCCAC TATCAATGCT 1380

CAGTCTCCTT GTTTCTGATA AAGCCCTGAG CCAAATCCTT AAGTGTACGA GCACCACTCA 1440

GTAACATTGC CGTCCTCAGC TCCGTCTTCA GGTGCTCAAT GACACTGGCA ACGCCCCCGA 1500

CACCACCTGC TGCGATGCCA TAAAGAACAG GACGTCCGAC CGCAACAGCC GTTGCCCCAA 1560

GAGAGATAGC CCTTACAACA TCAACCCCCC TGCGAATACC GCTGTCAAAA ATGACCGGAA 1620

CTTTGTGCCC GACTCTTGCA GCAACTTCCT GCAACTGGCT GATGGCAGAA GGAACACCAT 1680

CAATCTGGCG ACCACCATGA TTAGACACCT GGATGGCATC TGCTCCTGCA TCAATGGCGA 1740

CCACTGCATC CTCACCTCTG AGGATGCCCT TGACAATGAC TGGCAGCCCG GTGATTTTTT 1800

TTACAAACTC AATATCAGCC GGGGTCAGCT CAACTTTTTG GTTAAAAAAA TCACCTTTGC 1860

CACCGTAACG GGGGTCATGA TTACCGAACG TCGCTCCTGC AGGGAAAGGC GAGCTCATGC 1920

TGAGAAAAGC ATCACTTGTC CCGGGACCAA GCGCATCCGC TGTGATAATA ATGGCTGAAT 1980

AGCCTGCCGC TTTTGCACGC TCCAGTAAAC TTCGGGTCAC ACCAGCATCC GCGTTAAAAT 2040

ACAGCTGGAA CCATTTAGGT CCTTTACTGG CTTTTGCAAT ATCCTCCAGA GAGCGGTTGG 2100

ATGCCCCTGA TGATTCATAA AGTGCCCCGG CCTTTTCTGC ACCCGCTGCA GCAATCACCT 2160

CCCCTTCCGG ATGGACGAAC ATATGCGCGC CCATAGGTGC TATCAGCAGG GGATGTTCCA 2220

GATGATGGCC CAAAAGGTCA GTCCGGATAT CAATGCTGTG GGCAGCAACT CCACTGAGTC 2280

GGTGAGGTAA CAAAGGATAA TCACTGAANT GCCTGCGGTT CTCATGATAC GTCCACTCAT 2340

CTCCAGCACC ATGAGCAATA TATGCATACG CAGCTTCCGT CATCACATCT TTTGCTGAAG 2400

TCTYCAGTCT GTCCAGACTG ATGATATGAA GAGATTTGCT GGTCGATGTA TCAGCATGTC 2460

CAGACGTTTT ACTGATGATA TGTGCCGTTG AAGATGAGAT ATTTTTGGCA AGGGCCGGCG 2520

CAGTTGACAG CCTGCGGCAG ATATTCCTAA AACGGCATTC TGAATAAAAT TACGTCGGGA 2580

AAGAGGCATA ATAAGCTCCA TATATTATAA ATAAGCCAGG TCTCCCTGGC TTATAATGAT 2640

CATGCCACGC CCTGAAGCGG GTTGGTGTTG AAGGTATAAA GGAAAATTTT CCATTCACCA 2700

TTAATTTTAC TGAGGACAAA AACTTCACGG TTCAGGTCAA TAATGGTTTT CTGCTCTTTA 2760

AAGTTCGTTA CAACAGAACC CACATGGTGG TGAGTGCGGA CAACCGCGGT ATCTCCGTTG 2820

ATCCAGATAG AGTCAAACGC AAAATCGGTC TCAAACTTTT CACGCTTGAA CAGATCATCG 2880

TACTGCCCCT GGCGTTTTTC TGTATTGTCA GCCGTCAACT TATCATTCCA CTGGGAATAA 2940

CTTTCATCAG CAAACAGGCC CAGGATGGTT TTTGTATCCC CGGCATTCAG TGCGTTCTGA 3000

TACTTGATTA TCGTGTCATA CACGTTCTTC TGCTCAGTAG CAATCTTACT GTCTGTGGAG 3060

TATTTGAATG TACCGCCGGA TTGTTCAGGT GAGCTTTCCT TCTGTGCTGT CGACGATGAG 3120

GCAGCCAGAG CATTAGAGCC GAAAAGAAGG GATGATGCCA TGACTGCTGT TGCTATAAAA 3180

TGTTTCATAT ATTCTCCATC AGTTCTTCTG GGGATCTGTG GGCAGCATAT AGCGCTCATA 3240

CTATGCTGCT GTTTCAATAT TAGCGGCAGA CGTCAGCCTT ACCGCACTAC TTATTGGATA 3300

AGAATATCAA AAGTGACCGT GAAGTCAATT TTATCACAAC ACAGAAGGCC ACTATTTATG 3360

CCCAGAAAAT ATGAATCGTC CTCATCATGC ACGAAAGACT CGTAGTTGCA GCCCGGAAAA 3420

AACTGCCAGG ACACGACAGC AGATAGCCCG GGCAGCACTT GAGGAGTTCT CTGCACAAGG 3480

GTTCGCTCGC GCCACATNCA GCAATATCAG CAAGCGCGCA GGAGTAGCTA AAGGCACGGT 3540

ATATAACTAC TTCCCAACAA AGGAATTATT GTTTGAAGCG GTTCTGAAGG AGTTCATTGC 3600

TACCGTCCGT ACTGAACTGG AATCTTCCCC CCGCCGCAAC GGGGNAAACC GTAAAAGCCT 3660

ATCTGTTGAG AGTGATGTTA CCTGCCGTCA GGAAAATTGA CGACGCATCA ACAGGCAGAG 3720

CCAGAATAGC CCACCTGGTT ATGACAGAAG GGAGCCGGTT CCCGGTAATC GCTCAGGCTT 3780

ATTTACGGGA AATACATCAG CCACTACAGC AAGCCATGAC CCAACTGATT CAGGAAGCAG 3840

CATCAGCCGG AGAGTTAAAA GCAGAGCAAC TGCTCTGCKT CCCCTGTTTA TTGCTGGCTC 3900

CAAACTGGTT TGGCATGGTG TATAACGAAT TCTGAACCCG GCAGCACCGG TCAGTACAGG 3960

CGATCTTTTT GAAGCCGGAA TTGGTGCTTT TTTCCGATAG ACACATAACT GTCAGTATTA 4020

TGACCATGCC GTCAGGAGGA GGTATACCAG TGATACCCTG CCATGACCCG GTAACGTCTC 4080

CTGGCTGCCT TAAACCTGAA AGACCTGGCC CCACCACACT GCCGGTTACG CATCAAGATG 4140

CAGCAACCCT TGCATAAGGC TGTTTTGTGC AGAGGGCTAC CGGAAAGATA ATAACGTCAC 4200

AGCCCGTATG CATCAGATAA AACAGTGTAT TTTATCTGTC AGCAGTCACT GGAGCGGATT 4260

GTGGGGCGAG ATTCAGGTGC TGATACTGTA ACGACTCTGC GCCGCTGCTG CGGTAAAAGC 4320

GGCTGCCACC AGGCACGGTT ATCAGAGGAG GATGACCGTG TCCGCCCCTG GTGGTGATGA 4380

ACTCTCCATC ACAATCAATA ATGCCGCCGG GTGGATGAAG CAGACAGGGA TGGCAAGTCC 4440

CACTATCCCG GATAAAATGG GCTCTGGGCG CTCAGAAGAC CTGTGTGTCA GGCAGGGGTG 4500

AGAACGGTGA TGTTTTTTGT TGTCTGAAAG TCCAGCTCCA GCATTGCCTG CCAGCCTCAA 4560

GACTTCCGCT TTCTGCCCTT TCCGGCATTT TCTTCCGTTA CCATCATTCT GTTAATTCAG 4620

AGGCGTAGTA GTAGTAAACG TAATACATAT CCGGGAGGAT GAAGTCATCT AATCCTGCTC 4680

CCCGAATATC ATACAGCCAT TCCTGAGTGT GACTGCACCA TTTCCAATTA TGCAGTCTGT 4740

CCTCATCACA AAAATGTTGC AAGCAGTGCG GAGTCACGTT CCGTATTCAT GCCCTCTGCC 4800

AGATATTGAG CGGGGGAGAA ATGTGTAAGC GTCAACAGAG CGCCGTATTG ACACTTATTT 4860

ATCGGTGAAA ACTACGTTCC ATGGCAGCAG TTCGTCAACA CGGTTGGAGG GCCATTCCGG 4920

CAGTACGCTC AGGATATGGC GCAGATACGC TTCTGGATCG ATACCGTTCA ACCGACAGCT 4980

CCCGATTAGT CCGTACAGCA GAGCTCCGCG CTCGCCTCCA TGATCGTTGC CGAAGAACAT 5040

GTAATTCTTT TTCCCGAGAC AGACGGCACG AAGCGCTCTT TCTGCTGTGT TATTGTCCGC 5100

CTCCGCCAGA CCGTCATCAC TGTAATAACA GAGGGCGTCC CACTGATTCA GGACATAGCT 5160

3NSDOCID <WO 9822575A3 IA>

GAACGCTTSR CCCAGTCTGG ATTTTTTCGA CAACGTGCCA TTCTTCTCCA CCATCCATTC 5220

ATGCAGCGAC GTCAGTAACG CTTTGCTTCG CTGCTGCCTG GCTGCAAGAC GTTCAGACTC 5280

CGGTAAGCCC CGTATTTCAT CMTCAATGGC GTACAGTTCA CTGATGCGCT TCAGAGCTTC 5340

TTCTGCCGTC GTACTTTTGC TGCTGATGTA TACATCGTGG ATTTTTCGCC GGGCATGGGC 5400

CCAGCACGCA ACTTCTGTCA GTGCACCACC TTCACGTTCG GCACTGAACA GCCGATCGTA 5460

ACCGCTGAAT GCATCCGCCT GCAGGATACC CCGGAAGGGA CGAAGGTGTT GTACCGGATG 5520

TTTTCCCTGC CTGTCTGGTG AGTAGGCGAA CCAGACCSCC GGTGGCTCTG ATGAGCCCGC 5580

ATTCCGGTCA TCCCSGACAT ACGTCCAGAT GCGTCCTGTT TTTGCCTTTT TTCTGCCCGG 5640

TGCCAGCACT TTTACTGGTA TGTCGTCAGT GTGAACCTTG CGGGTGTTCA TCACGTAACG 5700

GTACAGGGCA TCATTCAGCG GAGTCATTAA CTGGCAGCAC GCGTCAACCC AGTTGGAGAG 5760

TAATGCACGG CTCAGTTCGG CACCCTGTCG GGCAAAGATT TCACTCTGAC GATACAGTGG 5820

CAGGTGTTCG CAGTATTTTC CCGTTAACAC GCGGGCAAGT AATCCGGAGC CCGCGATGCC 5880

GCGCTCTATC GGGCGGGACG GCGCTGGCGC TTCAACTATA CAGTCACATT TTGTACAGGC 5940

TTTTTTTACC CGAACAGTGC GGATCACTTT CAGGGCGCTA CTCACCAGTT CCAGCTGCTC 6000

AGCACTAACT TCACCCAGAT AATCCAGCTC ACTGCCACAC TCCGGGCAAC AACTTTCTTC 6060

AGGCTCCAGG CGGTGTATTT CACGGGGAAG ATGTGCTGGT AACGGACGAC GATGACGTGA 6120

TTGTCGCAAC TGGCGGGGAA CTGCGGGTCA TCCTCACGCC CACTGTAACG ATCGCTTTCC 6180

TGTTCGCGTT GTTTCAGTTG GGCCTCAGCC TGTTCAACCT CACGCTGCAG TTTTTCAGAA 6240

CGGGTACCGA ACAGCATCCG GCGCAGTTTT TCTATCTGGG CCCTCAGATG TTCTATTTCC 6300

CGCTCCTCCT CTTCGATCTT TTCTTCGGCA CGTGCCARTG CAGAGCGCAG GAAGGCCTCC 6360

GTCTCTTCAA CCAGACTCAG TTGCTGATCT TTCTGACGGA GGGCTTCAGC CTGCTCAGAG 6420

AGTAGCCTTT CCAGCTCAGT GATACGAATG AGGTATTTCC GACTCATGAC CGTTTTTATA 6480

ATCCGGCCAT GACATTTTTA CAACATTGTC AGTGCATTAA GGCGGGATGT TTTGGGTTGA 6540

CGCCAGTCCA GTTTATCGAG GAGCATTGCC AGCTGCGAGC GGGTAATGGA TACCTTACCG 6600

TCACGCACCG CAGNCCAGAT AAACTGGCCT TCCTCCAGAC GTTTGGTGAA CAGGCACAGA 6660

CCATCAGCAT CAGCCCACAG GATTTTAATC GTGTCACCCC GTCGGCCGCG AAAGATAAAC 6720

AGGTGACCGG AGAAGGGGTT CTCATCCAGC ACATGTTGTA CCTGTTCACC CAGACCGTTG 6780

AAGGATTTAC GCATATCAGT AACGCCGGCA ACCAGCCAGA TTCGAGTGTC TGATGGGAGC 6840

GAGATCATCG TCCTCTCCCG GTCAGTTCAC GGATCAACAC CGTGAGCAGC TCTGGTGAAG 6900

GATTTTCCAG CGTCATGTTA CCGTGGCGGA ACTCAACTTT ACAGGAACTG GCACTGACTG 6960

TGCTTTGTGA AGGAGTGGAT AAAAGCGGAG TAAGAGCCGC CATAGGCTCT TTCTGCTCAT 7020

CAGGCGTTAT CTCAACAGGT AATAATTCAA CGCCAGCGCC AGAAGAGGTT GTTACCGGAA 7080

GACGCCGCGA TATACGCCCT TCGTTCTGCC AGAGCCTGAG CCATTTGAAC AGGAGGTTAT 7140

CATTGATATC GTGTTCCCTG GCAATACGGG CAACAGAGGC TCCTGGTTGT GAAGCCAGTT 7200

TAACCATTTG AAGTTTAAAC TCATTTGAAA ATGTTCTGCA GGGTTCTGCG GATAATATTT 7260

TCTGTTCCAT AACAGGTGTC CACTAGTTGA AAAAGTGGGC ACCTACGTTA CCAATACTGG 7320

CTTAATGGCT ACATACGGCG GTCAGTTTAC GCTTACAGAA ATGTAATGAA CACGTCCTAC 7380

CATTAACTGA AGAGCATGGT GACGGATGAA GGAAAAAGCA GGAGTGTGTG GTGCCTCACA 7440

GATTTCCGAC ATCATAGCTG TCAACGACGG ATGAAAAGCG GCTCTTCCGC AACTTGGGTG 7500

GAAGAAAATG GATGAAACTT TCTGGTGTGA GAACCTTAAG GAAACAACAT GTTGGGTGGA 7560

GCGGACAATC CAAATGGTGA ATTACCGTCT TATATCACTG GCGCTGACAT TCCGGGCGTC 7620

TTCTCCGCCA CAACGCCATT TGCAGTGCAT CACAGGCCAG TTGTGCTGTC ATTCGCGGTG 7680

ACATCGACCA GCCAATAACG GCGCGTGACC ACAGGTCGAT GACTACTGCG AGATACAACC 7740

AGCCCTCATC GGTACGCAAG TAMGTGATGT CACCCGCCCA MTTCTGGTTC GGAGCCTGGC 7800

GCTGAAGTTC CTGCTCCAGC AGATTCTCCA ATACGGGCAG GCCATGTGCA CGGTAGCTGA 7860

CCGGGCTGAA CTTCCGGCTG CTTTCGCCCG CAGCCCCTGA CGACGCAGGC TGGCGGCAAT 7920

GGTTTTAATA TTGAACTCCG GCATTTCGTC AGCAAGGCGG GGAGCACCGT ATCGCTGCTT 7980

TGCCTCAATG AATGCCTTAT GGACAGCGGC ATCGCAGGTG AGCCGAAACT GTTGGCGCAG 8040

GCTCATCTGG TGACGACGCC TGAGCCAGAC ATACCAGCCG CTGCGGGCAA CCCGAAGTAC 8100

ACGACACATC GCTTTGATGC TGAACTCTGC CCGATGATTT TCGATGAAGA CATACTTCAT 8160

TTCAGGCGCT TCGCGAAGTA TGTCGCGGCC TTTTGGAGGA TGGCCAGTTC CTCAGCCTGC 8220

TCCGCCAGTT GTCGTTTAAG GCGGACATTT TCAGCGGCCA GTTCGCTTTC GCGCTCTGAC 8280

GAACTCATTT GTTGCTGCTG TTTACTGCGC CAGGCATAAA GCTGAGATTC ATACAGGCTG 8340

AGTTCACGGG CTGCGGCGGC CACACCGATG CGTTCAGCGA GTTTCAGGGC TTCGTTACGA 8400

AATTCAGGCG TATGTTGTTT ACGGGGCTTC TTGCTGATTG ATACTGGTTT TGTCATGAGT 8460

CACCTCTGGT TGAGAGTTTA CTCACTTAGT CCTGTGTCCA CTATTGGTGG GTAAGATCAC 8520

TCAGCAACGT ATCAAAAGTC TGTAAAATCA TGGGCGTTTC GCGTGATACA TTTTATCGTT 8580

ACCGCGAACT GGTCGATGAA GGCGGTGTGG ATGCGCTGAT TAATCGTAGT GCCGCGCTCC 8640

TAACCTTAAG AACGTACCGA TGAGGCAACT GAACAGGCTG TTGTTGATTA CGCCGTCGCT 8700

TTCCCGGCAC ACGGTCAGCA CCGGACCAGC AAACAAGCTG CGTAAACAGG GC 8752

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

NSDOCID: <WO 9822575A3_IA>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TGGTCAAAGA TGCAACTGCA TTTCGTCGCG GCTTTGCGGC AAATACTTAC ATCGCAGAAA 60

TACTGTGCGG AAATCTGCAT CCATTTCCAC TTGCTGTATG GCATAACTTT TCAGGCGGTC 120

CGGATACTGC CGAAGATTAT TATGCCACAT ACCACCCGTT ATGGGGGCAA TATCCGGAAG 180

CATTGCTGTT TGTAAACTGG CTCTATAATC ATTCCTCTGT GCTGCATGAA CGGGCAGAAA 240

TCATTAAATG CGCCGAAATG CTGATGCAGG AAGATGATTT CGAAATATGC GAAAGTATTT 300

TAAGACAGCA GGAGAAGTTG CGTGAAAGAA TTGATGAGAC GCTTTCTGAG AAAATTGTAC 360

AGAAATGCAG AAATATGAAT GGTGAATATG TCTGGCCCTG GATATTGCCG TTTTCAGCGG 420

CAGGCATGAA ACATACTGGC ATACAGTATC AGTAGATATT GCATTAGTGT ATCCTGCACA 480

CAAGTAATAA TTTATCCACC AATAATAACA CTGTTAATGT CCCCTTCCCC TGGTTGTCAG 540

CCAGGGGTTA TCTTCTGAAT ATTTCTTTTG AAAAGGATAA CACAATAAAT TATTTTTATG 600

AATTATCCCA TGGACTCATT AACACCCTTT CATAATGTTT TATTGTCAAA CACGTTATGG 660

CTGACATCAA AAAAAACCGG ATTTCCTCTG CCAGCGGGTA ATCACCTCCC CGGTGTTTTC 720

GGTTGGTCTG GTTACTCCTG TCTGGTTATT AGCAAGATAA TTGCTATAAA CAGTGGAAAA 780

CTCATCGTAC ATAATCTGGT GATGAACATT ACGCTTATTT TCCCTTGACC GGAAGAATCA 840

GAGGCTGCGG TTTCAGACTG TCTGCCGGTA CATTCCTCTC TCCGTTAAAA ACCATAATGG 900

GTTCATTATC TTCGTCTGTC AGTAGATTGA ATGGCGGTAT ATTTTCAGTA CGAATGCCGG 960

TCAGCCACTG AAAAATACCT GCGAAATGAC GGGCACTGAT TTTTCTGCTG ACGGACTGAT 1020

GAGACGTGAT GTCACTGGCG GTAATAATCA GGGGAACGCT GTAGCCTCCC TGCACATGAC 1080

CATCATGATG AACAGGATTA GCACTGTCGC TGACCGACAG CCCATGGTCA GAAAAGTAAA 1140

GCATGACGAA ATGACGGGAA TGCCGGCGAN GGATACCATC AAGCTGACCG AGAAAGTTAT 1200

CCAGTTTACT GATGCTGGCG AGGTAACAGG CAACCTTTCG GGGATACTGC TCCAGGTAAT 1260

GATTCGGCCA GGAGTGAAGC CGGTCACACG GGTTCGGATG AGACCCCATC ATGTGCAGGA 1320

ATATCACCTT CGGAGAGGAT TTATCCGCCA GCGCACGTTC TGTTTCCTGT AACAACAACA 1380

TGTCATCCGT TTTACGGGAA GCGAATGCSC TTTCTTGAGG AAAACGGTAT GCTCCGCATC 1440

AGAAGCAATA ACAGAGATGC GTGTGTCATG CTCTCCCAGT TTTCCCTGAT TGGATATCCA 1500

CCATGTGCTG TATCCTGCTT TTGCTGCCAG CGCCACCACG TTGTTGCCGG AATCAGGGTT 1560

CTGCTCATAG TCATAAATCA GTGTCCSGCT CAGGGAAGGT ACGGTACTGG CTGCTGCCGA 1620

TGTATAGCCG TCAATAAATA AACCGGGAGC TGTCATTCCA GCCACGGCGT GGTTGGCCAC 1680

GGGATAACCA TATACCGACA TATAATCCCT GCGCACACTC TCACCAGTGA CAATCACAAT 1740

CGTGTCATAT AACGGTGTTC CCCGGCCAGG ATTTTCCCAG TTGTCAGCCC CGTGCTGACT 1800

NSDOCID <WO 9822575A3 IA>

CAGTTGTTTA TAATGCTGCA TTTCACGCAA TGTGTCAGTT GTCCCCACAA CAGTTCCTTT 1860

AACCATCCGC AACGGCCAGC TGTTTACTGA GCATAATACG AACAGCAGCA GTGCCAGCCA 1920

GTTACGGTGA CCACGGCGGT GTGTTCGCCA GAAAATCACC ATGAATACCT GAATCGCGGC 1980

ACTGACCAGA AAATGATAAA CAGGAATCAT CCCGGTAAAC TCCGCTGCCT CATCAGTTGT 2040

GGTCTGCAGC AACGCGACAA TAAAACTGTT GTTGATTTTA CCGTACGTCA TACCGGCAGG 2100

CGCATACAGT GCACAACAGA ACAGAAATAA CAGCGCTGTA ATGGATGTGA GGGTATTTCT 2160

GTGTGCAAGG AGCAGAAGGA GAAACAGAAG CAGCACATTT CCTGTTGCAT TCCTCTCAGT 2220

GTATCCGCAT GCAATTGTGG TTATTGCAGA CACAACAAAA AAGAATAAAA ACAATAAAAT 2280

CCGGGGGGGG TTGCCCGGAC AAAACAGTTT TCTGATATTC ATCGGAGTAT ATCGACAACA 2340

TTATTATGAA GAGAACAGGA TAATAAAAAT CAGAAATTAT TGTAAAACAG ATAAAAGCAN 2400

CNATGCAGTA ATAGACT 2417

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGACAAAAAC CAGTTACGGT TATCACGTAC CAGCCCCCGT ATTTCCAATT TATAATCCTG 60

GCCATCAATT ACTGGGATCT CTTCTTCTCC ATAGAAGGCA TTAAAAGGGA ATGGAGTGGT 120

AATGTCCTCT GGAAGATATT CTGGTGCCAC ACTGTTTTTG CTGAACAGAA AACTTTGAAT 180

CCGGTCATTA AATCTGGATA TACGGAACAA TGCTTTTTCA ATATCATCAT TATTGCTTAT 240

ATCACAGCCA GTCAGCATCA TAATTCCCCC AAGCGTCAGT CCCTGTTGGA GTAAACGACG 300

TCTGTCCGGC GCAAGGATTT TTTCTGCATC TTTCACCACG TAATGGGCAT CACTGTCAGA 360

CAAAAAACGT TTTTTCTTCA TTAGTGACCC CGTATCATAG ATAACAATGC ACGCGGAACC 420

AATAACACCA TAACCAGGTG AATAATAATG AACAGTACCA TAATGTTCAT GCACAGAAAG 480

TGGATATAAC GCGCTGTATC ATAACCACCG RATAGTATAG TCAGAAGGGA AAACTGAACG 540

GGTTTCCATA AAACCAGACC AGACAATAGA AGAGCAGCGC CATCTAAAAT AATCAGAATA 600

TAGGCGACTT TTTGCACCAT ATTGTATTCC TGCATATTCG TATGATGCAG CTTTCCATAC 660

AGTGCCTGCG TAAGGGATTT TTTCAGTGAG GTCCATGACA GCGGGAAAAA CTTGCTCCGG 720

AAACGTCCGC TACAAATTCC CAGAGTAAGA TAGATCGTGG CATTAATCAG CAGAATCCAC 780

ATCAGGGCGA AGTGCCACAG TAACGCACCG CCAAGCCAGC CACCGAGAGT TAATGCTGCC 840

GGATAGTTAA AAGAAAACAA AGGAGAAGCA TTATAAATGC GCCATCCACT ACATATCATG 900

CCTGCGACAG TAACAGCATT AATCCAGTGG CAACAGCGTA ACCACAGAGG RTGTATTTGT 960

TTTAACGGTA ATGGCTGCAT TATGTGATCT CTGTCTGTAA ACTAAGTATA TTATGGAAAG 1020

GAATGTTCAT CACATCCTCA CAAGAGTTTA AAAAAAATGT GACAANTCAT CGTCAAATGC 1080

TGGGGTAAAA TTCAGATAAA GAATATGTGG ATAACTTTTG ATGAATAACG TAAAAAAAAT 1140

ACTGCTGATG GAAGATGATT ATGATATTGC AGCTCTGTTG CGGCTTAATC TGCAGGATGA 1200

AGGGTATCAG ATAGTTCATG AAGCGGATGG CGCCAGAGCT CGTTTATTAC TAGACAAGCA 1260

GACCTGGGAT GCCGTAATAC TTGATCTTAT GCTGCCTAAT GTTAATGGGC TGGAGATTTG 1320

CCGTTATATC CGTCAGATGA CCCGTTATCT GCCTGTGATT ATCATCAGTG CCCGTACCAG 1380

CGAAACCCAC CGCGTCCTGG GACTGGAAAT GGGGGCTGAT GACTATCTAC CGAAACCCTT 1440

TTCCATTCCT GAGCTGATTG NCCCGCATCA AAGCGTTGTT TCGTCGTCAG GAAGCCATGG 1500

GGCAAAATAT TCTCCTGGCA GGTGGACTGA TTTGCTGTCA CGGTCTGTGC ATCAATCCAT 1560

TTTCACGTGA AGTTCATTTG CATAATAAAC AGGTTGATCT TACCCCACGC GAGTTTGATC 1620

TGCTGCTCTG GTTTGCACGT CATCCTGGCG AAGTTTTTTC CCGTCTTTCA CTGCTGGATA 1680

ATGTCTGGGG GTATCAGCAT GAAGGATATG AGCATACAGT CAACACGCAT ATCAACCGTC 1740

TTCGTGCCAA AATTGAACAG GATGCAGCAG AGCCAAAGAT GATCCAGACC GTCTGGGGAA 1800

AAGGGTATAG GTTTTCAGTT GACAATGCAG GAATGCGATA AATGAATTGT AGCCTGACAT 1860

TAAGCCAGAG GTTAAGCCTA GTATTTACAG TCGTTTTGCT GTTTTGCGCC GTGGACATGT 1920

GGCGTTCATA TTTACAGCAG TAATCTGTAT GGCAATGCAA TGGTACAGCG TTTATCTGCA 1980

GGCTGGCGCA ACAGATTGTC ATCACGGAGT CTCTGCTGGA TAATCGTGGG CAGGTGAATC 2040

ACCGGACATT AAAGAGTCTG TTTGAGCGTC TGATGACGCT TAATCCCAGT GTGGAGCTGT 2100

ATATTGTCTC GCCGGAAGGT CGGCTGCTTG TGGAGGCCGC CCCTCCAGGT CATATCAAAC 2160

GTCGGTATAT CAATATAGCG CCCTTGAAAA AATTTCTCTC CGGTGCTGTC TGGCCCGTAT 2220

ATGGTGATGA TCCCCGAAGT GTAAATAAGA AAAAAGTTTT CAGTACCGCA CCGCTTTACC 2280

TGAGGGATGA TCTGAAAGGA TATCTGTATA TTATTTTACA GGGAGAGGAA CTTAATGCTC 2340

TTACTGATGC AGCCTGGACA AAGGCACTAT GGAATGCACT GTACTGGTCG CTGTTTCTGG 2400

TAGTGATATG TGGTCTGCTG TCGGGTATGC TGGTCTGGTA CTGGGTAACC CGTCCCATAC 2460

AGCAACTAAC TGAAAATGTC AGCGGGATAG AGCAGGACAG TATTAGTGCC ATTAAACAAC 2520

TGGCAATTCA GCGCCCTGCC ACCCCCCCTA GCAACGAGGT CGAGATATTA CACAATGCCT 2580

TCATTGAACT GGCCCGTAAA ATATCCTGTC AGTGGGATCA ACTTTCAGAA AGTGATCAAC 2640

AGCGCCGTGA ATTTATTGCC AATATCTCCC ATGATTTACG GACGCCATTA ACATCACTTC 2700

TGGGATATCT GGAAACCCTG TCAATGAAGT CGGATTCGCT ATCATCAGAG GACTGTCATA 2760

AATATCTGAC AACAGCTCTC CGGCAGGGAC ACAAGGTGAG GCATCTGTCC TGTCAGCTTT 2820

USPOCID: <WO 9822575A3 IA>

TTGAGCTGGC ACGTCTTGAG CATGGTGCTA TAAAACCTCA ACTGGAGCAA TTTTCTGTCT 2880

GTGAACTTAT TCAGGATGTA GCTCAAAAAT TTGAGCTCAG CATAGAAACC CGTCGATTGC 2940

AACTAAGAAT TATGATGTCA CATTCCCTGC CTCTTATCAG GGCAGATATT TCAATGATAG 3000

AGCGTGTGAT AACAAATTTA CTGGATAATG CTGTACGCCA CACACCTCCG GAAGGCTCGA 3060

TCAGGCTGAA AGTCTGGCAG GAAGATAATC GGTTGCACGT CGAAGTGGCT GACAGCGGCC 3120

CTGGACTAAC TGAAGATATG CGAACTCATC TTTTCCGGCG GGCATCAGTG TTATGTCATG 3180

AACCGTCAGA AGAGCCCCGG GGAGGACTGG GATTGCTGAT TGTACGCAGG ATGCTGGTAC 3240

TACACGGTGG TGATATCAGG TTGACTGATT CAACGACTGG AGCCTGCTTT CGTTTTTTTC 3300

TTCCATTATA ACATCAGGCG GCATATTTTG GGGTGGTTAT GTGTATCTGC CTTTGTAAAA 3360

GGGATACAAG TTCTGTAGTG GAGCACAAAA TCAGGACACC GGAATAACCT GTTTCCACTT 3420

TTCTTCATGT AAGCAAGGCG GTAAACCATC GTTGTTCGTG TGAGGTCGAT AAACGTTGTA 3480

ATAACCATTA ATCCACTGGT TTATATCACG TACCGCATGG ATAAAATCAC CATAACCACC 3540

TTTCGGAAGC CATTCATTTT TAAGGCTGCG AAAGACTCTT TCCATCGGCG AATTATCCAG 3600

GCCATTCCCT CTGCAACTCA TACTTTGCAT TACCCCATAA CGCCAGAGTA ACTTTCTGTA 3660

TTTATTGCTT TTATACTGAA CACCTTGATC TGAATGAAAC AGCAGGCGGC CATCACGCGG 3720

TCGAGTTTCC AGTCCGTTAC GCAAAGCCCT ACACACCAAC TCAGCATCAG CGGTTAATGA 3780

GAGGGCTGAA CCGATAATCC GCCGTGAATA TAAATCAACA ACGAGCGCGA GCTAACACCA 3840

TTTGTCCTGC AGGCGAATAA AACTGATGTC GCGCACCAGA CGCAGTTTGG TGCGGCGGGG 3900

TGAAATTGCC GGTTCAGTAA ATTTGGCAAT GGCGGACTTT TGTCTTCGTT TACCCGGTTG 3960

TGATGTTTAA CCGGCTGTCG ACTTGTCAGC CCTCATTCCC GCATCAGTCG TCATGCCAGC 4020

CACCGGCCTG CATCAACGCC ACTCTGGCGC AACATCTGAC TGATTGCCCG GCTACCCGGC 4080

TGCGCCACGA CTGAGAGCAT GGAAAGCCCT CACCCGGCTT CGTAATTCAA TTCTTTGCAC 4140

ATTAACAGGA CGCTTCACCT GCGCGTAATA AACGCTACGG TTAATACCGA ATAAATGACA 4200

AATAACCCAC ACTGGCCACT TTGCTTTCAG CTGTGTGATT AGCGCGACAG CTTCCCGGGG 4260

ATTTCGCTCA TCAGCACGGC AGCCTGCTTT AGTATTTCTT TTTCCATCTC AACGCGCTTT 4320

ATCTGCGCTT TAAGCTGCTG AATTTCGCGT TGTTCAGGGG TAATAGCATT ACCAGCTGGC 4380

TCAATACCCT GAAGTTCCTG CTTATACAAC CGTATCCATT TACGCAAATG GTCAGGGTTG 4440

AGCTCGAGTG CCTGCGCGAC TTCTCTGACA TCACGCTGGT ATTTAACCAC CACCTGCTCG 4500

AAAGCTTCAA GCTTGAACTC CGGGGAAAAG GTACGTTTAG TCCGACGAGT TTTGATCATG 4560

CATCACCTCA TTTTCACTGT TTTAACATTA ACAGGATTTC GAGGTGTCCT GAATTACCGA 4620

TCCACTACAA AGTACGACAG GTACTGTGGA GGTACTCCCG TAAAGACGGC CATCAAGCTC 4680

CCGCTCCGAC ATACCTGCGG GCAGAGGCCA TGAAAAGCCA GCTTTGCGAA AGCGCACGAA 4740

NSDOCID <WO_ 9822575A3_IA>

CATACCACAA GCTGTTGATT TTGGTACGCC CAGGCGACGC CCGACCACAA CCTGGGGTAA 4800

ATGTTCTTCA AAGTGAAGAC GTAAAGCTTC AGTGATCCAA GTCCGGTGTT TCATACGATA 4860

GTGTCCATTA AAAATGATGG ACATTATTTT TGTAAAACCG GAGGAAACAG ACCAGACGGT 4920

TTAAATGAGC CGGTTACATG TAATCCATAC TCATCCAAGG TTTAATTCTG ACACAATAAG 4980

AAAATATGGA AAGTCTCGCT CTAGAGATGG GGAGAGGGAT ATTGAAGTGT ATGATATTCC 5040

AAGAACTGCC GGAGATATCC TCGTAAATGG ATTTTCCAGT GCAAACTGAT AACAAATTCG 5100

AAGTCATTAT CTGCAACAAG ATTGATTGAT GTAGGGGATA TGTTAGAGCA TTATAATGCT 5160

CAAGGATTTG GCGTGATGAC ATCTGCGCCA ATTGATGCGA CACTATATGA TAAACTGGAT 5220

GCTATTTGCA GTAAGTGTAA AATAGAACAA ATAAATTTTT CAGTATTAGA GTCAGAACGC 5280

GCACTATATT ATGACGATAT ATTAAGATGC CGTTACTTTG GTAAATAMCA TAAAATTAAT 5340

CAATATGGTA ATATATCAGT TGTAATTGAT CGAAACAAAG CACATAAATG CCATCTTATA 5400

AAGATGGTGT TTKTTAAGCA TATAAAATAT ATTTTCTATA AGATATAGGG CAAACTAAAT 5460

TTCTTGACTT CTATGATGGA CTAACTAGAT ATACATGCCG CCAGTTTTTA TAAAACGACG 5520

GCATATATAA TCATTTATAT ATCTTTTGAT TTTATTCGTA ACCACTCATG TTGATCTAAA 5580

CCTATTCTTG ACAGATTAGC AACAATATCA GTTGTTATTT TTTGCGCGTA CGTTGTTTTT 5640

ATTTCCCCGA TCCATTTCAA TACTTTTGGA GTAGATATTT TTTCAACGAG TAAAGGAACG 5700

AATGAGATAT AGTCAGTATT AACTAGATTG TTCTTTTTCC CTATGATGAC ACCGTTTCCA 5760

TTTTCGACTC CAAATGAAAA TGAAATAATA TTAGAAGCTT TTGCCGGCAT TTTAATTTTA 5820

TAAAAACCGC CATATTCATC TTCGATTAAC AAATTGTAAT TATTATCGTC CAGTGTTCCC 5880

CTGAGGAATA AAAAATCGGC TTTTTCATGC AATCTGACGC TATCACATAA TGGTTGTATG 5940

CATAGATAGA CAAAATTATA TGCATCTAAA AGTAAAGTTC CTTGTTTTAA GGACACATTA 6000

TCTATATGAG AATGATATCT TAAACTCCTG CGCGTGATTT CCAGAGAGCA TAATTGCATT 6060

AACTTTTTAT CTTCTTCACC ATCTTGGCTT AAGTATTCCT TTTTACCTAA AGATGCGTGT 6120

TCAATAGCGT GTTGAATTTC TTCTAAAGAA TCAGCAGAGA GTATATTCCT TAGATGTTCT 6180

ACTGATAAGT CTTTTTGTTT TTTTCCAGTT AATAGAAAAT TCTTACAACC ATTTTTTGCA 6240

TAGTGAAAAA TAGGCCAATG GGATAAGGAG TTTTTGCTTA GAGATTTCTG GGGA 6294

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

VSDOCID: <WO__9822575A3_IA>

TATTCCTTTC TCTCCCATGA TAGGGCGAAA GGCTTTATTA CTATCCACTG CTGGTTTATT 60

AATTGCATCA TCGTCGATTA ATTTGCTGGA GGTTCCAATA GTCAACCACC TCTCTTCAAA 120

TTCATCGGTT GTCATACCTA ATCCATCATC TCTCAAGATA AGAAGATTTT CTTTCCTAAA 180

AAAATCAACT TCGACATTAT CAGCATAGGC ATCATGAGCA TTTTTAAATA ACTCACTCAA 240

GGCAGTAGGT ATACCTGCAA TTTGTTGTCT GCCAAGCATG TCCAAAGCTC GAGCCTTTGT 300

TCTTATTTTA GCCATATATC TATGAATCCT TATTAGTACA ATTTTCTATG AGATGTAGCC 360

CAAATAGTCT AGCGAGTTCG CAAGGTACAG CATTGCCGAT TTGCTTTGCC ATTGAATTCA 420

GCGAACCTTT AAAAACATAG CTTAAAGGAA ATGTTTGTAA TCTTGATGCT TCTCTTATGC 480

TAATTGCTCT ATGTTGAGTG GGGTCAGGAT GCCCAAAACG ACCATTGGAG TAACTATTAC 540

ATTTCGTCGT AAGTGTAGGC GCAGGCTTAT CCCAACTCAT TCTTCCATAA GTATCTGTGT 600

GGCCATCATA ATTTTTATGG CATTTATTAA CTAACTCTTC TGGCCAATTT CTTCTATCCC 660

CTCCTTCTGG AGTGTGCATA AKTCTTTTTA GGTTAAGAGG GCTCAGTGTT CCAGCCCTAT 720

GTAAAGGATC TTTGGGGTCG GTTTCTCCTG AACATAACTT TGTGAAGTCC TGGATATAAT 780

CTCGTACAGT TTTGAATGGG ATTTTATTTT TACCATGGGT TATCTCTGGT AGGGTAACTT 840

TACCTACTCG ACTAGCTAAG AGCACGAGTC TTTTTCTTCT TTGGGGAATC CCATAGTTCT 900

CAGCATTGGC TATAAAAGAT ATATAGTTAT ACTCTAACTC TTTAAGTAGC TTAATAAACT 960

CCTGAAATGG GCCTTCTTTT TCTTCATCAA TTTTTTGCAT TCCAGGAACA TTTTCAAGCA 1020

TAATATATTC AGGAAGAAGT TCTCTAATAA AACGATGAGT TTCATTTAGT AGATTTCTCC 1080

TTGAGTCGTC ACTAGTTTTA TTTTTATTCT GTTGCGAAAA TGGTTGACAT GGTGCACATG 1140

CACTCAGTAA CAAAGGCCGT TTAGCTTTAA TATCAATGAT GTCGGAGATA TCTTGAGGTT 1200

CGATTTTCCT AATATCATCT TGGATGAATT TTGCATCAGG GAAATTAGCT TTAAATGTTT 1260

CTGATGCTTG TTGGTCAATA TCTAATCCAA GCTCGATATC AAAGCCAGCC TGACGTAGCC 1320

CTTCACTGGC TCCACCACAG CCACAAAAAA AATCTATAAC TATCAATTTG ATACCTTCTT 1380

TGAACTAAAT AAAACAACTC GAATAAGTTG ATATTTTAAA TAAAAATAAT TGGTATGGAT 1440

ATGAACTTTG GTCACGCTAC CGCCCTGAGK TCATGGCCAT CCCCAGACCT TTTAAAGGGA 1500

TTATGAACAA CACCCAGCCG ACGTTCAACG GTGTTACCCA TACATATCAC AAAGTTAGTT 1560

AATTGGTTGG TCGTAAATTG ACCTAAAATG GATTGAGGGC AATGCAAAAA TCATTGGGAA 1620

ATCCAGGCGA CACAGATGTT CGGAAGAGAC TGAATGTTAA AAATATAGAA TGTATATTCT 1680

CAAAAAAGAG ATATTTCATT ACATTTTATA TGTGTATAGG AAAGTGAGAT TGGCGAATCA 1740

CCTCCCAATC ATCCCGCCAG CGCTCCATTC AGCGCCACGC CAACCCTCAC TCCAGCCCAC 1800

GTCATCGCCC CCAGCCAGAA TGTCGGCAAC ACCAGAAACA TCAACCTCAT CACCAGATTG 1860

ATAATCACGT CATCCTGCGT ATTCTGGATC CCGGCTAAAT TCCAGCTACT GTGGGTATCG 1920

CTGTTGTAGA GCACATCCAG CAGCCAGCTA TCAAGCCACC GTGCCAGTTC CCACCAAAAG 1980

GTGAGGAAAA ATAGTGCAAA CTGCACAAAC GTCAGCGTCA TCACTACTTT CACATCCCAC 2040

GCCGAACAGA GCGTTATCAG CGGAATACAG ATCACCAGCG CTATTTGCAG TGCGCCTGTA 2100

CCATCGGTAG TGCCTAACGC ACGCTGTCGA ATGCCGTACA TGCCGCTATG CTGCCGAGGA 2160

TATTTCTAGC GCCGGATGCC AACCGGGTGG CGGCATTGGC GACGGTGCCA TCAACGTTAC 2220

CGCCATAGCT TGGATAAACG CGCCCATTCT GCGATACCTG CATATTTCGT TCACTGACCC 2280

GCGAGCGCAG CACGGCCTCT TCATACACTA CCTGCGACTG GTCGATTTTT TTAAACGCCG 2340

TCCAGATATC TAGGGCAGGA AGTTGCAGTA GACGGGCTTT CAGCCCAAGC GGTGTCGTCG 2400

GCCCACCGCT GTTTACAAGT GGGATAGCCG CCCGCGCCCG TATCGGCCAG CCCGGCATCG 2460

CGCGATGCAC TGTACGGCCA AGCACTGTGT GGTGAAAGCG CATGGTCGGA AAAGGCCTGT 2520

TCAGCTAACC AAGCACATCC CACCATCACA AGAATCGCCA GAAAACCAAA CTCAGTCAGA 2580

ATAACTCTTC CTGATTCAGG CTTTGCTCCT GCATTATGGC TACCACTATT GTTTGCCTGC 2640

ACGTATCATC TGATAACGGT TAATTAACTG ATTTAGCGCC ATTTCAGCCT GTTTTTGCTG 2700

CTGTTCACTG CCATTCTGGT TACGGACTTC ACCGTAGCGA CGTAACTGCT CTTCCGCCGG 2760

GATATGCCGG TTAAAAGCCT GCATGATGCC AAACACCTCC GTTTTCAGTT CACTGACCGT 2820

CATGTATTTT CCCCGCTGTT CATCCTGACG GTTCAGGCGC TCAGCCAACT GCTGTAAGCG 2880

GATCATGCCT TCGTTCCAGC CCGTCATCGC CTCTTCCGGG AGCGCACGAC TCCTTACACT 2940

CTTCTGCCAG TTATCCACCA TTTCCTGAAC ACGGGGATTG CCGGGGACAA GAACCCTCAG 3000

TTGCTGCAGC AGCTGCGCAC TGCACCGCAG GTTGTATGCT GGAGGTAATT CTGCCAGTCG 3060

CGTTATCTGC TGACCGGAAA GGGTTATCCA GTGCACTCAG GGCAGATACC GGATTCAGGT 3120

TAATTTTTTC AAACAGGGAA GCATATACGC TGTCGCCGGT ATGCGTTTCA GATACCACAC 3180

TCTCTGCGAC GTTCTTTTCT TTCTGTACAG ACATCAGCAT TTTCTGTAAG CGTACAGCGA 3240

GGGCCGTATT GACGGGGATG TGTTATTCAG CTGGCAGTGC TATGCGCCAC GGAAGCAGTT 3300

CGCTGACCCG GTTGACCGGC CAGTCTGCTA TGACGGCAAG CACATGGCGA AGGTAGCTTT 3360

CTGGATCCAC GTCATTCAGT TTGCACGTCC CGATCAGGCT GTACAGTAGC GCTCCCCGCT 3420

CACCACCATG GTCAGAGCCG AAGAACAGGA AGTTTTTACG ACCCAGACTG ACCGCCCGCA 3480

GGNCATNTTT CAGCGATGTT GTTGTCGATT TCCACCCAGC CATCGTTCGC ATAGTACGTC 3540

ATGCCGGCCA CTGGTTAAGT GCGTACGCGA ACGCCTTCGC CACCATCAGG CTGGACAGGG 3600

GACTTTCACC CCCAAGCTGC TGAACATGCC CGGCACACAA AGAAGATCTC GGCTCAGTGG 3660

CCGGGATTAG TTATACAATT ATCTGATTGA TTTTTAATAT ATCTTTTCTT AAATCATCGT 3720

TAATATCTGA CGGTTCTAGC TGGTTTATAA GTTGCCTTAT TTGGGTAAAG GTACTTTTCT 3780

GATCTTTTAG ATCTTCTCCT TTTATCGTTG ATAAAGCTGC AATTAGTTCA CCATCGTAAT 3840

ATTCACCCGC TAACGGCTCT TTAGTTAGAA CTTCCAACAC TCTTGGCATC AACTGATCAA 3900

TACATAAATT TTGTCGGATA GCGCGGCAAA GATCTTCCAC TGTTAACTTT TCAAGAGGCA 3960

CATCTATGAT ACGTTCGAAC CAGAGTTCAA GCGGTGATTG TTGCTCAGGC TCTTTTGTCA 4020

TATTGATGTT TCCAATCAAT TTACGTAAGG TAATCATATT CCATATCCTT TCAAGGCTGA 4080

TTCTATTTTA TTAATAGCAT CTGTTGCTCT GCCATACGCA GCCTGAGCTT CAGGATTGTT 4140

GACGTTTTTC AACGTATCCG CATGATTTCT TAATCCTCTG AGCGTATTTT GCATTTCCTG 4200

CATATGATCC CAATATCCTC CATTCTCTTT AGGAACTGGC TTACCATCCA TATCCTTGAG 4260

AGTTCCAATT AATATCATGA ATCTTTTCAG ANCATTTTTT TAATAGTGGT TAATCGANTC 4320

TTCTTTAANT CGGCAACTTT TCTTGGCCTT CCTGGAATTA AAGGCTTTAA TCCTAACAAG 4380

TTTTTTTCTC AATTTTTGGC TGGCTTTAGG GAATCAATTT TTCCCGGATT GGGTGGGTGG 4440

GTGGTAACCC GGGTTTCCCT TGAAGCCCGG GAAACCCGGC CCCAAGTTCT TACTTTTTTT 4500

CCCGCAATCG GGTCAAGAT 4519

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATTACAGAAT GTGGAAATTA AGTATGATTC GAAAAAAGAT TCTGATGGCT GCCATCCCCC 60

TGTTTGTTAT ATCCGGGGCA GACGCTGCTG TTTCGCTGGA CAGAACCCGC GCGGTGTTTG 120

ACGGGAGTGA GAAGTCAATG ACGCTTGATA TCTCCAATGA TAACAAACAA CTGCCCTATC 180

TTGCTCAGGC ATGGATAGAA AATGAAAATC AGGAAAAAAT TATTACAGGG CCGGTTATTG 240

CCACCCCTCC GGTTCAGCGC CTTGAGCCGG GTGCGAAAAG CATGGTCAGG CTGAGTACCA 300

CACCGGATAT CAGTAAACTT CCTCAGGACA GGGAATCACT GTTTTATTTT AATCTCAGGG 360

AAATACCGCC GAGGAGTGAA AAGGCCAATG TACTGCAGAT AGCCTTACAG ACCAAAATAA 420

AGCTTTTTTA TCGCCCGGCA GCAATTAAAA CCAGACCAAA TGAAGTATGG CAGGACCAGT 480

TAATTCTGAA CAAAGTCAGC GGTGGGTATC GTATTGAAAA CCCAACGCCC TATTATGTCA 540

CTGTTATTGG TCTGGGAGGA AGTGAAAAGC AGGCAGAGGA AGGTGAGTTT GAAACCGTGA 600

TGCTGTCTCC CCGTTCAGAG CAGACAGTAA AATCGGCAAA TTATAATACC CCTTATCTGT 660

CTTATATTAA TGACTATGGT GGTCGCCCGG TACTGTCGTT TATCTGTAAT GGTAGCCGTT 720

GCTCTGTGAA AAAAGAGAAA TAATGTACCG CAATAACGGT TAAATGCGGG TGGGATATTA 780

TGGTTGTGAA TAAAACAACA GCAGTACTGT ATCTTATTGC ACTGTCGCTG AGTGGTTTCA 840

INSDOCID <WO__9822575A3 IA>

TCCATACTTT CCTGCGGGCT GAAGAGCGGG GTATATACGA TGACGTCTTT ACTGCAGATG 900

AGTTGCGTCA TTACCGGATA AATGAACGGG GGGGACGCAC CGGAAGCCTG ACCGTCAGTG 960

GTGCACTGCT GTCCTCACCC TGCACGCTGG TGAGTAATGA GGTGCCGTTA ARCCTCCGGC 1020

CGGAAAATCA CTCTGCGGCA GCCGGAGCAC CTCTGATGCT GAGGCTGGCA GGATGTGGGG 1080

ACGGTGGTGC ACTTCAGCCC GGAAAACGGG GCGTTGCGAT GACAGTCTCC GGCTCACTGG 1140

TAACCGGTCC CGGAAGCGGA AGTGCTTTAC TTCCTGACCG TAASCTATCC GGCTGTGACA 1200

TCTTGTTATA CAC 1213

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACGCTCTAGT ATTCTCTGTC GTTCTGCCTG GGCCACTGCA GATAGAATAG TGACAACCAT 60

TTTACCCATC TCCCCATCGG TACTGATTCC GTCATCAATA AACCGAATGG ATACACCTTG 120

GGCGTCAAAC TCTTTTATTA ACTGGATCAT GTCAGCAGTA TCGCGCCCAA GGGGTTCAAG 180

TTTCTTCACC AAGATGACGT CACCTTCCTC CACCTTCATC CTCAGCAAGT CCAGCCCTTT 240

CCGATCGCTT GAACTGCCCG ATGCCTTGTC AGTAAAGATG CGATTTGCTT TCACGCCTGC 300

GTCTTTGAGT GCCCGAACCT GAATATCGAG AGATTGCTGG CTGGTTGATA CCCGTGCGTA 360

ACCAAAAAGT CGCATAAAAA TGTATCCYAA ATCAAATATC GGACAAGCAG TGTCTGTTAT 420

AACAAAAAAT CGATTTNAAT TAGACACCNT T 451

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GACAAGGCTT ATAAACTCAC TGACGGGGCT GGCATGTTCC TGCTGGTACA TCCTAATGGT 60

TCCCGTTACT GGCGTCTCCG TTATCGTATT CTGGGTAAGG AGAAGACTCT GGCACTTGGT 120

GTGTATCCAG AAGTTTCTCT CTCCGAAGCT CGTACAAAAC GGGATGAGGC CCGAAAACTG 180

ATTTCGGAGG GGATTGACCC TTGCGAACAG AAAAGAGCTA AAAAAGTAGT CCCTGATTTA 240

CAGCTCTCTT TTGAACATAT TGCACGACGC TGGCATGCCA GTAATAAACA ATGGGCACAA 300

TCACACAGCG ATAAAGTACT CAAAAGCCTC GAAACACACG TTTTCCCCTT TATCGGCAAC 360

CGGGATATCA CAACACTCAA TACCCCGGAT CTGCTTATCC CTGTTCGTGC TGCAGAAGCT 420

AAACAAATTT ATGAAATCGC CAGTCGTCTG CAGCAAAGAA TATCTGCCGT AATGCGTTAT 480

GCCGTACAGT CTGGCATCAT CAGATATAAT CCTGCTCTGG ATATGGCTGG CGCATTGACT 540

ACGGTAAAAC GCCAGCATCG CCCCGCTCTT GATCTTTCAC GTCTGCCTGA ACTTCTGTCG 600

CGTATTAACA GTTATAAAGG NCAGCCTGTC ACCCGGCTTG CGTTGATGCT GAATTTACTG 660

GGTTTTTATT CGTTCCAGTG AACTCAGATA CGCCCGCTGG TTCTGAAAAT TGATATTGGA 720

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

NCNTTAATTT TATATCTCGT AAAATAAAAT GTTTTCTGTA CCGCTCTCCG GAGGGGGGAA 60

TGATTCGTTT ATCATTATTT ATATCGTTGC TTCTGACATC GGTCGCTGTA CTGGCTGATG 120

TGCAGATTAA CATCAGGGGA AATGTTTATA TCCCCCCATG CACCATTAAT AACGGGCAGA 180

ATATTGTTGT TGATTTTGGG AATATTAATC CTGAGCATGT GGACAACTCA CGTGGTGAAG 240

TCACAAAAAC CATAAGCATA TCCTGTCCGT ATAAGAGTGG CTCTCTCTGG ATAAAAGTTA 300

CGGGAAATAC TATGGGAGGA GGTCAGAATA ATGTACTGGC AACAAATATA ACTCATTTTG 360

GTATAGCGCT GTATCAGGGA AAAGGAATGT CAACACCTCT TACATTAGGT AATGGTTCAG 420

GAAATGGTTA CAGAGTTACA GCAGGTCTGG ACACAGCACG TTCAACGTTC ACCTTTACTT 480

CAGTGCCCTT TCGTAATGGC AGCGGGATAC TGAATGGCGG GGATTTCCGG ACCACGGCCA 540

GTATGAGCAT GATTTATAAC TGAGTCATAC CCAAATGAAT AACTGTAATT ACGGAAGTGA 600

TTTCTGATGA AAAAATGGCK CCCTGCTTTT TTATTTTTAT CCCTGTCAGG CTGTAATGAT 660

GCTCTGGCTG CAAACCAGAG TACAATGTTT TACTCGTTTA ATGATAACAT TTATCGTCST 720

CAACTTAGTG TTAAAGTAAC CGATATTGTT CAATTCATAG TGGATATAAA CTCCGCATCA 780

AGTACGGCAA CTTTAAGCTA TGTGGCCTGC AATGGATTTA CCTGGACTCA TGRTCTTTAC 840

TGGTCTGAGT ATTTTGCATG GCTGGTTGTT CCTAAACATG TTTCCTATAA TGGATATAAT 900

ATATATCTTG AACTTCAGTC CAGAGGAAGT TTTTCACTTG ATGCAGAAGA TAATGATAAT 960

TACTATCTTA CCAAGGGATT TGCATGGGAT GAAGCAAACA CATCTGGACA GACATGTTTC 1020

AATATCGGAG AAAAAAGAAG TCTGGCATGG TCATTTGGTG GTGTTACCCT GAACGCCAGA 1080

TTGCCTGTTG ACCTTCCTAA GGGGGATTAT ACGTTTCCAG TTAAGTTCTT ACGTGGCATT 1140

3NSDOCID <WO 9822575A3 IA>

CAGCGTAATA ATTATGATTA TATTGGTGGA CGCTACAAAA TCCCTTCTTC GTTAATGAAA 1200

ACATTTCCTT TTAATGGTAC ATTGAATTTC TCAATTAAAA ATACCGGAGN ATGCCGTCCT 1260

TCTGCACAGT CTCTGGAAAT AAATCATGGT GATCTGTCGA TTAATAGCGC TAATAATCAT 1320

TATGCGGCTC AGACTCTTTC TGTGTCTTGC GATGTGCCTA CAAATATTCG TTTTTTCCTG 1380

TTAAGCAATA CAAATCCGGC ATACAGCCAT GGTCAGCAAT TTTCGGTTGG TCTGGGTCAT 1440

GGCTGGGACT CCATTATTTC GATTAATGGC GTGGACACAG GAGAGACAAC GATGAGATGG 1500

TACAGAGCAG GTACACAAAA CCTGACCATC GCAGTCGCCT CTATGGTGAA TCTTCAAAGA 1560

TACAACCAGG AGTACTATCT GGTTCAGCAA CGCTGCTCAT GATATTGCCA TAAATGGTTT 1620

ATCCGGAGCC GGATAGTGTG TTGTGGATAT CTGGCATGCC CCGGGAAGTC ACCTTTCAGA 1680

CGGGCGGAGG GCTGGTGAAT TATCCGCGAT TACTGAGCAG TATGGATAAT CCTTTTTCAC 1740

AGACTTGTCA GCAGCCAGCA TTTATGTTCT TTTATCTGAG GGAATTTATC TGTACGCTGT 1800

GCCGGGATAT CTCAGTTATA CAGAAATCAG GCAGGAATAA ATTGTAGTGG AAAGTCGATG 1860

TTTACCGGAT GACTGATGCG CGCTTGTACA CAGACAGTGT GTTTCAGTAA TATGGAGAAT 1920

AATGAAATGA ATAACACAGA CACATTAGAA AAAATAATCA GACACCAAAA AAACAAAGAC 1980

CCCGCATATC CTTTCGGGAA CATTTGTTGA TGCAGCTCTG TATTCGCACA AATAAAAGAA 2040

TGCAGGATAA TATATCTGAA TTTCTGGGGG CGTATGGAAT AAATCACTCA GCATATATGG 2100

TCCTCACCAC ATTATTCGCA GCGGAGAACC ATTGTCTGTC ACCTTCAGAG ATAAGCCAGA 2160

AACTTCAGTT TACCAGAACT AATATTACCC GCATTACAGA TTTTTTAGAA AAAGCCGGAT 2220

ATGTAAAAAG GACGGATAGC AGGGAGGATC GCCGTGCTAA AAAAATCAGT CTGACATCTG 2280

AAGGTATGTT TTTTATTCAG AGGCTCACTC TTGCACAAAG CATGTATCTG AAAGAAATCT 2340

GGGATTATCT GACCCATGAT GAACAGGAAC TGTTTGAAGT CATTAATAAA AAATTACTGG 2400

CACATTTTTC TGATGCCAGC TCATAAAGTG CGAAATATCT GAGGATGCCG GATAGCTTCA 2460

GGCAAAATAA TAATGATTCT TGCAGATGTG TTTTTCCGGA TACAAAAACA AATGATAAAA 2520

ATTGCAGCGC CAGGCACCTT TCAAAGCAGG GAGACCTGTA CCGCGTCGAA AATTTCAGCC 2580

AGTTAATATC ATTGTCTGAA CCAGGCACTT TGCCCGGGCA GGAGAAGGAG TTGTGGCGGT 2640

CTCAGCCCGG AACAATTTGA AAACCATAAT CTCGCTTAGG GCCGTGTCCA CATTACGTGG 2700

GTAGGATCAC TCCTGGATTT TCTCTTTTTG GACATTGACG TCTCCATTGG TTTAAACACG 2760

GCAATGGAGA CTGCGGTGAA AAGAGTTAAT TCCCGGAGTG ACTGGCTGGA TGCCAATCAA 2820

TGATCGGAAG CATGCCAAAC TGTGAACGGA GATGGATGCC GCCAAATCAT GATCGATTCA 2880

GATGCCATAT TTGCAATATC GCGTTAATCG TCAGTTCAGC 2920

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

NSDOCID <WO 9822575A3_IA>

(A) LENGTH: 1678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGTAAGGAAG TTATATATAT GAGCAACTAT ACATCTTAGA TGTATGATAA AGAAAAAGAT 60

AACAGTTCTT TAGAATATGT ATATTGAAGA GAATGCAATA GCATGGTTTA TATAAATTAC 120

GCATAAAAAT AAGCATATGT AAGCATTTTG GTTTGCTTTT TTTAACCTGC CACCGCAATG 180

AATGCTTTTT TTATGTTAAT GTGCGTTATG AAACTAAATG CAAGAAACAT ATTTAAAGGA 240

TTAATATCGT TCTCTCACAG ACTCCGTTTA CTTATTCAAG AATATAATTT AATTTATAGT 300

GAGCTTATTA TGAATATGAA CAATCCATTA GAGGKTCTTG GGCATGTATC CTGGCTCKGG 360

GGCCAGTTCC CCATTACACA GAAACYGGCC AGTTTCTTTG TTTGCAATAA ATGTATTACC 420

TGCAATACGG GGCTAACCAA TATGCTTTAT TAACCCGGGG ATAATTACCC TGTTGCATAT 480

TGTAGTTGGG GCTAATTTAA GTTTAGAAAA TGAAATTAAA TATCCTAATG ATGTTACCTC 540

ATTAGTCGCA GAAGACTGGA CTTCAGGTGA TCGTAAAKGG TYCATTGACT GGATTGCTCC 600

TTTCGGGGAT AACGGTGCCC TGTACAAATA TATGGGAAAA AAATTCCCTG ATGAACTATT 660

CCGAGCCATC AGGGTGGATY CCAAAACTCA TGTTGGTAAA GTATCAGAAT TTCACGGAGG 720

TAAAATTGAT AAACAGTTAG CGAATAAAAT TTTTAAACAA TATCACCACG AGTTAATAAC 780

TGAAGTAAAA AACAAGACAG ATTTCAATTT TTCATTAACA GGTTAAGAGG TAATTAAATG 840

CCAACAATAA CCACTGCACA AATTAAAAGC ACACTACAGT CTGCAAAGCA ATCCGCTGCA 900

AATAAATTGC ACTCAGCAGG ACAAAGCACG AAAGATGCAT TAAAAAAAGC AGCAGAGCAA 960

ACCCGCAATG GGGGAAAACA GACTCATTTT TACTTATCCC TAAAGATTAT AAAGGACAGG 1020

GTTCAAGCCT TAATGACCTT GTCAGGACGG CAGATGAACT GGGAATTGAA GTCCAGTATG 1080

ATGAAAAGAA TGGCACGGCG ATTACTAAAC AGGTATTCGG CACAGCAGAG AAACTCATTG 1140

GCCTCACCGA ACGGGGAGTG ACTATCTTTG CACCACAATT AGACAAATTA CTGCAAAAGT 1200

ATCAAAAAGC GGGTAATAAA TTAGGCGGCA GTGCTGAAAA TATAGGTGAT AACTTAGGAA 1260

AGGCAGGCAG TGTACTGTCA ACGTTTCAAA ATTTTCTGGG TACTGCACTT TCCTCAATGA 1320

AAATAGACGA ACTGATAAAG AAACAAAAAT CTGGTAGCAA TGTCAGTTCT TCTGAACTGG 1380

CAAAAGCGAG TATTGAGCTA ATCAACCAAC TCGTGGACAC AGCTGCCAGC ATTAATAATA 1440

ATGTTAACTC ATTTTCTCAA CAACTCAATA AGCTGGGAAG TGTATTATCC AATACAAAGC 1500

ACCTGAACGG TGTTGGTAAT AAGTTACAGA ATTTACCTAA CCTTGGATAA TATCGGTGCA 1560

GGGTTAGATA CTGTATCGGG KATTTTATCT GCGRTTTCAG CAAGCTTCAT TCTGAGSCAT 1620

INSDOCID <WO__ 9822575A3_IA>

GCAGATGCAG ATACCGGRAC TAAAGCTGCC AGCAGGTGTT GGATTNACCA ACGGAANT 1678

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGGATTACT TTGGAATCTG ACAACAAAGT TACTATGAAA AAGAACTAAC AAAGTTATAT 60

AATGACGCTA AAAATGCTTT GAAAGATGTG CAATCTAAAG CAAATAGGTT AATTTCTGAT 120

AATAAGANAA AACATAAGAG TGAACTAAAA AACATTTCTT ATGAATTCCA ATCAACTAAT 180

CTCAATGGCA AAGATACTGC GTATATATTG GATGTARAAA GAAATCTAGA AAGTAAAATT 240

GAGAATACTT CAAACGAATG AGTGTAATGA AATAAGAAAA CTAACCGACC AGATTGCAAT 300

AATTAGTGAT AGTACCACTT CTGAAAATTT ATCATCGGCT CAAGTAACTG AAGCAATCGA 360

AACTGAACTT GAACATTTAC GAGACCAACA AGCAAATAAC GCAGAGTTAA TACTACTTGG 420

CATGGCTCTT TCTGTAGTAC ATCATGNATT TAATGGTAAT ATTAGGGCAA TTAGAAGTGC 480

GCTAAGGGAA TTAAAAGCAT GGGCTGACAG AAATCCTAAG CTTGATATTA TATACCAAAA 540

AATCAGAACT AGTTTTGATC ACTTAGATGG TTATTTAAAA ACCTTTACAC CATTGACAAG 600

ACGTTTAAGT CGCTCTMAAA CCAATATAAC TGGAACTGCC ATTTTAGAAT TTATCAGAGA 660

TGTATTCGAT GATCGTCTTG AGAAAGAAGG AATTGAATTA TTCACTACCT CAAAGTTTGT 720

TAATCAAGAA ATTGTAACTT ACACATCAAC CATTTACCCT GTCTTTATAA ATCTAATTGA 780

TAACGCAATA TACTGGCTTG GGAAAACAAC TGGAGAAAAA AGACTTATAC TTGATGCKAC 840

TGAAACAGGA TTTGTTATTG GTGATACTGG TCCCGGTGTT TCAACTAGAG ATCGAGATAT 900

AATATTTGAT ATGGGATTTA CACGAAAAAC AGGAGGGCGT GGAATGGGAT TATTCATTTC 960

CAAAGAGTGT TTATCTCGAG ATGGATTTAC TATAAGATTG GATGATTACA CTCCTGAACA 1020

GGGTGCTTTC TTTATTATTG AGCCATCAGA AGAAACAAGT GAATAGCGGA TATAAATAAA 1080

TGACAAGCTC TACTGATTTN CATAAACTTT CTGAAGACTG CGTTCGCCGT TTTTTACATT 1140

CTGTAGTTGC TGTAGATGAC AATATGTCTT TTGGAGCTGG TAGTGATACT TTCCCTACAG 1200

ACGAAGATAT TAATGCTTTA GTTGATCCCG ACGATGATCC TACACCAATA ATAACAGCAT 1260

CAGCATCCCC AAGGATAGAA TCAACTAAAT CAAAAGCAAA GGTAAAAAAC CATCCTTTTG 1320

ATTACCAAGC TCTAGCAGAA GCTTTCGCCA AAGATGGTAT TGCTTGTTGC GGATTATTAG 1380

CTAAGGAAGG TGCGAATAAG CGGGGAAATT CTTCTCGGCT GACTCAGTCA TTTCATTTCT 1440

TCATGTTTGA GCCGATTTTT TCTCCCGTAA ATGCCTTGAA TCAGCCTATT TAGACCGTTT 1500

CTTCGGCATT TAAGGCGTTA TCCCCAGTTT TTAGTGAGAT CTCTCCCACT GACGTATCAT 1560

TTGGTCCGCC CGAAACAGGT TGCCCAGCGT GAATAACATC GCCAGTTGGT TATCGTTTTT 1620

CAGCAACCCC TTGTATCTGG CTTTCACGAA GCCGAACTGT CGCTTGATGA TGCGAAATGG 1680

GTGCTCCACC CTGGCCCGGA TGCTGGCTTT CATGTATTCG ATGTTGATGG CCGTTTTGTT 1740

CTTGCGTGGA TGCTGTTTCA AGGTTCTTAC CTTGCCGGGG CGCTCGGCGA TCAGCCAGTC 1800

CACATCCACC TCGGCCAGCT CCTCGCGCTG TGGCGCCCCT TGGTAGCCGG CATCGGCTGA 1860

GACAAATTGC TCCTCTCCAT GCAGCAGATT ACCCAGCTGA TTGAGGTCAT GCTCGTTGGC 1920

CGCGGTGGTG ACCAGGCTGT GGGTCAGGCC ACTCTTGGCA TCGACACCAA TGTGGGCCTT 1980

CATGCCAAAG TGCCACTGAT TGCCTTTCTT GGTCTGATGC ATCTCCGGAT CGCGTTGCTG 2040

CTCTTTGTTC TTGGTCGAGC TGGGTGCCTC AATGATGGTG GCATCGACCA AGGTGCCTTG 2100

AGTCATCATG ACGCCTGCTT CGGCCAGCCA GCGATTGATG GTCTTGAACA ATTGGCGGGC 2160

CAGTTGATGC TGCTCCAGCA GGTGGCGGAA ATTCATGATG GTGGTGCGGT CCGGCAAGGC 2220

GCTATCCAGG GATAACCGGG CAAACAGACG CATGGAGGCG ATTTCGTACA GAGCATCTTC 2280

CATCGCGCCA TCGCTCAGGT TGTACCAATG CTGCATGCAG TGAATGCGTA GCATGGTTTC 2340

CAGCGGATAA GGTCGCCGGC CATTACCAGC CTTGGGGTAA AACGGCTCGA TGACTTCCAC 2400

CATGTTTTGC CATGGCAGAA TCTGCTCCAT GCGGGACAAG AAAATCTCTT TTCTGGTCTG 2460

ACGGCGCTTA CTGCTGAATT CACTGTCGGC GAAGGTAAGT TGATGACTCA TGATGAACCC 2520

TGTTCTATGG CTCCAGATGA CAAACATGAT CTCATATCAG GGACTTGTTC GCACCTTCCC 2580

TAAGAGTTTT AATGTTTGAA GAAAGAGATA TAATTACAGC ATCATCCCAC AAAGCAGATA 2640

TTACAATACC TTGACTGGGN TATTGCCAAG CGGATA 2676

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAATTTGTCC TCCGGNTCTT TTCCCGTGGA TACGGGCATT GAGACCCGAA AGGSCCTGTA 60

TTTGCGACCG GAGAGGCATC CTGGGGGCTC AGTAAACCAG TGGTCGCTGT ATGGCGGGGC 120

TGTGCTTGCC GGTGATTATA ATGNCACTGG SAGCCGGTGC CGGCTGGGAC CTGGGTGTGC 180

CGGGGACCCT TTCCGCTGAT ATCACGCAGT CAGTAGCCCG TATTGAGGGA GAGAGAACGT 240

TTCAGGGAAA ATCCTGGCGT CTGAGCTACT CCAAACGGTT TGATAATGCG GATGCCGACA 300

TTACGTTCGC CGGGTATCGT TTCTCAGAGC GAAACTATAT GACCATGGAG CAGTACCTGA 360

ACGCCCGCTA CCGTAATGAT TACAGCAGTC GGGAAAAAGA GATGTATACC GTTACGCTGA 420

ATAAAAACGT GGCGGACTGG AACACCTCTT TTAACCTGCA GTACAGCCGT CAGACATACT 480

GGGACATACG GAAAACGGAC TATTATACGG TGAGCGTCAA CCGCTACTTT AATGTTTTCG 540

GACTGCAGGG TGTGGCGGTT GGATTGTCAG CCTCAAGGTC TAAATATCTG GGGCGTGATA 600

ACRRTTCTGC TTACCTGCGT ATATCCGTGC CGCTGGGGAC GGGGACAGCG AGCTACAGTG 660

GCAGTATGAG TAATGACCGT TATGTGAATA TGGCCGGCTA CACTGACACG TTCAATGACG 720

GTCTGGACAG CTACAGCCTG AACGCCGGCC TTAACAGTGG CGGTGGACTG ACATCGCAAC 780

GTCAGATTAA TGCCTATTAC AGTCATCGTA GTCCGCTGGC AAATTTGTCC GCGAATATTG 840

CATCCCTGCA GAAAGGATAT ACGTCTTTCG GCGTCAGTGC TTCCGGTGGG GCAACAATTA 900

CCGGAAAAGG TGCGGCGTTA CATGCAGGGG GAATGTCCGG TGGAACACGT CTTCTTGTTG 960

ACACGGATGG TGTGGGAGGT GTACCGGTTG ATGGCGGGCA GGTGGTGACA AATCGCTGGG 1020

GAACGGGCGT GGTGACTGAC ATCAGCAGTT ATTACCGGAA TACAACCTCT GTTGACCTGA 1080

AGCGCTTACC GGATGATGTG GAAGCAACCC GTTCTGTTGT GGAATCGGCG CTGACAGAAG 1140

GTGCCATTGG TTACCGGAAA TTCAGCGTGC TTAAAGGGAA ACGTCTGTTT GCAATACTGC 1200

GTCTTGCTGA TGGCTCTCAG CCCCCGTTTG GTGCCAGTGT AACCAGTGAA AAAGGCCGGG 1260

AACTGGGCAT GGTGGCCGAC GAAGGCCTTG CCTGGCTGAG TGGCGTGACG CCGGGGGAAA 1320

CCCTGTCGGT AAACTGGGAT GGAAAAATAC AGTGTCAGGT AAATGTACCG GAGACAGCAA 1380

TATCTGACCA GCAGTTATTG CTTCCCTGTA CGCCTCAGAA ATAAATGAAA GTCCGGAATA 1440

TTAACGGCTG ATTGAATTGC GGTTTATGCC ATTTTCCCGG ACCAA 1485

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTACCAATTT CATCGTCCGG TACATCCTCC AGAACATCTC GCAATAAACT CTCGTCTGCC 60

TCATTCCATG CCACACCAGC ATTTGGGAAA CGAGGATCGA TCTCTCTTTC CTTCTTCTCC 120

TTCTTACTTT GCTCTTTTCG GGATGATACA GATACGACAG AACGTTCTTT TACCGCTGTA 180

ATTGCCATAA CTGCATTGAG CAGAGATCTG CGCTCCACAT CGTTCAGCAT TTTTCCTTCA 240

CAGATCAAAT CATTCAGGAT GTCAATGACT AGATTCAGAC TTTCTTCTGT TAGCTTCATA 300

TTTCAGACCT TGAAGTATGT AGATAATCAG CACAATTACT AATGTGATAA ATATCAGAAG 360

ATAATTTACA GGTAAACCGG AAAATACATC TGAAGAATAA AGGCCTCAGC TTAACGTTTC 420

SDOCID: <WO 9822575A3 IA>

AGCCAGTTTG TGAGCTGATT GAGGTACGGC GATGACATTA ACGGGAATTA CTCCCCTATA 480

GCTCTGAGCT TATTTTTCAC CCTGGCAACA TATGGTGGCT ACTGCGCATG GTTTTGGAGT 540

AGATATCTTA CTACTCGTAG AATTGTGCTT ACTGGTCAGG CCAGCGCACA GGCATTCCGT 600

GCAATCAATA GAACACTGGT TTTTTAGTCT TCCGTTACCC ATCAGGATGT TAGTGCAGAT 660

TCCGGTGTAT TCGATCAGTT GTTCGGCGAA TCAGCGATCG ATCACGATGC GATTTCGTAT 720

GTTAGGGATG CTGGTATGAT TACTCGCTGA AAAATAATGT GAAAAGGCAG TTTTTCTTTA 780

GACATTTAGC TCATTCATGC TGTTGTTTTA CGTTTTGCTG TCGTGTGCAG GATTATCTTT 840

TCGTTACGGG ACGATTCATT CCGTTTTAAT CAGGAGCTAT TGGCGTTGCT CATTGGTGGG 900

ATGCCGTAAA GTTTTACCGC GGCGATTAAT GATGTGAAGT CAATCCAAAT CAACGGAGAT 960

CTCTCATCAT GAATCAACCA ATACACAATG ATTACTGGTT ATCCCGTTTT GAAAGTATTC 1020

TCAACAGTGC CCTGGTGCAA CACCGTGCCG TCTCGTTAAT CTGGGTGGAT TTACGTTTCC 1080

CTGAGCATAT GCCTGTCACC ATCATGGATC CCGATCCGGA TTCAGCGGTG ATTTCTCGTT 1140

TTTTCGAATC CCTGAAAGCC AAAATTCAGG CTTACCAGCG GAAAAAACGA CGTACCAACA 1200

AGCGTGTGCG TGCAACCACC CTGCATTATT TCTGGTGTCG GGAGTTTGGC AAGGAAAAAG 1260

GCAGGAAACA TTATCACGTG ATATTACTGC TCAACAAAGA TACCTGGTGC TCGCCAGGGG 1320

ATTTCACCGT TCCTTCTTCG CTGGCGACGC TGATCCAACT GGCATGGTGT AGCGCTCTGC 1380

ATCTTGAGCC CTGGCAGGGT AATGGACTGG TTCATTTTTC CAGGCGGACG CYTTTCCGTA 1440

AACCGGTATC ATCTGATGCT CGCCCTTCTT CCGATGATAC GCCTTTGTCG GGTGGATGTT 1500

CTGAAACCAG GAAGGCTTCA GACAAAAAGC CGGGTGAAGC CGCTGTTCTC TGGATCAAGC 1560

GTGGTGATGT GGAAGCGATG CAGAAAGCCA TGGAGAGAGC CCGTTATCTC GTGAAGTATG 1620

AGACGAAGCA GCATGACGGT TCTGGTCAAC GTAATTATGG TTGCAGCCGT GGAGCGGGGC 1680

GTCTACTGGA TGGCAGGTGA ACCCTGTAAA ACGGCATCCG GTGCCAGAGT ATATGTCACA 1740

GTAAGGGCGT GGTTGATGCC CTTAGCTCGT TTTCTGAAAA AGTCGTCCTG AAGTCATGTG 1800

TCACGAACGG TGCAATAGTG ATCCACACCC AACGCCTGAA ATCAGATCCA GGGGGTAATC 1860

TGCTCTCCTG ATTCAGGAGA GYTTATGGTC ACTTTTGAGA CAGTTATGGA AATTAAAATC 1920

CTGCACAAGC AGGGAATGAG TAGCCGGGCG ATTGCCAGAG AACTGGGGAT CTCCCGCAAT 1980

ACGGTTAAAC GTTATTTGCA GGCAAAATCT GAGCCGCCAA AATATACGCC GCGACCTGCT 2040

GTTGCTTCAC TCCTGGATGA ATACCGGGAT TATATTCGTC AACGCATCGC CGATGCTCAT 2100

CCTTACAAAA TCCCGGCAAC GGTAATCGCT CGAGAGATCA GAGACCAGGG ATATCGTGGC 2160

GGAATGACCA TTCTCAGGGC ATTCATTCGT TCTCTCTCGG TTCCTCAGGA GCAGGAGCCT 2220

GCCGTTCGGT TCGAAACTGA ACCCGGACGA CAGATGCAGG TTGACTGGGG CACTATGCGT 2280

AATGGTCGCT CACCGCTTCA CGTGTTCGTT GCTGTTCTCG GATACAGCCG AATGCTGTAC 2340

3NSDOCID: <WO___9822575A3_IA>

ATCGAATTCA CTGACAATAT GCGTTATGAC ACGCTGGAGA CCTGCCATCG TAATGCGTTC 2400

CGCTTCTTTG GTGGTGTGCC GCGCGAAGTG TTGTATGACA ATATGAAAAC TGTGGTTCTG 2460

CAACGTGACG CATATCAGAC CGGTCAGCAC CGGTTCCATC CTTCGTTGTG GCAGTTCGGC 2520

AAGGAGATGG GCTTCTCTCC CCGACTGTGT CGCCCCTTCA GGGCACAGAC TAAAGGTAAG 2580

GTGGAACGGA TGGTGCAGTA CACCCGTAAC AGTTTTTACA TCCCACTAAT GACTCGCCTG 2640

CGACCGATGG GGATCACTGT CGATGTTGAA ACAGCCAGCC GCCACGGTCT GCGCTGGCTG 2700

CACGATGTCG CTAACCAACG AAAGCATGAA ACAATCCAGG CCCGTCCCTG CGATCGCTGG 2760

CTCGAAGAGC AGCAGTCCAT GCTGGCACTG CCTCCGGAGA AAAAAGAGTA TGACGTGCAT 2820

CCTGGTGAAA ATCTGGTGAA CTTCGACAAA CACCCCCTGC ATCATCCACT CTCCATTTAC 2880

GACTCATTCT GCAGAGGAGT GGCGTGATGA TGGAACTGCA ACATCAACGA CTGATGGCGC 2940

TCGCCGGGCA GTTGCAACTG GAAAGCCTTA TAAGCGCAGC GCCTGCGCTG TCACAACAGG 3000

CAGTAGACCA GGAATGGAGT TATATGGACT TCCTGGAGCA TCTGCTTCAT GAAGAAAAAC 3060

TGGCACGTCA TCAACGTAAA CAGGCGATGT ATACCCGAAT GGCAGCCTTC CCGGCGGTGA 3120

AAACGTTCGA AGAGTATGAC TTCACATTCG CCACCGGAGC ACCGCAGAAG CAACTCCAGT 3180

CGTTACGCTC ACTCAGCTTC ATAGAACGTA ATGAAAATAT CGTATTACTG GGACCATCAG 3240

GTGTGGGGAA AACCCATCTG GCAATAGCGA TGGGCTATGA AGCAGTCCGT GCAGGTATCA 3300

AAGTTCGCTT CACAACAGCA GCAGATCTGT TACTTCAGTT ATCTACGGCA CAACGTCAGG 3360

GCCGTTATAA AACGACGCTT CAGCGTGGAG TAATGGCCCC CCGCCTGCTC ATCATTGATG 3420

AAATAGGCTA TCTGCCGTTC AGTCAGGAAG AAGCAAAACT GTTCTTCCAG GTCATTGCTA 3480

AACGTTACGA AAAGAGCGCA ATGATCCTGA CATCCAATCT GCCGTTCGGG CAGTGGGATC 3540

AAACGTTCGC CGGTGATGCA GCCCTGACCT CAGCGATCGT GGACCGTATC TTACACCACT 3600

CACATGTCGT TCAAATCAAA GGAGAAAGCT ATCGACTCAG ACAGAAACGA AAGGCCGGGG 3660

TTATAGCAGA AGCTAATCCT GAGTAAAACG GTGGATCAAT ATTGGGCCGT TGGTGGAGAT 3720

ATAAGTGGAT CACTTTTCAT CCGTCGTTGA CATCATGCAA TGTTTCCTGG TTTTCATGCA 3780

TCCATCATTT GTCGCTGCGA TGCCAGACTT CTGGATGCAC ACATGTTGTT TTACTTTTGT 3840

CAGCATCATA AATGCGCCGG GACTGGTGAA TGGAGATAAG CCATTTTATT ATCGACGTCA 3900

GCGAACATAC TCACCATGCC GGTATGTTCC TGAACTGAAC AATAAGTTTT GCGCTGATTA 3960

CAGTATGTGA AGGAGGTCCG TTACAATGAA TTCCGCTTAT ATGCAATCCT TGCAGACATC 4020

CCACCACTTC CCAGCTGATT TAACCTACAG ATTATTTCCT AGTGAGCTTG CATATCTCAT 4080

TGACGACTTA TATGAAAGTA CCCAACTTCC GCTGGAGCTC ATTTTTAATA CTGTACTGGC 4140

AACGCTCTCA CTCTCCTGTC AGTCACTGGT TGACGTTGTT CATCCTCACA CCAACATGCC 4200

GGAACCCTGC TCACTTTATC TGTTGGCAAT CGCAGAGCCA GGCGCGGGAA AAACAACGAT 4260

AAACAGACTG GTGATGAACC CCTGTTACGA ATTTGCCGAT CGACTCATTC AACAATACGA 4320

AGAGAGAAAC AAAGATTATA AGACTGAACT ACAGATCTGG AATACCCGGC AGAAAGCGCT 4380

TGCTGCCAAT TTAAGAAAGG CTGTTAACCG GGGGTATCCG GGGGAACAGG AAGAAGAGGC 4440

GCTGCGTAAT CACGAAAGAA ATAAACCGAC ACGTCCGGTT CGACCGAATT TTATCTATGA 4500

AGATGTTTCG CTTAAAGCGC TTGTGGAAGG GCTCAATGAA CATCCTGAGG CAGGGGTTAT 4560

TTCTGACGAG GCGGTCACTT TTTTCAGAAG CTATCTGAAA AATTATCCGG GCCTGTTGAA 4620

TAAAGCATGG AGTGGACAAC CGTTTGATTT TGGACGGGCT GACGAGAAAT ACCATATCAC 4680

GCCACGTCTG ACATTTTCGT TAATGTCCCA GCCGGATGTC TTTACGAATT ATATAAATAA 4740

AAATGACGTA CTGGCGTGGG GAAGCGGATT TCTTTCCCGG TTTCTGTTCA GTCAGACCGG 4800

AAGTCCTTCC CGGGTACGGG ATTATACGAG AGGCGAGTTC AGAACAAAAC CAACCCTGGA 4860

GAAGTTTCAT AAAAAGATTA ACGGATTTCT GTTAAGCCAT AACATTAATT CCCCCGGTAT 4920

GAGCACCGAA AGGAAAACAT TAAAACTTGC AAAGAAAGCG TTGGGGGAGT GGCAGGAAAA 4980

CCAGATTAAG ATTGAAAGAA AAGCGCTTGC AGGAGGGGAG TGGGAACACA TCAGAGATAT 5040

TGTTCTGAAA GCAGGTTCTA ATATACTGAG GATAGCTGGA ATATTCACCT GCTATTGCTA 5100

TAAAGATGCT GAGGAAATTG AATCAATTGC GCTTTTTAAA GCTATGCATC TCATGGGCTG 5160

GTATCTGGAG GAGGCGAGCA CAATATTTTA TCCCATGTCT GCACGATGCC AGTTTGAACA 5220

GGATGCCTGT GAACTGTATG CATGGATTAT GACCCGAATA AGGCAGAATA ATTGGCGTGC 5280

TATCAGGAAA ACAGACATTG AAAGATATGG TCCCAATCGT CTGAGAAGAG CAGAAAAACT 5340

TACACCTGTA CTCAATCAGT TAATCGYTCA GAATTATTTC CGTATCATCM AAGATGCGAT 5400

CGCATCAGGC ACTTTATGTT TCTGCTCTTG ATAATAATGG TTACATCCTT CCTTTCGGCG 5460

CAATGTCTTA CGAACCGTTT GATATTGTTC CACCCCAGTA TAACCATAAT GCGAAAACAT 5520

ATTCCGTTGT TATTCCACCG GCATTAATTC AGTCATTTAC ACCTGATTCC TCAGCTTACA 5580

CCTTATTTTA AAACAATTTT GTGAGTAGAA AACGAAAATC ATAATCCTTC GAATGAAGGT 5640

TAATGATAAG GTGTGTTGCA TATCCTGCAC CTGTGCAAAT ATTCACCAAT CATTGGGTGT 5700

GAATGAAAAT TTCTCTGAAA AAATCGCTAT GGTAGCAACA GTAGCAGCAC ATACACTACA 5760

TCTGTGATTT GGTTTTGTTT TCATAATGAC CTGCTGTCAG AGCTGATTGA ATGCTGGGAT 5820

GTGCGCACTG GTGGAAGAGT GGTTTTCGTT TCAGATATAA CGAAAGGTAA TCGAAAGATT 5880

GTTTTAAACA TGGATTAAAG CTAATAATTA ACCATATTGT GTGAGTTTTT ATATATAAGT 5940

TTGTTTGATT CTTGCCGTGA TGAGTGCTGG GGTATATGAC GATGTCGCTC TCTTTCTGAA 6000

TAACAAATTA TTATTCGTCT GTTACTGATA AGGGATGCGA TTCATGTTTT AATAGAGGGT 6060

TGAAGAAAAT TAATTTGATA TTTTTTTGTA AGGGAATGGA ACTGTCCGGA ATATGTTCAG 6120

AACGGCGGAT TTCTCATTTC CATTCATTAA ACATGGATAA TTTTAATTTA GGTTTATTAC 6180

3NSDOCID <WO_ 9822575A3 IA>

TATTATTATA CTCACTCCCT TTTTCATACA ATCTCTATTG TTATTTACTT CCTGTCTTTA 6240

CTCACTCTCT ATCTTTACGA TTATATTCAC TCTATCGTTA CACATTCCAT TAGTATTACT 6300

CTTGTTATCG TATTCATTCC ATCCCTCAAT CATATTTACT GTAACTCATA TGATGTTCAG 6360

GTAAGTTATT CTCTACCATT CTACTGATGA TATCCATCTG TTCTCATTTT CAGTGAAACA 6420

GCAATTGATT TTAATCTTAT CCATCATGAA CTGTATTTGC TTAACAATGA TTGTTTATCT 6480

GAAGTGTTTT AACTATTCTG GTTGGAAACA ATTTCTCTGT CATCACAGAT TAACTGAATG 6540

TTTACTCTTT GATAAGGTAT CCATGATTCC GTCATGTTTA ACAGCGCAGG ATAAACAACA 6600

GAATTAACAG AGTGAATTTC TGATTATATT TGTTGCCGGT TGTATTGTTT AAGGTACTGG 6660

GTGAAAATTA TTCATCCATG GTATGTTGTC TTATGCTATC GTGTGTCGTT AACGTTCATA 6720

TCCTGGAGAA CAGATTGAAT GAGCGCATAT AAGTTTATTG CATTGGCCTT GTACACGGTT 6780

TTTACAACCA CTGAGAGCAA GTTTGTAGTT TATGATGTGA TTGGTCGCAA TATGTTTCTT 6840

AACCTTCTGG TCGTGGTGTT TTATCGCGTA TTTTGCAGTA TTTCGTGATG TTTTATTGAG 6900

TCTGTATTTT CTTTACTCCT CGTTTATCTC ATCTCTTTAG CTAATACCAT CAGATAATCC 6960

ATTTCTTTCT GCATAATGCT GCGTATCGTT AATAACCCGT CGTATCCATT CTGCTACAGC 7020

ATGCCTGATA AATACCATCT GTAAGTTATT ACCGTTTTAG ATCTGATTAT GAGCGAAAGC 7080

ATTAATTCGT TCACAGAGCT TAAAACATCA TTAACTTTCA GGAGTCATCA ACATGCCTAA 7140

ATCTTACACA CCAAACTGGT TTTTTACCGC TTTACTTGAC AATCACATCA ATCAAATGAT 7200

GGCACGCTAT TCCTGCCTGC GGGCCTTACG CATGGATTTC TTCTACAGGA AAGATACGCC 7260

CGATTTCTTA CAACCTGATC ATCGCTGGCT TGAATTGCAG TTGCGTATGA TGCTGGAGCA 7320

GGTGGAACAA TTTGAAAATA TCGTTGGCTT CTTCTGGGTG ATTGAATGGA CGGCTGATCA 7380

TGGTTTTCAT GCGCATGCGG TTTTCTGGAT CGATCGTCAG AGGGTTAAAA AAATATATCC 7440

CTTTGCGGAG CGGATTACGG AATGCTGGCG GTCTATTACG CATAACAGCG GTTCGGCACA 7500

CCGCTGCACA TATCAGCCGC ATTATACATA CAACATCAAC ATTCCTGTGC GCCACAACGA 7560

TCCTGAAAGC ATCGATAATA TTCGCGGTGC CCTGCATTAT CTGGCGAAAG AAGAGCAAAA 7620

AGACGGGCTG TGTGCTTACG GCTGCAATGA AGTTCCTGAA CGTCCTGCTG CAGGGCGTCC 7680

TCGTAAGCCT CACTTCTGAA GCTTAAGGCC TGAGCCTTCG CTCCTGGAAA CACTCCGTCG 7740

GTAAAAACTT ACCGCCTTGA TTAATGATGT GAACTGAAGT CAACGGAGAT CATTCATCCT 7800

GAACCTGCAT CCGGTGTTTT GTTCCTTGTC TTCCCGTTCT GCTTCGGTTC TTCACTTATT 7860

CCATCAATCT CATTCCGCAA GCCATAACAC GTCAGCTCAT TCACGGGCAG GACGCATTGT 7920

GGGCTGCGCA TAACGGAACA TATCTTATGA ATGCTATTCC TTATTTCGAC TATAGCCTGG 7980

CACCCTTCTG GCCATCTTAT CAGAACAAAG TCATCGGCGT CCTTGAGCGT GCGCTGCGTG 8040

AGCAGTCCGG CTCACGGATA CGGCGGATCC TGCTTCGTCT GCCGTGGGAA CATGACAACG 8100

CCTTCAGCAG CAGAAAGATC TGGTTCGGTA TGGACTTTAT CGAAACCGTC AGTGCGCTGA 8160

TGAATGCGAA ACCCGGACGC GACCTTTGCT GGCTCCTGAC CCGTCATCCG GAAAAGCCGG 8220

AATACCACGT GGTGCTGTGC GTCAGACAGG AGTATTTCGA CGGCCCCGAA CTGGATCGGT 8280

TGATACTGGA TGCCTGGAGT AATGTGCTGG GTTTCGCGTC ACCAGGTGAA GCAAAGCCGT 8340

ACCAGAAGCA GATCACCCGG GATGTGGTAC TGGATCGCCG GTCACCGGAC TGCGAAGCCC 8400

TGTTTAAGGA CCTTATCTGG GCGTTCAGTG ATTTCGCCCG CGATCGCCGT GGAGTGTGCG 8460

ATCCGGAAGC CCGTTGCCTT GCCGGCAATC CCGGTTGGCA GTGCTGAAAG CAGCACGCCA 8520

TCCCATCCCC CGTATTACCC CATTCTTCAT AAATCTCACT GAGGACATTC TGACCATGTT 8580

GACCACAACA AGCCACGACA GCGTATTGCT GCGTGCCGAC GATCCCCTGA TCGACATGAA 8640

CTACATCACC AGTTTCACCG GCATGACCGA TAAATGGTTT TACAGGCTGA TCAGTGAAGG 8700

GCATTTTCCT AAACCCATCA AACTGGGGCG CAGCAGCCGC TGGTACAAAA GTGAAGTGGA 8760

GCAGTGGATG CAACAACGAA TTGAGGAATC ACGAGGAGCA GCAGCATGAA ACGTGTTGTG 8820

ATGCCAGTAC GTTGGCAATG TGCAAAATGC CAGCGCTGGT ATTGTGGAAA TCAGCCCTGT 8880

CCCTGGTGCT GGCGACATTC CCGCTTATCT TTCCGCTGAC ACCCTCCGGT CAGCCAACTG 8940

TTAGTCATCA TTTCCTGACT GATTCGTCAT TCCATTCTTA TTGATTATAA CTGGCATTAC 9000

ACCGGTGCTG GCGTGCTTTC CTGCGTGTCT GCACCGGTTT GACAAAATTC AACAGGGTTT 9060

GAAAAGGAAC ATTTCGTGCA AATAACCGAA GCCTTAATTT CAGAGCCGGG AGACATCCGG 9120

CGTTTTATTC AACATGCTGT TGACCACTGG CCGCGTCTGC TGGCAGTCCA CTTCATACTC 9180

CATTCGACAG AAGGAAACAT CTACGGGCAA CAGATTCATG CATTCTGCAC TTCCTTTTAT 9240

CGACAACTGC ATGAACGTAT TACTGAGAGC AATCACACTG CCAGTCCATC ATCGTCGGTG 9300

GTATTACGCT GGTTGCGGGA ACAACATGGA GGAGCAACAA TTCGATGCCT GTTGCTGCTC 9360

AGCCAGACGA GTATTTGTCA CCCGCGAGCC AGTGTCACAG TTGATGAACA ATGTTCGCAA 9420

GTGGTGGATT TACTGCAACA TAGCTGGCAG GTGATAAGTG CTGGCGGACA ATGCCGGGTG 9480

GAAAGGTGTT TTCGGGTTGC CCGGGGTGAT ACATCCGGTC AGTATGTTGC GTTAAAAACA 9540

GTCGCATTGT CTCTGGGGTT ACCGGTTGTG ACCGCCATTA CCCATCGTCC GGTACAGCGC 9600

TGTACATTGA TTACAGCTCA GTGAATCAGC GCTTTCTGGC TTTTCGTCGG TCATTCTGTC 9660

AACGCCACGA TGTTTGACCG TTATGGGGAT GCGGACGATT CCCTGCACAG CGTTGTTTCA 9720

CGGTGGTGGA TGACGCAACA CCGCTGTTAA AAACAGTCGT TCAGTCCTTT GTGTTACCGG 9780

TTGTGACAAC AATCAGTTGG TAATGGACGT GTGAACCATC TGCGCTTCCG TTGATTTTTA 9840

TGGACTGATA AAGTTTTGCC AGCTGAATCT TTATACGGAA TGCTCTTCAG TATGCGTACA 9900

CGAATTGACT ATCTGGCGGA TAAATACTCT TTTACCGAAC GGAATGAATC TCCACGCCTT 9960

CGCCGGCAGT GGCAGGATGT TCTGGAGGAG TGTCGGCTGA CAGAGGCCGG ACCAGAAGAA 10020

INSDOCID <WO__ 9822575A3_IA>

CGGCTGCGTA TTGCCCTGCT GAATGTGGAT TACGTCACCA GTTTTGAACT GCCTTTTCGC 10080

TTGTTGCTTA CTCGTACACC ACAACTGATT GCCGCGCTTC GGGAAGAATG GGGCCTCAGC 10140

CAGAAAAATG TGGTGTTCAA CGATAAACGG TTTGGCTGCG TGTACAGCCT GAAGGCCAGT 10200

CTTTCTGGTG TACCGGATAC ATTCCGGTAT CATCTGTCTC ATCGTATTCG CCGGATGGTT 10260

GGGAATGAAA ATACATCATC GCCATATCAG CAGATTGCCC GGGAAGTGAA AGTGCCCCGT 10320

GAACGGCTGA AGTATGCGCT GGAAGCCGGT TTACTGGTGA CTGCACTGGA CGGGCTGTTC 10380

TGGTCTGGTA GTCAGCGCAT TGCGGCTGAT ATCCTGAGAC TGAGAAAGAG CGGAATGCCG 10440

GTGGTGACAA CGTCCGTGGA AGCGAGCGAT AACCTGACGG GAACAACCCG CAAAATACCG 10500

GCATACCATC TCTGACATTG CGATGAAGGG CAGATTTCAC CTTGACAGGG GCAGAGTGCC 10560

GCTTTTTATA CTTTATTCCC GTGTCTGAAA AAAATGTGCA AAGGAAACGG GAATGGCAAG 10620

GTCCGATTAC GATTTTATCA ATCTGTCTCT GGGACATGAA CTGAATGAGT GGCTGGCAGA 10680

GAGAGGTTAT GCCGGACAGG CGGATAACCG GAACCGACTG GCAGAGGTGG TTACCCGCAA 10740

ATTGCGGGAC AGTTTTTATG CGGACGTCTC CTGGGATGCG CTGAATGTGG CATACAGTGA 10800

ACACCCTGAG TGGTTTTCAG AGCTTGCCTC CGGGGATGAG GATTAACAGG CAAATTATGC 10860

TGCTATCGGG CAGAGTGATT ACCTGCAGGG ATTTCCATTT ATAAGAATAC GCCGCTTCGG 10920

GAAAGCTCCG GTTCTCCGGA GAGTTACGAT TATTTTTACT CAAATTCACA ACACCTGAAC 10980

TGGAACTTGC GTTGTGTCCC GGATTGTTAC TCCGCAGAAG CATCCTTTTT ACCATACGGA 11040

TGTTTGTTTT CCATTTCCCC TCCGAAAAAT ACAACTCCGA TCACATTTCT GATATTTTCC 11100

CCGGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTAA ATTTCAGCAC 11160

TGACATTCCG CTTACGTTAA TTTACACTGG ATACCCCACG AGGAGAATAT GCAGCACCGG 11220

CAGGATAACT TACTGGCGAA CAGAAATTTG TTGCCTGGTA TGGTTTCCGG TCAGTACGCA 11280

TTCAGGATCC GTACCTTATC TCAGGTGGTA CGCTATTTTT CCCTCCTCCC CTGCCTTTGC 11340

ATTCTTTCAT TTTCGTCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG TGCAATTCAG 11400

CAGCAACAGC AGCAGTTGTT GGATGAAAAC CAGCGCCAGC GTGATGCGCT GGAGCGCAGT 11460

GCGCCGCTGA CCATCACGCC GTCTCCGGAA ACGTCTGCCG GTACTGAAGG TCCCTGCTTT 11520

ACGGTGTCAC GCATTGTTGT CAGTGGGGCC ACCCGACTGA CGTCTGCAGA AACCGACAGA 11580

CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCACGG GACTGACCGC GGTCACGGAT 11640

GCCGTGACGG ACGGCTATAT ACGCCGGGGA TATATCACCA GCCGGGCCTT TCTGACAGAG 11700

CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT GCAGCAAATC 11760

CGGGCGGAAG GCGCTGACCT TCCTGCCCGC ACCCTGAAGA TGGTTTTCCC GGGAATGGAG 11820

GGGAAGGTTC TGAACTGCGG GATATTGAGC AGGGGATGGA GCAGATTAAT CGTCTGCGTA 11880

CGGAGCCGGT ACAGATTGAA ATATCGCCCG GTGACCGTGA GGGATGGTCG GTGGTGACAC 11940

NSDOCID <WO 9822575A3 IA>

TGACGGCATT GCCGGAATGG CCTGTCACAG GGAGCGTGGG CATCGACAAC AGCGGGCAGA 12000

AGAATACCGG TACGGGGCAG TTAAATGGTG TCCTTTCCTT TAATAATCCT CTGGGGCTGG 12060

CTGACAACTG GTTTGTCAGC GGGGGACGGA GCAGTGACTT TTCGGTGTCA CATGATGCGA 12120

GGAATTTTGC CGCCGGTGTC AGTCTGCCGT ATGGCTATAC CCTGGTGGAT TACACGTATT 12180

CATGGAGTGA CTACCTCAGC ACCATTGATA ACCGGGGCTG GCGGTGGCGT TCCACGGGAG 12240

ACCTGCAGAC TCACCGGCTG GGACTGTCGC ATGTCCTGTT CCGTAACGGG GACATGAAGA 12300

CAGCACTGAC CGGAGGTCTG CAGCACCGCA TTATTCACAA TTATCTGGAT GATGTTCTGC 12360

TTCAGGGCAG CAGCCGTAAA CTCACTTCAT TTTCTGTCGG GCTGAATCAC ACACACAAGT 12420

TTCTGGGTGG TGTCGGAACA CTGAATCCGG TATTCACACG GGGGATGCCC TGGTTCGGCG 12480

CAGAAAGCGA CCACGGGAAA AGGGGAGACC TGCCCGTAAA TCAGTTCCGG AAATGGTCGG 12540

TGAGTGCCAG TTTTCAGCGC CCCGTCACGG ACAGGGTGTG GTGGCTGACC AGCGCTTATG 12600

CCCAGTGGTC ACCGGACCGT CTTCATGGTG TGGAACAACT GAGCCTCGGG GGTGAGAGTT 12660

CAGTGCGTGG CTTTAAGGAG CAGTATATCT CCGGTAATAA CGGCGGTTAT CTGCGAAATG 12720

AGCTGTCCTG GTCTCTGTTC TCCCTGCCAT ATGTGGGGAC AGTCCGTGCA GTGACTGCAC 12780

TGGACGGCGG CTGGCTGCAC TCTGACAGAG ATGACCCGTA CTCGTCCGGC ACGCTGTGGG 12840

GTGCTGCTGC CGGGCTCAGC ACCACCAGTG GTCATGTTTC CGGTTCGTTC ACTGCCGGAC 12900

TGCCTCTGGT TTACCCGGAC TGGCTTGCCC CTGACCATCT CACGGTTTAC TGGCGCGTTG 12960

CCGTCGCGTT TTAAGGGATT ATTACCATGC ATCAGCCTCC CGTTCGCTTC ACTTACCGCC 13020

TGCTGAGTTA CCTTATCAGT ACGATTATCG CCGGGCAGCC GTTGTTACCG GCTGTGGGGG 13080

CCGTCATCAC CCCACAAAAC GGGGCTGGAA TGGATAAAGC GGCAAATGGT GTGCCGGTCG 13140

TGAACATTGC CACGCCGAAC GGGGCCGGGA TTTCGCATAA CCGGTTTACG GATTACAACG 13200

TCGGGAAGGA AGGGCTGATT CTCAATAATG CCACCGGTAA GCTTAATCCG ACGCAGCTTG 13260

GTGGACTGAT ACAGAATAAC CCGAACCTGA AAGCGGGCGG GGAAGCGAAG GGTATCATCA 13320

ACGAAGTGAC CGGCGGTAAC CGTTCACTGT TGCAGGGCTA TACGGAAGTG GCCGGCAAAG 13380

CGGCGAATGT GATGGTTGCC AACCCGTATG GTATCACCTG TGACGGCTGT GGTTTTATCA 13440

ACACGCCGCA CGCGACGCTC ACCACAGGCA AACCTGTGAT GAATGCCGAC GGCAGCCTGC 13500

AGGCGCTGGA GGTGACTGAA GGCAGTATCA CCATCAATGG CGCGGGCCTG GACGGCACCC 13560

GGAGCGATGC CGTATCCATT ATTGCCCGTG CAACGGAAGT GAATGCCGCG CTTCATGCGA 13620

AGGATTTAAC TGTCACTGCA GGCGCTAACC GGATAACTGC AGATGGTCGC GTCAGTGCCC 13680

TGAAGGGCGA AGGTGATGTG CCGAAAGTTG CCGTTGATAC CGGCGCGCTC GGTGGAATGT 13740

ACGCCAGGCG TATTCATCTG ACCTCCACTG AAAGTGGTGT CGGGGTTAAT CTGGGTAACC 13800

TTTATGCCCG CGAGGGCGAT ATCATACTGA GCAGTGCCGG AAAACTGGTC CTGAAGAACA 13860

INSDOCID <WO 9822575A3 IA>

GCCTTGCCGG CGGCAATACC ACCGTAACCG GAACGGATGT CTCACTTTCA GGGGATAACA 13920

AAGCCGGAGG AAATCTCAGC GTTACCGGGA CAACGGGACT GACACTGAAT CAGCCCCGTC 13980

TGGTGACGGA TAAAAATCTG GTGCTGTCTT CATCCGGGCA GATTGTACAG AACGGTGGTG 14040

AACTGACTGC CGGACAGAAC GCCATGCTCA GTGCACAGCA CCTGAACCAG ACTTCCGGGA 14100

CCGTGAATGC AGCTGAAAAT GTCACCCTTA CCACCACCAA TGATACCACA CTGAAAGGCC 14160

GCAGCGTTGC CGGGAAAACA CTCACTGTCA GTTCCGGCAG CCTGAACAAC GGTGGGACAC 14220

TGGTTGCCGG GCGCGATGCC ACGGTGAAAA CCGGGACATT CAGTAATACC GGTACCGTCC 14280

AGGGGAATGG CCTGAAAGTT ACCGCCACTG ACCTGACCAG CACCGGCAGT ATTAAAAGTG 14340

GCAGCACACT CGATATCAGC GCCCGCAATG CCACACTGTC CGGTGATGCC GGTGCAAAAG 14400

ACAGTGCCCG CGTTACCGTC AGCGGTACAC TCGAAAACCG CGGCAGACTT GTCAGCGATG 14460

ACGTGCTGAC GCTCAGTGCC ACGCAGATAA ACAACAGCGG TACCCTCTCC GGGGCAAAGG 14520

AACTTGTGGC TTCTGCAGAC ACACTGACCA CCACAGAAAA ATCGGTCACA AACAGTGACG 14580

GTAACCTCAT GCTGGACAGC GCGTCTTCCA CACTGGCGGG TGAAACCAGT GCGGGTGGCA 14640

CGGTGTCTGT AAAAGGCAAC AGTCTGAAGA CCACGACCAC TGCGCAGACG CAGGGCAACA 14700

GTGTCAGCGT GGATGTGCAG AACGCACAGC TTGACGGAAC ACAGGCTGCC AGAGACATCC 14760

TTACCCTGAA CGCCAGTGAA AAGCTCACCC ACAGCGGGAA AAGCAGTGCC CCGTCGCTCA 14820

GCCTCAGTGC GCCGGAACTG ACCAGCAGCG GCGTACTTGT TGGTTCCGCC CTGAATACAC 14880

AGTCACAGAC CCTGACCAAC AGCGGTCTGT TGCAGGGGGA GGCCTCACTC ACCGTTAACA 14940

CACAGAGGCT TGATAATCAG CAGAACGGCA CGCTGTACAG TGCTGCAGAC CTGACGCTGG 15000

ATATACCGGA CATCCGCAAC AGCGGGCTTA TCACCGGTGA TAATGGTTTA ATGTTAAATG 15060

CTGTCTCCCT CAGCAATCCG GGAAAAATCA TCGCTGACAC GCTGAGCGTC AGGGCGACCA 15120

CGCTGGATGG TGACGGCCTG TTGCAGGGCG CCGGTGCACT GGCGCTTGCT GGCGACACCC 15180

TCTCACAGGG TAGTCACGGA CGCTGGCTGA CGGCGGACGA CCTCTCCCTC CGGGGCAAAA 15240

CACTGAATAC CGCAGGACCA CGCAGGGACA GAATATCACC GTGCAGGCGG ACAGATGGGC 15300

GAACAGTGGT TCCGTGCTGG CAACCGGTAA CCTTACTGCT TCGGCAACCG GTCAGTTGAC 15360

CAGTACCGGC GATATCATGA GCCAGGGTGA CACCACGCTG AAAGCAGCCA CCACGGACAA 15420

CCGGGGCAGT CTGCTTTCGG CCGGCACGCT CTCCCTTGAT GGAAACTCAC TGGATAACAG 15480

CGGCACTGTC CAGGGTGACC ATGTCACGAT TCGCCAGAAC AGTGTCACCA ACAGTGGCAC 15540

GCTCACCGGG ATCGCCGCGC TGACGCTTGC CGCCCGTATG GTATCCCCTC AACCTGCGCT 15600

GATGAATAAC GGAGGTTCAT TGCTGACCAG CGGCGATCTG ACAATCACCG CAGGCAGTCT 15660

GGTAAACAGC GGGGCGATCC AGGCGGCTGA CAGCCTGACT GCACGTCTGA CGGGTGAGCT 15720

CGTCAGCACA GCGGGCAGCA AAGTCACCTC GAACGGTGAA ATGGCGCTCA GTGCACTGAA 15780

TTTAAGCAAC AGCGGACAAT GGATTGCAAA AAATCTGACC CTGAAGGCGA ACTCACTGAC 15840

CAGTGCGGGT GACATCACCG GTGTGGATAC TCTCACGCTC ACGGTGAATC AGACGCTGAA 15900

CAATCAGGCG AACGGAAAAC TGCTCAGTGC AGGTGTGCTG ACGCTGAAGG CAGACAGTGT 15960

CACAAACGAC GGGCAATTAC AGGGAAATGC CACCACCATC ACGGCAGGAC AACTCACAAA 16020

CGGCGGGCAT CTGCAGGGCG AAACGCTGAC GCTGGCCGCC TCCGGTGGCG TGAACAACCG 16080

TTCCGGTGGT GTTCTGATGA GCCGGAATGC ACTGAATGTC AGTACTGCGA CCCTGAGTAA 16140

CCAGGGCACG ATACAGGGTG GTGGCGGGGT TTCCCTGAAC GCCACTGACC GTCTGCAGAA 16200

CGACGGCAAA ATCCTCTCCG GCAGTAACCT CACGCTGACG GCGCAGGTGC TGGCGAACAC 16260

CGGCAGCGGA CTGGTACAGG CTGCCACCCT GCTGCTGGAT GTGGTGAATA CTGTCAACGG 16320

CGGACGCGTA CTTGCCACCG GCAGTGCCGA CGTTAAAGGA ACCACGCTGA ATAATACCGG 16380

TACGCTTCAG GGTGCGGACC TGCTGGTGAA TTACCACACA TTCAGCAACA GCGGTACCCT 16440

GCTGGGAACC TCCGGGCTTG GCGTCAAGGG CAGTTCACTG CTGCAAAATG GTACAGGGCG 16500

GCTGTACAGT GCAGGCAACC TGCTGCTTGA CGCTCAGGAC TTCAGTGGTC AGGGGCAGGT 16560

GGTGGCCACC GGTGATGTCA CACTGAAACT GATTGCTGCC CTCACGAATT ACGGTACCCT 16620

GGCCGCAGGG AAAACCCTTT CCGTCACGTC GCAAAATGCC ATCACCAACG GCGGTGTCAT 16680

GCAGGGTGAT GCCATGGTGC TCGGTGCCGG AGAGGCATTC ACCAACAATG GAACGCTGAC 16740

TGCCGGTAAA GGCAACAGTG TTTTCAGCGC ACAGCGTCTT TTCCTTAACG CACCGGGTTC 16800

ACTTCAGGCC GGTGGCGATG TGAGTCTGAA CAGCCGGAGT GATATCACCA TCAGTGGTTT 16860

TACCGGCACG GCAGGCAGTC TGACAATGAA TGTGGCCGGT ACCCTGCTGA ACAGTGCGCT 16920

GATTTATGCG GGGAATAACC TGAAGCTGTT TACAGACCGT CTGCATAACC AGCATGGTGA 16980

TATCCTGGCC GGCAACAGTC TGTGGGTACA GAAGGATGCT TCCGGCGGTG CAAACACAGA 17040

GATTATCAAT ACTTCCGGGA ATATTGAGAC GCATCAGGGC GATATTGTTG TAAGAACCGG 17100

GCATCTTCTG AACCAGCGGG AGGGATTTTC TGCCACAACA ACAACCCGGA CTAACCCCTC 17160

ATCCATTCAG GGAATGGGAA ATGCTCTGGT TGATATTCCC CTTTCCCTTC TTCCTGACGG 17220

CAGCTATGGC TATTTCACCC GTGAAGTTGA AAATCAGCAC GGTACGCCCT GCAACGGGCA 17280

CGGGGCATGC AATATCACAA TGGATACGCT TTATTATTAC GCTCCGTTTG CTGACAGTGC 17340

CACACAGCGC TTTCTCAGCA GCCAGAACAT CACAACAGTA ACCGGTGCTG ATAATCCGGC 17400

AGGCCGCATT GCGTCAGGGC GTAATCTTTC TGCTGAGGCT GAACGACTGG AAAACCGGGC 17460

GTCATTTATC CTGGCGAATG GGGATATCGC ACTCTCGGGC AGAGAGTTAA GCAATCAGAG 17520

CTGGCAGACG GGGACAGAGA ATGAATATCT GGTATACCGC TACGACCCGA AAACGTTTTA 17580

CGGTAGCTAT GCAACAGGCT CTCTGGATAA ACTGCCCCTG CTGTCACCGG AATTTGAAAA 17640

CAATACCATC AGATTTTCAC TGGATGGCCG GGAAAAAGAT TACACGCCCG GTAAGACGTA 17700

INSDOCID <WO__9822575A3_IA>

TTATTCCGTT ATTCAGGCGG GCGGGGATGT TAAGACCCGT TTTACCAGCA GTATCAATAA 17760

CGGAACAACC ACTGCACATG CAGGTAGTGT CAGTCCGGTG GTCTCTGCAC CTGTACTGAA 17820

TACGTTAAGT CAGCAGACCG GCGGAGACAG TCTGACACAG ACAGCGCTGC AGCAGTATGA 17880

GCCGGTGGTG GTTGGCTCTC CGCAATGGCA CGATGAACTG GCAGGTGCCC TGAAAAATAT 17940

TGCCGGAGGT TCGCCACTGA CCGGTCAGAC CGGTATCAGT GATGACTGGC CACTGCCTTC 18000

CGGCAACAAT GGATACCTGG TTCCGTCCAC GGACCCGGAC AGTCCGTATC TGATTACGGT 18060

GAACCCGAAA CTGGATGGTC TCGGACAGGT GGACAGCCAT TTGTTTGCCG GACTGTATGA 18120

GCTTCTTGGA GCGAAACCGG GTCAGGCGCC ACGTGAAACG GCTCCGTCGT ATACCGATGA 18180

AAAACAGTTT CTGGGCTCAT CGTATTTTCT TGACCGCCTC GGGCTGAAAC CGGAAAAAGA 18240

TTATCGTTTC CTGGGGGATG CGGTCTTTGA TACCCGGTAT GTCAGTAACG CGGTGCTGAG 18300

CCGGACGGGT TCACGTTATC TCAACGGACT GGGTTCAGAC ACGGAACAGA TGCGGTATCT 18360

GATGGATAAC GCGGCCAGAC AACAGAAAGG ACTGGGATTA GAGTTTGGTG TGGCGCTGAC 18420

AGCTGAACAG ATTGCTCAGC TTGACGGCAG CATGCTGTGG TGGGAGTCAG TCACCATCAA 18480

CGGACAGACA GTCATGGTCC CGAAACTGTA TCTGTCGCCG GAAGATATCA CCCTGCATAA 18540

CGGCAGCGTT ATCAGCGGGA ACAACGTGCA GCTTGCGGAC GGCAATATCA CCAACAGCGG 18600

CGGCAGCATC AACGCACAGA ACGACCTTTC GCTCGACAGT ACCGGCTATA TCGACAACCT 18660

GAATGCAGGG CTGATAAGCG CGGGCGGTAG CCTGGACCTG AGCGCCATCG GGGATATCAG 18720

CAATATCAGC TCAGTCATCA GCGGTAAAAC CGTACAACTG GAAAGCGTGA GTGGCAACAT 18780

CAGCAATATC ACCCGGCGTC AGCAATGGAA TGCGGGCAGT GACAGCCGAT ATGGTGGTGT 18840

GCATCTCAGC GGTACGGACA CCGGTCCGGT TGCGACCATT AAAGGCACTG ATTCACTTTC 18900

ACTGGATGCA GGGAAAAACA TTGATATTAC CGGGGCAACG GTCTCGTCCG GTGGAGACCT 18960

TGGAATGTCT GCGGGTAATG ACATCAACAT TGCCGTAAAC CTGATAAGCG GGAGCAAAAG 19020

TCAGTCCGGT TTCTGGCACA CTGATGACAA CAGTTCATCA TCCACCACCT CACAGGGCAG 19080

CAGCATCAGC GCCGGCGGTA ACCTGGCGAT GGCTGCAGGC CATAATCTGG ATGTCACAGC 19140

ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTTCTGCA GGTAACGACC TGAGTCTGAA 19200

TGCAGTCAGG GAAAGCAAAA ACAGTCGCAA CGGCAGGTCA GAAAGTCATG AAAGCCACGC 19260

AGCTGTGTCC ACGGTGACGG CGGGCGATAA CCTCCTCCTT GTTGCCGGTC GTGATATTGC 19320

CAGTCAGGCT GCCGGTATGG CTGCGGAAAA TAACGTGGTC ATCCGGGGCG GACGTGATGT 19380

GAACCTGGTG GCAGAGTCTG CCGGCGCAGG CGACAGCTAT ACGTCGAAGA AAAAGAAAGA 19440

GATTAACGAG ACAGTCCGTC AGCAGGGAAC GGAAATCGCC AGCGGTGGTG ACACCACCGT 19500

CACCGCAGGA CGGGATATCA CCGCTGTTGC GTCATCCGTT ACCGCAACCG GCAATATCAG 19560

CGTGAATGCC GGTCGTGATG TTGCCCTGAC CACGGCGACA GAAAGTGACT ATCACTATCT 19620

JSDOCID <WO 9822575A3 IA>

GGAAACGAAG AAAAAAAGCG GAGGTTTTCT CAGTAAGAAA ACCACCCACA CCATCAGTGA 19680

GGACAGTGCC TCCCGTGAAG CAGGTTCCCT GCTGTCGGGG AACCGCGTGA CCGTTAACGC 19740

CGGTGATAAN CTGACGGTAG AGGGTTCGGA TGTGGTGGCT GACCGGGATG TGTCACTGGC 19800

GGCGGGTAAC CATGTTGATG TTCTTGCTGC CACCAGTACA GATACGTCCT GGCGCTTTAA 19860

GGAAACGAAG AAATCCGGTC TGATGGGTAC CGGCGGTATT GGTTTCACCA TTGGCAGCAG 19920

TAAGACAACG CACGACCGCC GCGAGGCSGG GACAACGCAG AGTCAGAGTG CCAGTACCAT 19980

CGGCTCCACT GCCGGTAATG TCAGTATTAC CGCGGGCAAA CAGGCTCATA TCAGCGGTTC 20040

GGATGTGATT GCGAACCGGG ATATCAGCAT TACCGGTGAC AGTGTGGTGG TTGACCCGGG 20100

GCATGATCGT CGTACTGTGG ACGAAAAATT TGAGCAGAAG AAAAGCGGGC TGACGGTTGC 20160

CCTTTCCGGC ACGNTGGGCA GTGCCATCAA TAATGCGGTC ACCAGTGCAC AGGAGACGAA 20220

GGAGAGCAGT GACAGCCGTC TGAAAGCCCT GCAGGCCACA AAGACAGCGC TGTCTGGTGT 20280

GCAGGCCGGA CAGGCTGCGG CAATGGCCAC CGCAACCGGT GACCCGAATG CGACGGGAGT 20340

CAGCCTGTCG CTTACCACCC AGAAATCGAA ATCACAACAA CATTCTGAAA GTGACACAGT 20400

ATCCGGCAGT ACGCTGAATG CCGGGAATAA TCTGTCTGTT GTCGCAACCG GCAAAAACAG 20460

GGGAGATAAC CGCGGAGATA TTGTGATTGC AGGAAGCCAG CTTAAGGCCG GTGGTAACAC 20520

AAGCCTGGAT GCCGCGAATG ATGTTCTGTT GAGTGGCGCT GCAAACACAC AAAAAACAAC 20580

GGGCAGGAAC AGCAGCAGTG GCGGTGGCGT GGGTGTCAGT ATCGGTGCCG GTGGTAACGG 20640

TGCCGGTATC AGCGTCTTTG CCAGCGTTAA TGCGGCAAAA GGCAGCGAGA AAGGTAACGG 20700

TACTGAGTGG ACTGAAACCA CAACAGACAG CGGTAAAACC GTCACCATCA ACAGTGGTCG 20760

GGATACGGTA CTGAACGGTG CTCAGGTCAA CGGCAACAGG ATTATCGCCG ATGTGGGCCA 20820

CGACCTGCTG ATAAGCAGCC AGCAGGACAC CAGTAAGTAC GACAGTAAAC AGACCAGCGT 20880

GGCTGCCGGC GGCAGTTTTA CCTTTGGCTC CATGACCGGC TCAGGTTACA TCGCTGCCTC 20940

CCGGGATAAG ATGAAGAGCC GCTTTGACTC CGTTGCTGAA CAAACCGGGA TGTTTTCCGG 21000

AGATGGCGGC TTCGATATCA CGGTCGGCAA CCACACCCAG CTCGATGGTG CGGTTATCGC 21060

TTCCACGGCG ACGGCAGATA AAAACAGCCT CGATACCGGG ACGCTCGGCT TCAGCGATAT 21120

TCACAACGAA GCGGATTATA AAGTCAGTCA CAGTGGAATC AGTCTGAGCG GTGGTGGCAG 21180

CTTCGGGGAT AAATTTCAGG GTAACATGCC GGGTGGCATG ATATCCGCCG GAGGTCACAG 21240

CGGACATGCG GAAGGAACGA CTCAGGCCGC AGTGGCAGAT GGCACAATCA CCATCCGGGA 21300

CAGGGACAAT CAGAAGCAGA ATCTGGCGAA CCTGAGCCGT GACCCTGCGC ACGCTAATGA 21360

CAGTATCAGC CCGATATTTG ACAAGGAGAA AGAGCAGAGG CGTCTGCAGA CAGTGGGGCT 21420

TATCAGTGAC ATTGGCAGTC AGGTGGCGGA TATCGCGCGG ACGCAGGGGG AACTGAATGC 21480

GTTGAAGCTG CGCAGGATAA ATATGGGCCT GTTCCGGCGG ATGCGACGGA AGAACAGCGG 21540

3NSDOCID: <WO___9822575A3_IA>

CAGGCATATC TGGCAAAACT GCGTGATACG CCGGAATACA AAAAGGAACA GGAAAAGTAT 21600

GGTACCGGCA GCGATATGCA GCGCGGTATC CAGGCTGCAA CGGCTGCACT TCAGGGCCTG 21660

GTGGGCGGCA ATATGGCAGG CGCGCTGGCA GGTGCTTCAG CGCCGGAGCT GGCGAACATC 21720

ATCGGTCATC ACGCGGGTAT TGATGACAAT ACAGCGGCAA AAGCCATTGC CCATGCCATT 21780

CTCGGTGGTG TGACAGCAGC CCTTCAGGGC AACAGTGCGG CAGCAGGCGC AATTGGTGCG 21840

GGTACTGGTG AAGTGATCGC GTCAGCCATT GCGAAAAGCC TCTACCCGGG CGTAGATCCG 21900

TCGAAACTGA CAGAAGATCA GAAGCAAACT GTAAGCACGC TGGCAACGCT GTCAGCGGGT 21960

ATGGCCGGCG GCATTGCCAG TGGCGATGTG GCTGGCGCGG CTGCTGGAGC TGGTGCCGGG 22020

AAGAACGTTG TTGAGAATAA TGCGCTGAGT CTGGTTGCCA GAGGCTGTGC GGTCGCAGCA 22080

CCTTGCAGGA CTAAAGTTGC AGAGCAGTTG CTAGAAATCG GGGCGAAAGC GGGCATGGCC 22140

GGGCTTGCCG GGGCGGCAGT CAAGGATATG GCCGACAGGA TGACCTCCGA TGAACTGGAG 22200

CATCTGATTA CCCTGCAAAT GATGGGTAAT GATGAGATCA CTACTAAGTA TCTCAGTTCG 22260

TTGCATGATA AGTACGGTTC CGGGGCTGCC TCGAATCCGA ATATCGGTAA AGATCTGACC 22320

GATGCGGAAA AAGTAGAACT GGGCGGTTCC GGCTCAGGAA CCGGTACACC ACCACCATCG 22380

GAAAATGATC CTAAGCAGCA AAATGAAAAA ACTGTAGATA AGCTTAATCA GAAGCAAGAA 22440

AGTGCGATTA AGAAGATCGA TAACACTATA AAAAATGCTC TGAAAGATCA TGATATTATT 22500

GGAACTCTCA AGGATATGGA TGGTAAGCCA GTTCCTAAAG AGAATGGAGG ATATTGGGAT 22560

CATATGCAGG AAATGCAAAA TACGCTCAGA GGATTAAGAA ATCATGCGGA TACGTTGAAA 22620

AACGTCAACA ATCCTGAAGC TCAGGCTGCG TATGGCAGAG CAACAGATGC T 22671

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT 60

ATCAGGGTTA TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGGCA ACTGAAACCC 120

GCTGACGGAT NANGTGTACA GTGGCATCAG TGGACGGMTT ACAGCATAAG TGCTTAAGGC 180

GCGTGACCAT ACAGMTACGG TCGCTGCAGA GAACAGGGAG AATATCATCC GGAACACGGT 240

GGCCATAAAC CGTAACACCA GGGGGCTGCT TTCCCCGGGA GAGGTGCTGG AGATGCATGC 300

GGACGTCTGA ACAGTCAGCA GGGCTGATTA ATGAGAATCA CGAGGAAATG AAGCGGGAGC 360

CGTACAGTGA GGATAAATTT AACGCCATAG CGGCTGTGGG CGGGTATAGT GCCAAGCAGA 420

CTGCTTAAAG GCAGGTACTA CTTTCAGTGG CGCCTATGTT TCCTGGAATG TGGGTGTCAA 480

CTGGTAGTTC TGAACCCGGG CCTGAGTCAC CGGGGAGGCA GTTTTCGGTA TGAAGTAATG 540

ATTCGCTGCC TGTTTTTCTC CCCGATGGCA TAACTGACTG TTCCCGGGTA TTCCTGAAGA 600

TCTGAGAGGA AGAGTGTATA TGCTGAACTA TCGCATAAGG TCAGTGCAGC TATTTATTGT 660

AAACGGTCGG GCTGACAGGG CGCAGGTGCG TCTGGAATGC GACGATGAAG CCGTTTTTGA 720

ATGTTATCTT CTTGCTGAAG GGGAAGGGGA ACTGAAAGAA CTGAGCCTGT CAGAGCTGGA 780

AGAGCGGGCG CTGATGTATG CGGCAGACAG TTTCCGTTAT GAATGATAAG TCAGTTATAC 840

CGGTAATGGT AAACGGAGCC GGTATCCGGG ATACAAGGGG CAGAGAGTAT GCTGATTATT 900

ATTATGACCC GGGACAGATA TCTGGAATAT GGCCTGATGC GTATACTGAG CGGATATCAG 960

GTCACGACAG GCAGAGAGCT GTTTAATGCC GGAAAGCAAC GTCAGTCACT TCCCGAAGAC 1020

AGTTATGTGA TTCTCTGTGA CCGTAATCTG GAAAGGCTTA CATACTCTAT GTTCTGTGGG 1080

CGTCGGTTTC TTGTCATTCC TGTTTCCTCT GTGAGATGCC TGACAGATAT CAGGCAAACC 1140

ATCCGCCGTG GAGCGTGGCT GTTCGGACAT ACGGCAAGGC CACTGACCCG GACAGAGATG 1200

GTGGTGGTCT TCGGGGTTGT TTTCCATGAC TACGGGTTTA CCTTTCTGGC AGACCGGCTG 1260

GGGATAACCA TGAAGACGGT ATGTGCGCAT CTTTACAATG CGATGGAGAA AAATGGTATG 1320

CGCGGCGTCA GTATTAAATA TCTCTGCAAC ACCATAGACC GGTAAAAAGA TGGTTTTCTG 1380

ATAAAGGCTG TTGCGACGGG GATTTCTGTG CATGCTGTGT CACGGGCATC CCAGCTCTCC 1440

GGATAATTAA TGTTATGTAG TCAGGCGTGA TAAATTTCAT ATGGAACAGG TATGCGTTTT 1500

ATTTGTGATA ACAGTTAATG AGGTGTTTCC ATACACACTG AAGTTACCTG TAATATTAGC 1560

GGGGGATTTG AATGATGTTG CGTGTCTGCG ACCACTCGTT TATTCATGCA AATAAGTGGA 1620

CTGCTGGATC CACGGTAAGA GTACAGCGAG GGCCGTATTG ACGGGGATGT GTTATTCAGC 1680

GGGCAGTGCT ATGCGCCACG GAAGCAGTTC GCTGACACGG TTGACCGGCC AGTCAGCTAT 1740

GACGCCAAAC ACATGGCGAA GGTAGTTTTC TGGATCCTCG TCGTTCAGTT TGCACGTCCC 1800

GATCAGGCTG TACAGTAGCA CTCCCCGCTC ACCACCATGC TCAGAGCTGC GTATTACCGT 1860

GAAGGAGATC GGTGAGTAAC CCTCTGTGTC GGCACATTAT AGCCGTCACA TCGGATAACT 1920

GTTATCCTTC TGTTCTGATG TATTCTGGGA GGTGATGTTT CACTCCTGAT AAGAGCATTA 1980

CTAATTACAG CTGCTTTTCG GATAACATTC GGGCAGTTTT CTTTAATTCT GAAGTCTGAA 2040

AGAGATATCA GTAATTGTAT TGCTTTTAAA CATTGTCAGT ATTTATTTGT CCAAATCGTT 2100

CACGTTTCTC ATAATCTTCC CGACAGTCAC CATCACAAAA CAATCCAGTC TTAACAGGTT 2160

CTCCGCAGTT ATAGCAGAAT CCTGTTTCAG GGAGTCTATT CCGGATACGA TTTTTTAGTC 2220

TGATGCTCAT GCTGAATTGT TCATTTTCAT AAGCAATATC TGCACTATCT GCCATAAACG 2280

ATCCTCTGAG GAGACCACAT CTTTATAACC CACCACCGAA ATATTACAAA GTAATACTCA 2340

NSDOCID <WO___9822575A3_IA>

TTGTATAATC TTTAACCRGG GGCAGGATAA TTGTATCCTG CCCCT 2385

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 746 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CTTTCAGACC AGCGTTTCCT GTCAGGAGAT GAGGAAGAAA CATCAAAGTA TAAAGGCGGC 60

GATGACCATG ATACGGTATT CAGTGGCGGT ATTGCGGCCG GTTATGATTT TTATCCGCAG 120

TTCAGTATTC CGGTTCGTAC AGAACTGGAG TTTTACGCTC GTGGAAAAGC TGATTCGAAG 180

TATAACGTAG ATAAAGACAG CTGGTCAGGT GGTTACTGGC GTGATGACCT GAAGAATGAG 240

GTGTCAGTCA ACACACTAAT GCTGAATGCG TACTATGACT TCCGGAATGA CAGCGCATTC 300

ACACCATGGG TATCCGCAGG ATTGGCTACG CAGAATTCAC CAGAAAACAA CCGGTATCAG 360

TACCTGGGAT TATGAGTACG GAAGCAGTGG TCGCGAATCG TTGTCACGTT CAGGCTCTGC 420

TGACAACTTC GCATGGAGCC TTGGCGCGGG TGTCCGCTAT GACGTAACCC CGGATATCGC 480

TCTGGACCTC AGCTATCGCT ATCTTGATGC AGGTGACAGC AGTGTGAGTT ACAAGGACGA 540

GTGGGGCGAT AAATATAAGT CAGAAGTTGA TGTTAAAAGT CATGACATCA TGCTTGGTAT 600

GACTTATAAC TTCTGACGAC ACTGCTCCTG AACGATAATT GCGTATATTC TGTAATTAAG 660

ATAATTGCAT ATCKTCTGCA ATTAARCAGA AATACCCTGC AGTCTATTAC TGCAGGGNTG 720

TCTTTTATCT GTTTTACAGA NAATTT 746

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TCTGTTTGTC GTTTTTTCCC CGTTGTAGCG GYTCTGCTCC TGGCTTCCCT GATAGTCAGC 60

CCGCAGGCGC CAGGGCCCCA GATTCCCCCC CACAGTCCCG TTATAACTGA ACTGATGAGA 120

GTCTCCTCCC TGATAATTAC GGGAAACCGT CCCGTTGAGG TTATAATCCA GCATCAGTCC 180

GGGAATGCCG TCGTCCCAGC GTGAGGGAGG CAGCCAGGTG GCATCAGAAT ACTCAAGCCC 240

AGCTGCGGCA TATTGATGCG TAATACGCCC GCTCCGGTAT CAGGACGAAT ATCCACTCCC 300

GGCAACCCAT GAAAATCCGC ACACTGACCA TCATGCCAGT AAACAACTTT ATCCAGAGAT 360

NSDOCID <WO_ 9822575A3_IA>

TCTGCTGTTA ACCCCATCAG TCTGACCATA TCTGATGTCA GACAGGCCTG C 411

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 977 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TATTATCGCG CGCGCGCTGC ACAGGGGTTA TCTACATCTG CTGCTGCTGC CGGTTTAATT 60

GCTTCTGTAG TGACATTAGC AATTAGTCCC CTCTCATTCC TGTCCATTGC CGATAAGTTT 120

AAACGTGCAA ATAAAATAGA GGAGTATTCA CAACGATTCA AAAAACTTGG ATACGATGGT 180

GACAGTTTAC TTGCTGCTTT CCACAAAGAA ACAGGAGCTA TTGATGCATC ATTAACAACG 240

ATAAGCACTG TACTGGCTTC AGTATCTTCA GGTATTAGTG CTGCKGCAAC GACATCTCTT 300

GTTGGTGCAC CGGTAAGCGC ACTGGTAGGT GCTGTTACGG GGATAATTTC AGGTATCCTT 360

GAGGCTTCAA AGCAGGCAAT GTTTGAACAT GTTGCCAGTA AAATGGCTGA TGTTATTGCT 420

GAATGGGAGA AAAAACACGG TAAAAATTAC TTTGAAAATG GATATGATGC CCGCCATGCT 480

GCATTTTTAG AAGATAACTT TAAAATATTA TCTCAGTATA ATAAAGAGTA TTCTGTTGAA 540

AGATCAGTCC TCATTACTCA ACAACATTGG GATATGCTGA TAGGTGAGTT AGCTAGTGTC 600

ACCAGAAATG GAGACAAGAC ACTCAGTGGT AAAAGTTATA TTGACTATTA TGAAGAGGGA 660

AAGCGGCTGG AAAGAAGGCC AAAAGAGTTC CAGCAACAAA TCTTTGATCC ATTAAAAGGA 720

AATATTGACC TTTCTGACAG CAAATCTTCT ACGTTATTGA AATTTGTTAC GCCATTGTTA 780

ACTCCCGGTG AGGAAATTCG TGAAAGGAGG CAGTCCGGAA AATATGAATA TATTACCGAG 840

TTATTAGTCA AGGGTGTTGA TAAATGGACG GTGAAGGGGG TTCAGGACAA GGGGTCTGTA 900

TATGATTACT CTAACCTGAT TCAGCATGCA TCAGTCGGTA ATAACCAGTA TCGGGNAATT 960

CGTATTGAGT CACACCT 977

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCTTAAGT CCGGCATTGC CACGCGTAAC CCCCACTTCA ACCGCATGAT TGAGCAGATC 60

GAAAAAGTGG CGATCAAATC CCGCGCGCCG ATTCTGCTTA ACGGTCCAAC CGGCGCGGGC 120

NSDOCID <WO 9822575A3 IA>

AAGTCATTTC TGGCGCGACG CATCTTAGAG TTAAAACAGG CGCGGCATCA GTTTAGCGGC 180

GCKTTTGTGG AAGTGAACTG CGCCACCCTG CGCGGCGATA CCGCCATGTC GACGCTGTTT 240

GGTCATGTAA AAGGCGCGTT TACCGGGGCG CGGGAATCTC GTGAAGGTTT ATTACGCAGC 300

GCCAACGGGG AAATGTTGTT TCTTGATGAG ATTGGCGAAC TGGGCGCGAC GAACAGGCAA 360

TGCTGCTGAA ACCCATTGAA GRGGAAAACC TTTTACCCGT 400

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GTATGCGTTT TCATTAAGAT ATTCTCTGCT GTAGAGAAAC TTATAGCAAT ATAATCTGAT 60

AATATCTTTT ATGTAAAATT TAAATAGTTC ACCTGTGACA GATATATGTT TTCTGCTCAG 120

TAACTCCTGT GTATTAAGCC ATTCCCGTGA CCGAAGCACA CCCTTGTGAA AACTTTTTCT 180

TACTTGCTTT GAGGCACGGC ATTGATGTAA TATTTTTGCG TCCTCAATAA TTCTCTTTCC 240

CGTTTTATTT TTTGCAGCAT CTCTTACTCC ATAAAATATC TCCCGGTCCA GACTTTTGTC 300

ATATTTACTG ATTATACGAC AAATATTCCT GACCCGACGA TTCTCTTTAT TTCGCTTCCA 360

TAGCTTATAA TGATCATCGC ATAACCTTAA GGCATTTGCC TCATCAAATT CTGAAACAGG 420

ATTACTGCAT TTTTTATTCC GACAAATACC TTTGTTTTTA GCCATACTCT TCTTCCCGTC 480

AATGGAAAAA TTTTCACACC CATATTACCT GAATGATAAA CCGGATTAGT GTGATCCGGT 540

TCAGTGAAAT CAACAGGATA CCGGTATGCC ATTCAGCAAT TCTTCCCTCT CCGCGCAAGT 600

GAAATCATAT CTGACGTTTC TTCCTGAAGA AATACGCCAG AAAATCCTTG AACATCTCCA 660

CGGTGTTATT CATTACGAGC CCGTGATTGG CATTATGGGT AAATCCGGCA CCGGCAAGAG 720

CAGCCTGTGT AATGCCATTT TTCAGTCCCG TATCTGCGCC ACGCATCCCC TGAACGGCTG 780

CACCCGCCAG GCTCATCGTC TTACCCTGCA GCTCGGTGAA CGCAGAATGA CGCTGGTCGA 840

TCTGCCCGGC ATTGGTGAAA CACCGCAGCA TGATCAGGAA TACCGAGCGC TTTATCGTCA 900

GTTACTGCCG GAACTGGATC TGATTATCTG GATCCTGCGG AGTGATGAAC GTGCGTATGC 960

TGCCGATATT GCCATGCATC AGTTTTTACT GAATGAGGGC GCAGATCCCT CGCGCTTTCT 1020

GTTTGTTCTC AGCCATGCCG ATCGCATGTT TCCTGCTGAA GAATGGAATG CCACAGAAAA 1080

ATGCCCGTCC CGTCACCAGG AACTCTCACT GGCGACAGTA ATAGCCCGGG TGGCCACCCT 1140

GTTCCCTTCA TCATTTCCGG TACTCCCTGT AGCCGCACCT GCAGGCTGGA ACCTTCCAGC 1200

GCTGGTGTCA CTGATGATCC ACGCGCTGCC ACCACAGGCA ACCAGCGCAG TTTATTCACA 1260

TATCAGGGGG GAAAACCGCT CTGAACAGGC CGGGAAACAC GCACAACAGA CTTTTGGTGA 1320

TGCCATCGGG AAAAGTTTTG ACGACGCCGT TGCCCGGTTC AGTTTTCCGG CCTGGATGTT 1380

ACAGCTTCTG CGTAAAGCCC GGGACCGCAT TATCCACCTG CTGATCACAC TGTGGGAGCG 1440

TCTGTTCTGA CACACTCACG CCGACAGATG TGTCGCTGGA TTAACGAGCA TTCTTCTTTT 1500

TATGAAATCA TGCTTAAAAA TCAGATAATT ARAAGAATAT TTTTTCTGCT GCATTTTATT 1560

CCTGATTATC CGGATGCGAC ACATCCTTTC AACATCATGA TGCATAATAA CATCATGAAA 1620

TAAAAGATGT TTTCTTACGG AGTGCACATC TATGTCTGAT AATCGTTCCC GGCATGATCG 1680

CCTGGCGGTT CGCTTATCAC TCATTATCAG CCGACTGATG GCCGGAGAAT CTCTGTCACT 1740

AAAAACACTG TCAGATGAAT TTGGCGTTAC AGAACGTACT TTACAGCGCG ATTTTCATCA 1800

GCGTCTGGTT CACCTAGATT TAGAGTACAG AAATGGCAGG TACAGCCTCA GACGACAGAG 1860

CAGCCCAGGT GCGATCCCTG AAATGCTTTC TTTTATACAG AATACCGGGA TCGCACGGAT 1920

ACTTCCGCTC CGGAACGGAC GACTGATAAC CTGTCTTACC GACAACCAGG AGCCCTCTCC 1980

CTGCCTTATC TGGCTACCGG CGCCGGATAT CACTGCAACG TTCCCCGAGT GTTTCTCGCA 2040

ACTCATCCTG GCAATAAGAC AGTGTATCCA CATCTCTCTG ATGACTGAGC GATGGTATCC 2100

GTCACTGGAG CCCTGCCGGC TCATTTATTA CAGCGGTAGC TGGTATCTGA TCGCGTTACA 2160

GAAGGGAAAA CTGCAGGTCT TTCCTCTGGC AGATATCAAA TCAGTCAGCC TGACATCAGA 2220

ACGGTTTGAA CGGAGAGGCC ACATCCACAG TCTGGTCGCT GAAGAGCGTT TTATCTCCGC 2280

CCTGCCACAT TTCTCTTTCA TCCATAAACT TATCAACACC TTTAACCTGT GATCGCCGGC 2340

CTGCCAAAGC CGTCCCGACA GGTATGGAGA CAATATGTTG AACAGAAAAC TAAATATACG 2400

GCTACGTCAT TCCCTGAACA GTCACTGCAT ACCTTCCATC ATTATCAATA ACACCGTACG 2460

TTCATTTCAG AGGTCAGTCA TGAATACCAG AGCTCTTTTT CCCCTGCTGT TCACTGTGGC 2520

ATCATTCTCC GCCTCCGCCG GCAACTGGGC TGTCAAAAAC GGCTGGTGTC AGACCATGAC 2580

GGAAGATGGT CAGGCGCTGG TAATGCTGAA AAATGGCACG ATTGGTATTA CCGGCCTGAT 2640

GCAGGGATGC CCGAATGGTG TACAGACGCT CCTGGGCAGC CGTATCAGTA TTAACGGTAA 2700

CCTGATCCCC ACATCACAAA TGTGTAATCA GCAGACGGGA TTCAGGGCTG TTGAGGTGGA 2760

AATCGGACAG GCGCCGGAAA TGGTCAAAAA AGCCGTTCAC TCCATAGCAG AGCGTGATGT 2820

GTCCGTTTTA CAGGCATTTG GTGTACGAAT GGAATTCACC CGCGGTGATA TGCTGAAGGT 2880

CTGTCCGAAA TTTGTCACAT CACTTGCCGG TTTTTCCCCG AAACAGACGA CCACTATTAA 2940

TAAAGATTCC GTCCTGCAGG CTGCCCGGCA GGCATACGCC CGGGAATATG ACGAGGAAAC 3000

AACAGAAACC GCTGATTTTG GCTCTTACGA AGTAAAAGGC AATAAGGTTG AGTTTGAAGT 3060

ATTCAATCCT GAAGACCGTG CGTACGACAA AGTGACCGTC ACGGTTGGTG CTGACGGTAA 3120

TGCCACCGGC GCCAGCGTTG AATTTATCGG AAAATAGCCG GTATGTCGGA CTGCCACCCT 3180

INSDOCID <WO__ 9822575A3 IA>

GTTTTATTGC CCGAAGGCCC TTTCTCACGC GAACAGGCGA TGGCTGTCAC AACAGCTTAC 3240

CGCAATGTGC TTATTGAAGA TGACCAGGGA ACGCATTTCC GGCTGGTTAT CCGCAATGCC 3300

GAAGGGCAGC TACGCTGGCG GTGCTGGAAT TTTGAACCTG ATGCCGGAAA ACAGCTAAAT 3360

TCGTATCTCG CCAGTGAGGG AATTCTCAGG CAATAAACGT CTTCATTTCA TCCATCAGGC 3420

CGCGTCTTCT CCGGGAGACG CGGCCTTTTC GTTTATACCG CTAATTCATT CATAAGGAGC 3480

AAAGTATGCA ATTAGCCAGT CGTTTTGGTC ATGTAAATCA GATCCGTCGG GAGCGCCCAC 3540

TGACACGCGA AGAACTGATG TACCACGTCC CGAGTATTTT TGGAGAAGAC CGGCACACCT 3600

CCCGCAGTGA ACGGTATGCG TACATTCCCA CCATCACCGT CCTGGAAAAT CTGCAGCGGG 3660

AAGGCTTTCA GCCGTKCTTC GCCTGCCAGA CCCGTGTGCG CGACCAGAGC CGCCGGGAAT 3720

ATACCAAACA TATGCTGCGT CTGCGGCGGG CCGGACAGAT AACCGGTCAG CATGTGCCTG 3780

AAATTATTCT GCTCAACTCC CATGACGGTT CATCCAGCTA CCAGATGTTA CCCGGATATT 3840

TTCGTGCCAT TTGTACCAAT GGCCTGGTCT GCGGTCAGTC GCTGGGAGAA GTCCGGGTGC 3900

CACACCGGGG AAACGTGGTG GACAGGGTCA TAGAAGGTGC TTACGAAGTG GTGGGCGTGT 3960

TTGACCTGAT TGAGGAAAAG CGTGATGCCA TGCAGTCGCT GGTCCTGCCG CCACCGGCAC 4020

GCCAGGCGCT GGCACAGGCG GCGCTGACTT ACCGTTATGG TGATGAACAT CAGCCCGTCA 4080

CCACTACCGA CATTCTGACG CCACGACGCC GGGAGGATTA CGGTAAGGAC CTGTGGAGTG 4140

CTTATCAGAC CATCCAGGAG AATATGCTGA AAGGCGGGAT TTCCGGTCGC AGTGCCAGAG 4200

GAAAACGTAT CCATACCCGG GCCATTCACA GCATCGATAC CGACATTAAG CTCAACCGGG 4260

CGTTGTGGGT GATGGCAGAA ACGCTGCTGG AGAGCCTGCG CTGATACCGT TTCCCTGAAA 4320

GCGCAGTCCT GTTCACGGCT GTCCCTTCCC CCAGACATTC CACCATTCAT TTACTTTTTA 4380

TAAGGAATAA TCTCATGACA ACCTCTTCGC ATAATTCCAC CACACCTTCT GTTTCCGTGG 4440

CCGCTGCATC AGGGAATAAC CAGTCTCAGT TGGTTGCCAC TCCCGTCCCT GATGAACAGC 4500

GCATCAGCTT CTGGCCGCAG CATTTTGGCC TCATTCCACA GTGGGTCACC CTGGAGCCCC 4560

GTGTCTTCGG CTGGATGGAC CGTCTGTGCG AAAACTACTG CGGGGGTATC TGGAATCTGT 4620

ACACCCTGAA CAACGGTGGC GCATTTATAG CACCTGAACC GGATGAAGAT GATGGAGAAA 4680

CCTGGATACT GTTCAATGCC ATGAACGGTA ACCGCGCTGA AATGAGCCCG GAAGCTGCCG 4740

GCATTGCCGC CTGTCTGATG ACGTACAGCC ATCATGCCTG TCGTACGGAG AATTATGCCA 4800

TGACGGTCCA TTATTACCGG TTGCGGGATT ACGCCCTGCA GCATCCGGAA TGCAGCGCCA 4860

TTATGCGCAT CATTGACTGA AAGGGGCCGG AATAATGCAA CAGATTTCCT TTCTGCCCGG 4920

AGAAATGACG CCCGGCGAGC GCAGTCACAT TCTGCGGGCC CTGAAAACCC TGGACCGCCA 4980

TCTTCATGAA CCCGGTGTGG CCTTCACCTC CACCCGTGCG GCACGGGAAT GGCTGATTCT 5040

GAACATGGCG GGACTGGAGC GTGAAGAGTT CCGGGTGCTG TATCTGAATA ACCAGAATCA 5100

NSDOCID <WO___9822575A3 IA>

GCTGATTGCC GGTGAAACGC TCTTCACCGG CACCATCAAC CGCACGGAAG TCCATCCCCG 5160

GGAAGTGATT AAACGCGCCC TGTACCACAA TGCCGCTGCC GTGGTGCTGG CGCACAATCA 5220

CCCGTCCGGT GAAGTCACAC CCAGTAAGGC AGACCGGCTT ATCACCGAAC GTCTGGTACA 5280

GGCACTGGGC CTGGTGGATA TCCGGGTGCC GGACCATCTG ATAGTCGGTG GCAGCCAGGT 5340

TTTCTCCTTT GCGGAACACG GTCTGCTTTA ACCCGTCACC GTCACAATCA CCTTCATATC 5400

ACTTCAGTTT CTCTTTCTCA GCTGTTTCTT ACTTTCACAT TCAGGAGGAC TATTCTCATG 5460

AAAATCATCA CCCGTGGTGA AGCCATGCGT ATTCACCGTC AGCATCCTGC ATCCCGTCTT 5520

TTTCCGTTCT GTACCGGTAA ATACCGCTGG CACGGTAGCA CGGATACATA TACCGGCCGT 5580

GAAGTACAGG ATATTCCCGG TGTGCTGGCT GTGTTTGCTG AACGCCGTAA GGACAGTTTT 5640

GGCCCGTATC TCCGGCTGAT GAGCGTCACC CTGAACTGAA TCAGGACGGG CATTCAGAAG 5700

AGCAGAATTA TCGCCACCAC CGGACCATTC TTAACCAATT TTCTGTGAGG ATTTTATCGT 5760

GTCAGACACT CTCCCCGGGA CAACGCATCC CGACGATAAC AACGACCGCC CCTGGTGGGG 5820

GCTACCCTGC ACCGTGACGC CCTGTTTTGG GGCACGTCTG GTGCAGGAGG GTAACCGGTT 5880

GCATTACCTT GCAGACCGCG CCGGTATCAG AGGCCGGTTC AGCGACGCGG ATGCGTACCA 5940

TCTGGACCAG GCCTTTCCGC TGCTGATGAA ACAACTGGAA CTCATGCTCA CCAGCGGTRA 6000

ACTGAATCCC CGCCATCAGC ATACCGTCAC GCTGTATGCA AAAAGGCTGA CCTGCGAANC 6060

GACACCCTCG GCAGTTGTGG CTACGTTTAT ATGGCTGTTT ATCCGACGCC CGAAACGAAA 6120

AAGTAACTCT CCAGAATAAC CTTCTGCCCC GGCCTGGTGC TTTCACCACG CCACTTTTCC 6180

ATTTTTCATC TCTGCATATC AGGAAAATCT TCAGTATGAA CACATTACCC GATACACACA 6240

TACGGGAGGC ATCGCATTGC CAGTCTCCCG TCACCATCTG GCAGACACTG CTCACCCGAC 6300

TGCTGGACCA GCATTACGGC CTCACACTGA ATGACACACC GTTCGCTGAT GAACGTGTGA 6360

TTGAGCAGCA TATTGAGGCA GGCATTTCAC TGTGTGATGC GGTGAACTTT CTCGTTGAAA 6420

AATACGCACT GGTGCGTACC GACCAGCCGG GATTCAGCGC CTGTACTCGT TCTCAGTTAA 6480

TAAACAGTAT TGATATCCTC CGGGCCCGCC GGGCAACCGG CCTGATGGCC CGCGACAATT 6540

ACAGAACGGT AAATAACATT ACCCTGGGTA AGCATCCGGA GAAACGATGA AACTTTCCCT 6600

GATGCTGGAA GCCGACAGAA TTAATGTGCA GGCACTGAAC ATGGGGCGAA TTGTCGTTGA 6660

CGTCGATGGT GTTAATCTCA CTGAACTGAT TAACAAGGTC GCTGAAAACG GTTATTCACT 6720

CCGCGTGGTG GAGGAATCCG ACCAACAGTC AACCTGCACA CTACCACCGT TTGCAACCCT 6780

TGCCGGCATA CGCTGCAGTA CCGCACATAT CACGGAAAAG GATAACGCCT GGCTGTACTC 6840

GCTGTCACAC CAGACCAGTG ACTTCGGTGA ATCAGAATGG ATTCATTTCA CAGGTAGCGG 6900

ATATCTGTTA CGTACCGATG CGTGGTCATA TCCGGTTCTG CGGCTTAAAC GCCTGGGGCT 6960

GTCAAAAACG TTCCGTCGTC TGGTTATCAC ACTTACCCGA CGTTATGGCG TCAGTCTCAT 7020

TCATCTGGAT GCCAGCGCTG AATGCCTGCC GGGTTTACCC ACTTTCAACT GGTAACCAGG 7080

AACAACATGA AATCATTAAC CACGGAAACC GCACTGGATA TTCTGATTGC GTGGCTGCAG 7140

GACAATATCG ACTGCGAATC GGGAATTATC TTTGACAACA ATGAGGATAA AACGGATTCA 7200

GCAGCACTGT TGCCCTGTAT CGAACAGGCC AGAGAGGATA TCCGTACCCT GCGCCAACTG 7260

CAGCTTCAGC ACCAGAACCG GTGAGTCTCA CTCATCATCT CACTCACCAG ACTTCATTCC 7320

ACTSACGCCA GCCTGAACAC GGCTGGCGTT TTCATTTATC TGCAAAAAGG AATATCGATT 7380

ATGTCTGAAA TCACAGTCTC CCGTCCGGAA GTGGTCAACG AGAATACGGA CGTTATCTGC 7440

TCCACCTCAG TCAGGTACAG GTCACTGGAA TATGATAATT TTCCGGAAAT CAGCGAAGCG 7500

AACATTCTGA GCACATTTGA ACAACTGCAC CAGAACAAAG ATGAAGTGTT TGAACGGGGA 7560

GTGATCAACG TCTTCAAAGG GCTGAGCTGG GATTACAAAA CCAACTCACC CTGTAAATTT 7620

GGCAGTAAAA TTATCGTCAA CAATCTGGTG AGATGGGACC AGTGGGGATT TCATCTTATC 7680

AGTGGAATGC AGGCAGATCG CCTGGCTGAC CTGGAAAGAA TGTTGCATCT GCTCAGCGGT 7740

AAACCGATCC CCGACAACCG AGGGAATATC ACCATTAATC TGGATGACCA CATACAGTCC 7800

GTTCAGGGTA AAGGACGCTA TGAAGATGAG ATGTTCATCA TTAAATACTT TAAGAAGGGA 7860

TCTGCACACA TCACTTTCAA AAGGCTGGAG CTGATTGACA GAATTAACGA TATAATAGCC 7920

AGGCACTTTC CTTCTGTGCT CTCAGCCTGA CCCCGAGTTT GATTCCCTTT CGATATCAAA 7980

AGGGACTGCG GGTACAAAAG AGGGTACATC TTTCACCAAA CCAAACAAAA TAAACTAATA 8040

TCAACATGAT AGAAGCATTC TTCGATTCCG AGTCCGGCAC CAAATTCATA TAAACGGACC 8100

TCCACGGAGG TCCGTTTTTC GTTTCAGGAC GCCACGATTT AAGCGTCCTG CCGCCAAATC 8160

AATTCTACCG AACTCAACCA GATTCTCCCC ACATCACCAG CAATTTGCGG GCATATCCCA 8220

ATTCGGGAAA ATTTGTTTCT GAGCTATAGC GCTGACTGAC GTGAAATGTC GTGCGGCCCC 8280

GTGATGCTGT TGAAMGTCAA ATGACGTCAT CAGGAGCGTA ACGCACCCAT AAAGCACAAC 8340

ATCGGGCAGA ACGCCAACTG ATGAGATTTT CTGAATGAGA ACAAAGAGAA ATGTATCAGT 8400

CCGTTTGCTC ATGCAAAGAC TAACAATCCA TTAAAATAGT AAGCGCTCCG GACAATTTTC 8460

CATGGATTAT TTTCTGAACA TTTTTCTTTG GCAAAGATGA TGAATTTTGA TGGTAAGGAA 8520

AATTACTTCT GGTTCTCAGT AAAATCCTTT CGTAATACTA TGTAATCAAG AAGTTTATGG 8580

CTAGTAAAAA TAACGTCTTG CATTCACCAA TAATATGTAA ATAAACCCAT CTATAGATGG 8640

AAAAAATAGG TTATGGAATT ATCATTGCAT CATTCCCTTT TCGAATGAGT TTCTATTATG 8700

CAACAACCTG TAGTTCGCGT TGGCGAATGG CTTGTTACTC CGTCCATAAA CCAAATTAGC 8760

CGCAATGGGC GTCAACTTAC CCTTGAGCCG AGATTAATCG ATCTTCTGGT TTTCTTTGCT 8820

CAACACAGTG GCGAAGTACT TAGCAGGGAT GAACTTATCG ATAATGTCTG GAAGAGAAGT 8880

ATTGTCACCA ATCACGTTGT GACGCAGAGT ATCTCAGAAC TACGTAAGTC ATTAAAAGAT 8940

NSDOCID <WO 9822575A3 IA>

AATGATGAAG ATAGTCCTGT CTATATCGCT ACTGTACCAA AGCGCGGCTA TAAATTAATG 9000

GTGCCGGTTA TCTGGTACAG CGAAGAAGAG GGAGAGGAAA TAATGCTATC TTCGCCTCCC 9060

CCTATACCAG AGGCGGTTCC TGCCACAGAT TCTCCCTCCC ACAGTCTTAA CATTCAAAAC 9120

ACCACAACGC CACCTGAACA ATCCCCAGTT AAAAGCAAAC GATTCACTAC CTTTTGGGTA 9180

TGGTTTTTTT TCCTGTTGTC GTTAGGTATC TGTGTAGCAC TGGTAGCGTT TTCAAGTCTT 9240

GAAACACGTC TTCCTATGAG TAAATCGCGC ATTTTGCTCA ATCCACGCGA TATTGACATT 9300

AATATGGTTA ATAAGAGTTG TAACAGCTGG AGTTCTCCGT ATCAGCTCTC TTACGCGATA 9360

GGCGTGGGTG ATTTGGTGGC GACATCACTT AACACCTTCT CCACCTTTAT GGTGCATGAC 9420

AAAATCAACT ACAACATTGA TGAACCGAGC AGTTCCGGTA AAACATTATC TATTGCGTTT 9480

GTTAATCAGC GCCAATACCG TGCTCAACAA TGCTTTATGT CGGTAAAATT GGTAGACAAT 9540

GCAGATGGTT CAACCATGCT GGATAAACGT TATGTCATCA CTAACGGTAA TCAGCTGGCG 9600

ATTCAAAATG ATTTGCTCCA GAGTTTATCA AAAGCGTTAA ACCAACCGTG GCCACAACGA 9660

ATGCAGGAGA TGCTCCAGCA AATTTTGCCG CATCGTGGTG CGTTATTAAC TAATTTTTAT 9720

CAGGCACATG ATTATTTACT GCATGGTGAT GATAAATCAT TGGATCGTGC CAGTGAATTA 9780

TTAGGTGAGA TTGTTCAATC ATCCCCAGAA TTTACCTACG CGAGAGCAGA AAARGCATTR 9840

GTTGRTATCG TGCGCCATTC TCAACATCCT TTAGACGRAA AACAATTAGC CAGCACTGAA 9900

CACAGAAATA GATAACATTG TTACACTGCC GGAATTGAAC AACCTGTCCA TTATATATCA 9960

AATAAAAGCG GTCAGTGCCC TGGTAAAAGG TAAAACAGAT GAGTCTTATC AGGCGATAAA 10020

TACCGGCATT GATCTTGAAA TGTCCTGGCT AAATTATGTG TTGCTTGGCA AGGTTTATGA 10080

AATGAAGGGG ATGAACCGGG AAGCAGCTGA TGCATATCTC ACCGCCTTTA ATTTACGCCC 10140

AGGGGCAAAC ACCCTTTACT GGATTGAAAA TGGTATATTC CAGACTTCTG TTCCTTATGT 10200

TGTACCTTAT CTCGACAAAT TTCKCGCTTC AGAATAAGTA ACTCCCGGGT TGATTCATGC 10260

TCGGGAATAT TTGTTGTTGA GTTTTTGTAT GTTCCCGTTG GTATAATATG GTTCGGCAAT 10320

TTATTTGCCG CATAATTTTT ATTACATAAA TTTAACCAGA GAATGTCACG CAATGCATTG 10380

TAAACATTGA ATGTTTATCT TTTCATGATA TCAACTTGCG ATCCTGATGT GTTAATAAAA 10440

AACCTCAAGT TCTCACTTAC AGAAACTTTT GTGTTATTTC ACCTAATCTT TAGGATTAAT 10500

CCTTTTTTCG TGAGTAATCT TAGCGCCAGT TTGGTCTGGT CAGGAAATAG TTATACATCA 10560

TGACCCGGAC TCCAAATTCA AAAATGAAAT TAGGAGAAGA GCATGAGTTC TGCCAAGAAG 10620

ATCGGGCTAT TTGNCCTGTA CCGGTGTTGT TGCCGGTAAT ATGATGGGGA GCGGTATTGC 10680

ATTATTACCT GCGAACCTAG CAAGTATCGG TGGTATTGCT ATCTGGGGTT GGATTATCTC 10740

TATTATTGGT GCAATGTCGC TGGCATATGT ATATGCCCGA CTGGCAACAA AAAACCCGCA 10800

ACAAGGTGGC CCAATTGCGT ATGCCGGAGA AATTTCCCCT GCATTTGGTT TTCAGACAGG 10860

TGTTCTTTAT TACCATGCTA ACTGGATTGG TAACCTGGCA ATTGGTATTA CCGCTGTATC 10920

TTATCTTTCC ACCTTCTTCC CAGTATTAAA TGATCCTGTT CCGGCGGGTA TCGCTGTTAT 10980

TGCTATCGTC TGGGTATTTA CCTTTGTGAA TATGCTCGGC GGTACCTGGG TAAGCCGTTT 11040

AACCACGATT GGTCTGGTGC TGGTTCTTRK TCCTGTGGTG ATGACTGCTA TTGTTGGCTG 11100

GCATTGGTTT GATGCAGCAA CTTATGCAGC TAACTGGAAT ACTGCGGATA CCACTGATGG 11160

TCATGCGATC ATTAAAAGTA TTCTGCTCTG CCTGTGGGCC TTCGTGGGTG TTGAATCCGC 11220

AGCAGTAAGT ACTGGTATGG TTAAAAACCC GAAACGTACC GTTCCGCTGG CAACCATGCT 11280

GGGTACTGGT TTAGCAGGTA TTGTTTACAT CGCTGCGACT CAGGTGCTTT CCGGTATGTA 11340

TCCGTCTTCT GTAATGGCGG CTTCCGGTGC TCCGTTTGCA ATCAGTGCTT CAACTATCCT 11400

CGGTAACTGG GCTGCACCAC TGGTTTCTGC ATTCACCGCC TTTGCGTGTC TGACTTCTCT 11460

GGGCTCCTGG ATGATGTTGG TAGGCCAGGC AGGTGTACGT GCCGCTAACG ACGGTAACTT 11520

CCCGAAAGTT TATGGTGAAG TCGACAGCAA CGGTATTCCG AAAAAAGGTC TGCTGCTGGC 11580

TGCAGTGAAA ATGACTGCCC TGATGATCCT CATCACTCTG ATGAACTCTG CCGGTGGTAA 11640

AGCCTCTGAC CTGTTCGGTG AACTGACCGG TATCGCAGTA CTGCTGACTA TGCTGCCGTA 11700

CTTCTACTCT TGCGTTGACC TGATTCGTTT TGAAGGCGTT AACATCCGCA ACTTTGTCAG 11760

CCTGATCTGT TCTGTACTGG GTTGCGTGTT CTGCTTCATC GCGCTGATGG GCGCAAGCTC 11820

CTTCGAGCTG GCAGGTACCT TCATCGTCAG CCTGATTATC CTGATGTTCT ATGCTCGCAA 11880

AATGCACGAG CGCCAGAGCC ACTCAATGGA TAACCACACA GCGTCTAACG CACATTAATT 11940

AAAAGTATTT TCCGAGGCTC CTCCTTTCAT TTTGTCCCAT GTGTTGGGAG GGGCCTTTTT 12000

TACCTGGAGA TATGACTATG AACGTTATTG CAATATTGAA TCACATGGGG GTTTATTTTA 12060

AAGAAGAACC CATCCGTGAA CTTCATCGCG CGCTTGAACG TCTGAACTTC CAGATTGTTT 12120

ACCCGAACGA CCGTGACGAC TTATTAAAAC TGATCGAAAA CAATGCGCGT CTGTGCGGCG 12180

TTATTTTTGA CTGGGATAAA TATAATCTCG AGCTGTGCGA AGAAATTAGC AAAATGAACG 12240

AGAACCTGCC GTTGTACGCG TTCGCTAATA CGTATTCCAC TCTCGATGTA AGCCTGAATG 12300

ACTGCGTTTA CAGATTAGCT TCTTTGAATA TGCGCTGGGT GCTGCTGATG ATATTGCTAA 12360

CAAGATCC 12368

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ISDOCID <WO__9822575A3_IA>

GCACGGCACT CTGATGTANC TTTTATCTGT TCCCAGTGGA AGCATGCCCC ACAACTGAGT 60

CATTAAGTGT GGAAGAACAG TTTTGTCCCC GCCTGCAATC TCTCCCTTTC NAAAAACCAG 120

TATGTCGCCA TGCCTCGCCT TAATGGAGAG CGCTGAACCA TACCTTCTTT TTCCCAGTAA 180

TAACAGGTAA TAGCGTGCCT GGTAATCCGT TACCGCCAGC GCCTCCGCAA TTTCTGCGGT 240

TTTCCCTCCA TTATGCCTGT TCAGAAATYC CAGTATTTCA TTCTTCATAT ATTCACTCAT 300

CTCACTGTAA CAAAGTTYCT YCGAATAATA AAAATCATGC TTTCTGTTAT CAACGGAAAG 360

GTATTTTTAT TCTCTGTGTT TGCTTTATTT GTGAAATTTA GTGAATTTGC TTTTTGTTGG 420

CTTTATTTGN ATGTGTGTCA CATTTTGTGT GTTATTTTTC TGTGAAAAGA AAGTCCGTAA 480

AAATGCATTT AGACGATCTT TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA 540

GTGCATTCTT TTTGTTGGTG TTTTATTCTA GTTTGATTTT GTTTTGTGGG TTAAAAGATC 600

GTTTAAATCA ATATTTACAA CATAAAAAAC TAAATTTAAC TTATTGCGTG AAGAGTATTT 660

CCGGGCCGGA AGCATATATC CAGGGGCCCG ACAGAAGGGG GAAACATGGC GCATCATGAA 720

GTCATCAGTC GGTCAGGAAA TGCGTTTTTG CTGAATATAC GCGAGAGCGT AYTGTTGCCC 780

GGCTMTATGT CTGAAATGCA TTTTTTTTTA CTGATAGGTA TTTCTTCTCA TTC 833

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2916 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TGCACCATCA CTGATACCAC CGGGACCCCG GATTTTATCC GGTCCCCGCG GACTGACAGG 60

GTTTGTGACA CCTGAGTCAT ATCCGATGTA AACTTCATTT TCACGGGTTG TACAGGAAAA 120

CTCCCCTGTG CCATTGAGTT CTGATGTGTG CCCTTCGCCA CAACTCCCAC CGTCACGGCA 180

CCAGTTGCAT CTGACGCCGA CCAACTGCTG AGAGCCATGC CGTTTCCGGC TTTGTCGACA 240

ACGCATGCTG CAGTTCCCAG CGATGCGAAC TGGTCTGGCA TGCATTCACG AACCAACAGC 300

AGTGGTGCTA CGTCCGGATG CAATTCGCAT GAGCTCCAAC CGCGGTTGTA AGTTCAGCAG 360

CCCGGGCCTC TGCCCCCGGC ACAGTCGCAT AAGTATTCGA TACCGTGCGA CACCATTACC 420

TTCAGGATAC GCCACGGACC CGTCACCCTA CGAAAACGCC GGAGCACCGG CAATCAGCAA 480

AGGCAGCAGT GATAAAAGAC TGATATATTT CCTGTCATTA TTTTTCATAT TAATTTAACT 540

CCTGATTAAC CGGTTTTTAT TGATATGAGA AAGTAATAGT TGCAATAGCC TTCACACTTC 600

CAGGTGTAGT TGCATCAGCA ATTTTTATAT AATTGGCTCT TAAATTGATA TGTGGATTTA 660

CCTCTCCCCT GTAATCGGAG AAGTGCCATT GACTGCCATT TCCTTTCACA GGGGAGTCTT 720

CACCATAGCT GATGGCAGTT ACATCACTGT CTTTATATAG CCTGATGCCA AATCCTTTTG 780

CAGTGGATTC ACTGCTTAAG GTCAATATAT CTGTTCTGTT CACTGGCTGT GATGCATCTG 840

TCAATGTAGC ATAAACATCA ATTCCATCCG GGCATTGTAG GTGTATGTCA ATTTTACCTC 900

CCTGTATTTC TTTATACAAA GATGTGAACT GTGATTGATA TACGGTATTT AATGGCACCA 960

CATAGTTTTT TTGCCCCATG GTACATGTCT GACTCTGTAC CTGAATGCGC CCACCATTTA 1020

ACATAACAGG TGCTGTCAGT CCTTTATTAT TTAAACTTGT ACGTTTTGCT TCCAACAAAA 1080

TAGTACCAAG CTGCCTGGTG GGTATTGTTA TATATCCATT GGGTAATCTT CCCGTTGCGA 1140

CAAAAGCAAC AAACAAACGA GCTCCGAAGC TTGCTGTCGC ACCGTTATAA GTATTGGGGT 1200

TTGTATTGGC ACCTACAGGG TCAATATATA TACCTGAGCT ATTTATGGGG ACCAGAGGCG 1260

TTGCGGGCCA ATAGCCCGCC ATGCCAATAA TAATACCCAG TCCGGATACA CCAATATCAT 1320

AGATATCAAA ATCAGATGAA TCACGGCTGT TTCCTTGATG GAAAGTATAC GTAATACTTC 1380

CAATTTTAGG CAGTGCGGGT GTAAACTTTC CACGCATCAG AGCGATGGCA CCGCCATTAA 1440

AAACATACTG GTTACTTGTT CCCGCCAGCT CTCCTATCAC CCGGGGATAG GTATGGGCAT 1500

CAGCAGGACC AATCACAACA CCTGGCAATG TGGATGTATT AACCGCTATC TGCGAAGGCA 1560

CATAATCATC CGGACCCGCT ACCGCCAGCT TAGGGAGTAA AATTAAAAAC AATGGTATGA 1620

AAAAGATTCT TTTCATGTTT TTTCCTGATT AGGGTGCTGT ATACACAGAA CAGGAACGAG 1680

CTGAGATTGC ATATCATCTT TATTGTGTGC AACATGATAT ACAAATGAAC ATCTGTCTTT 1740

ATTATCTGGT CCCCATACAA CGCTGAGATG ACCTTTTTCA GGGAGTCCCC TGGTAAATAC 1800

CTTCCCGGCC TGAGCGACAT ATCCGGCCAA CTGTCCATGT TCATCCAGAA CTTCAGAAGC 1860

CATTGGAGGG GGATTGCCAG TAGACATACG AATATCAAAT AACAGACTTC TTCCTGTTTT 1920

AGTGTCAAAT TTYACTAACG TGGCGCTATT AGCACGAGGA ATGATTTCCT GCTCCGTCGC 1980

CGATAATTCA ACATTCAAAT CTAAATTGGA GGGATCGATG CTAATTTGAT TTTTCTCATA 2040

GGGTGTAACA TAAGGAACAA TACCATTTCC CCAAAAATCC AGACGACTAC CAGAGGCATT 2100

ATTGATGGCA GCCCCCTGAG CTCCTTCAGC ATGGATAATG GCAAAAGTAT CACTCAGGTC 2160

ATTACTCAAT GTCACTCCAT AGGGGTGTGC GACCACCGCT CCCGACGCAC CAAATGACCT 2220

TTGATTATTA TTCTGAGTAT CATGCCCGAC TGTTGTGGTT ATATTTACAT AAGGTGAACG 2280

ATAACCCCCA TTCATTGCAT AACCGGAAGG CCCGTTTTCC TGGCTGTTTC CTGAAAGACC 2340

ATAAGAGAAC TGATTATCCT CCCCGCCAGT ACCACTAATT GATGTCTGAA TACTATTTTT 2400

CTCTTCTTTG CTATAATTTA AAACAGTGGA AAACACCGGG CTTTGAACAC TTNCCTCCCA 2460

GAGGGAGAGT AAAATTAATA TAAAATCTGT CATCACGGCG TTGTTGCTCA TTATCTCTTG 2520

ACTGAGACAA TCCAATTTGA TAGCCGAGTT GTTTCCAGAA GTTGCTGTAC CCCATCTGGT 2580

ATTCATTACG ACTTCCTTTA TGTCCCCAGT AATTATAGGT TGTTCCTGTT AAATACATCC 2640

ISDOCID <WO 9822575A3 IA>

CACCCCATTT TTCACCTAAT TCCTGGTTGA TTGAAATCTG GAATTGATTC CTGGGACGAT 2700

AAAACGCTGT ACTTTTTACA GAAACATCAT CAATAAACGC GTTGTGATTA GCTGATAGCG 2760

CATCCTTCAG ATGATAAAAA TCTTTTGATG AATAACGATA AGCCGCCAGA GTTATATTTG 2820

TGTTTTGAGG GCTGGGAATA TTGGATGGCT AATAACTTGG AGTNGCAGGA CTAATAAACC 2880

TTTTACGGCG GTTACACCGG GAATACCNGG AAATGC 2916

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACCGCATCGC CAATCTCAGC GGCAGTGGTT TACATGTCTT CCGTGATGGA AGGTCATGGC 60

ATCAGCTACC TCCATCTGCT CTCCGTGGTC ATCCCGTCCA CCCTGCTGGC GGTTCTGGTG 120

ATGTCCTTCC TGGTCACTAT GCTGTTCAAC TCCAAACTCT CTGACGATCC GATTTATCGC 180

AAGCGTCTGG AAGAGGGCCT GGTTGAACTG CGCGGTGAAA AGCAGATTGA AATCAAATCC 240

GGTGCAAAAA CGTCCGTCTG GCTGTTCCTG CTGGGCGTAG TTGGCGTGGT TATCTATGCA 300

ATCATCAACA GCCCAAGCAT GGGTCTGGTT GAAAAACCAC TGATGAACAC CACCAACGCA 360

ATCCTGRTCA TCATGCTCAG CGTTGCAACT CTGACCACCG TTATCTGTRA ARTCGATACC 420

GACAACATTC TCAAYTCCAG CACCTTCAAA GCAGGTATGA GCGCCTGTAT TTGTATCCTG 480

GGTGTTGCGT GGCTGGGCGA TACTTTCGTT TCCAACAACA TCGACTGGAT CAAAGATACC 540

GCTGGTGAAG TGATTCAGGG TCATCCGTGG CTGCTGGCCG TCATCTTCTT CTTTGCTTCT 600

GCTCTGCTGT ACTCTCAGGC TGCAACCGCA AAAGCAYTGA TGCCGATGGC TCTGGCACTG 660

AACGTTTCTC CGCTGACCGC TGTTGCTTCT TTTGCTGCGG TGTCTGGTCT GTTCATTCTG 720

CCGACCTACC CGACACTGGT TGCTGCGGTA CAGATGGATG ACACGGGTAC TACCCGTATC 780

GGTAAATTCG TCTTCAACCA TCCGTTCTTC ATCCCGGGTA CTCTGGGTGT TGCCCTGGCC 840

GTTTGCTTCG GCTTCGTGCT GGGTAGCTTC ATGCTGTAAT GACCCATYGC GGGGCGTTCA 900

CGCCCCGCTT TCTTTCCCGC CGACTAACAT CCTTTCCCCG TCCGTTGTAT AGTGACCTCT 960

CTCTTGCGGT TCCATCTGTT CTTGCGAGGT GTTTATGCTT GATGAAAAAA GTTCGAATAC 1020

CACGTCTGTC GTGGTGCTAT GTACGGCACC GGATGAAGCG ACAGCCCAGG ATTTAGCCGC 1080

CAAAGTGCTG GCGGAAAAAC TGGCGGCCTG CGCGACCTTG ATCCCCGGCG CTACCTCTCT 1140

CTATTACTGG GAAGGTAAGC TGGAGCAAGA ATACGAATGC AGATGATTTT AAAAACTACC 1200

GTATCTCACC AGCAGGCACT GMTGAATGCC TGAAGTCTCA TCATCCATAT CAAACCCCGG 1260

AACTTCTGGT TTTACCTGTT ACACACGGAG ACACAGATTA CCTCTCATGG CTCAACGCAT 1320

CTTTACGCTG ATCCTGCTAC TTTGCAGCAC TTCCGTTTTT GCCGGATTAT TCGACGCGCC 1380

GGGACGTTCA CAATTTGTCC CCGCGGATCA AGCCTTTGCT TTTGATTTTC AGCAAAACCA 1440

ACATGACCTG AATCTGACCT GGCAGATCAA AGACGGTTAC TACCTCTACC GTAAACAGAT 1500

CCGCATTACG CCGGAACACG CGAAAATTGC CGACGTGCAG CTGCCGCAAG GCGTCTGGCA 1560

TGAAGATGAG TTTTACGGCA AAAGCGAGAT TTACCGCGAT CGGCTGACGC TTCCCGTAAC 1620

CATCAACCAG GCGAGTGCGG GAGCAACGTT AACTGTCACC TACCAGGGCT GTGCTGATGC 1680

CGGTTTCTGT TATCCGCCAG AAACCAAAAC CGTTCCGTTA AGCGAAGTGG TCGCCAACAA 1740

CGAAGCGTCA CAGCCTGTGT CTGTTCCGCA GCAAGAGCAG CCCACCGCGC AATTGCCCTT 1800

TTCCGCGCTC TGGGCGTTGT TGATCGGTAT TGGTATCGCC TTTACGCCAT GCGTGCTGCC 1860

AATGTACCCA CTGATTTCTG GCATCGTGCT GGGCGGTAAA CAGCGGCTTT CCACTGCCAG 1920

AGCATTGTTG CTGACCTTTA TTTATGTGCA GGGGATGGCG CTGACTTACA CGGCGCTGGG 1980

TCTGGTGGTT GCCGCCGCAG GKTTACAGTT CCAGGCGGCG CTACAGMACC CATACGTGCT 2040

CATTGGCCTC GCCATCGTCT TTACYTTGCT GGCGATGTCA ATGTTTGGCT TKTTTACTCT 2100

GCAACTCCCC TCTTCGCTGC AAACACGTCT CACGCTGATG AGCAATCGCC AACAGGGCGG 2160

CTCACCTGGC GGTGTGTTTA TTATGGGGGC GATTGCCGGA CTGATCTGTT CACCYTGCAC 2220

CACCGCACCG CTTAGCGCGA TTCTGCTGTA TATCGCCCAA AGCGGGAACA TGTGGCTGGG 2280

CAGCGGCACG CTTTATCTTT ATGCGCTGGG CATGGGCCTG CCGCTGATGC TAATTACCGT 2340

CTTTGGTAAC CGCTTGCTGC CGAAAAGCGG CCCGTGGATG GAACAAGTCA AAACCGCGTT 2400

TGGTTTTGTG ATCCTCGCAC TGCCGGTCTT CCTGCTGGAG CGAGTGATTG GTGATATATG 2460

GGGATTACGC TTGTGGTCGG CGCTTGGTGT CGCATTCTTT GGCTGGGCCT TTATCACCAG 2520

CNTACAGGCC AAACGCGGCT GGATGCGCGT GGTGCAAATA ATCCTGCTGG CAGCGGCATT 2580

GGTTAGCGTG CGCCCACTTC AGGATTGGGC ATTTGGTGCA ACACATACCG CGCAAACTCA 2640

GACGCATCTC AACTTTACAC AAATCAAAAC AGTAGAT 2677

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATCCTGATGA CGCCGTAAAT GTGCATTTGC CAGGATTGCC GCATAGAGGG CACGAAGAAA 60

AGGTCGGTTG TCAGGATGTA TCCAGATGAT TCTGCCACTG AAACCTTCAG GGATAAGACG 120

NSDOCID: <WO_ 9822575A3 IA>

ATTGCCAACT GCCAGTCCTT TAAGGGCAGC ATTCAGCGCC TTACGCGGGG CATTCTGCTC 180

CAGAAATACG TATGCCAAGT GAGCGTGTAC ATCAATAAAG TCATTCTCCT GTCGGGCAAG 240

GCGCCTGAGT TTGTTGATGT AACTTGTTTC GCTGATTTCA TCCGCATCGT ATGCATCAAT 300

CAGTTCTTCA AACTCATCCA GCAACGAGCC AAACCAGGTT TCCGGAAATA TGAAACAGCC 360

CTGGTTATCG TTCACTTCAA AGCGTAATTT GCCAGTCATA TTCTGAACCT GTAAAAAAGG 420

ATAGACCATA ATCTGCAGGC TATAAAAATT GTGGATGCCT GGCATCGGGT GTCCTTTTAT 480

TGTCCGGGAT TAACGTTGCC CATGATAATA CAGTGAATCC NGTTCTGTGG TAAGACG 537

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CGCTCGAGCA CCAGATTCAC TGACATGCGC AAACTCATGT GTAAATCCTG TCTGGGCATC 60

TATCTCAAGT AACAGTTCCG TTAAATCTAC CGGTGGGAGT AGCTGTTTGA TCCGATTATT 120

TAGACGAAGC AATGATGGTG GCTCTTCCTG TTTCTCCAGA CAACTGATAG TCAGGGATGG 180

ATATTTACCT TCATTACAGA TATGAACTTC CGCATTCTTT TCAAATCGTG ATGCCAGGCT 240

TTCCAGGTCT CATCCAGCTG AATAGCCAGT TGTTGCACAC CTTTACGTCC ATCGACAGGA 300

TGTCCCAGTG CCCGACAGAC AGGAATACGC TGAGTCTGCC ACTCTTCACC TTGCAACAAC 360

TTCTCGCGAG GATCTCCCCA GCGATCACTG TTTTCAAGCC CAGATGTCCC CGGCGGCGCA 420

RTGCATCCTG AAGGCGTTCC AGCAAACATA GTGAATAACC TGCACGCTGT ATCCCGTCCC 480

TCCGCATCGT ATACGAGGCG TTTCCAGGGA CCGGTGATAA TATGTTCAGC GCATCATCAA 540

GGATGCGCTT TTTCGAACCA TTCAGTTCTG CCAGATAATG AATCGCAGCC AGTACATGTC 600

ACCTGCCGGT GCCGCACGGA AATGCAGGTC CCGCAACACC GCCGGAAGAA AACGTTTAAC 660

CCGACCGTAC TGCTCAACCA TTTCGTCATG GAAATTATTG TTCTGTGGAC GAGCAAGTTC 720

ATTAACCTTG CTTACAGATT CTGCCAGTCT GTTTTTGGGT ACGCACTTGA AGATAACCTG 780

CCTGAGATCT GGGACATCTG TATTATCATC CAGCAACAAT GCACATGCCC GCGCCAGTAA 840

CAATGCGGCC TGATCAAGAT CTTTCAGTGT CCTGAGTCTT TTTTTTTGCC CGGTTTTCTT 900

TGCTTCGCGG ATAATGTCCA GAATTAGCAT ATCAAGCACA TCAACGGCAT CGTCTAATGC 960

CGTTATTTCC TGTGCTTTAA CGAATGCAGT AAGTACAGCA AGCTTTCTCT GCTGTGGCAT 1020

TCGAGCGATA TATTTTACCG ACGCCATGCC AGCATGAACG AGCCAGATTA CGCNTTGGNA 1080

ATGGTCAGGC AGACCGGGAA AAGTTCCAGT CGGGNAAAAC TCCAAGAA 1128

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGNTGATAAA AATCYTTTGA TGAATAACGA TAAGCCGCCC AGAGTTATAT TTGTGTTTGA 60

GGCTGGAATA TTGATGCTAT AACTTGAGTG CAGACTATAA CCTTTACGCG TTACACCGGA 120

ATACCTGAAT GCTGTTCTGG ACAATGTAAT GTCAGATGCT ATAGCACCCA GATGGGTATT 180

AAAGGCCAGG CCAGCTAACC CCGCTGTATA TCCTGAAGCT GTGGTAAGAC CACTGTTTAA 240

AGTAATATCA TTCGTCAGGC CGTATTGATA GGTGCCTTGT GCTATTAAAT CATTATATGT 300

TTTATTCGCA TAACGATACT TTCCCACTGA CATTTGCCAG CGACTAAATC CGGGACGAAT 360

GAGTTGAGCA ACGGCCGCAA AAGGAACCGT GAACATTCGT GTCTGGCCAT TAGACTCTGT 420

TATCTTAACG AGAAGGTCAC CAGCATATCC ACTGGGATAT AAATCATTGA TGACAAATGG 480

TCCGGCTGGC ACCGTCGTTT CATAGAGGAT ATGAGCATTT TGATAAATGG TTACTTTAGC 540

ATTACTGTTA GCTATTCCCC GGACAGCAGG RGCATAGCCA CGTAAAGAAC CGGGTAACAT 600

TCGTTCATCC GATGCTAACC TGACTCCCCG CAAACTGAGG CTATCCATTA GCTCACCATT 660

CGTATAAAAA TCCCCTAATG TGAATTGTGC TCTCAATGGG GCAAGGTCAT GCATTATACT 720

TGTTTCTATA TTCTGATATC CGGCAGGATA GCTATTATTC CAGCTCTCAC TGCCACGGTG 780

GCGCAAAGCC ATCCCCACAA ATTGAATCCA GCTTTTAATC CCAGATAAGT CTGTTCGTTA 840

CTCGTCCCGG AAGAGCTATA CTGGTAATAG TTAGCATCAT AGTTTATAAA TGCTGCAGGA 900

ACACCACTTT GCCACTGAGA AGGGGAAATA TATCCTCTTG GACGTGTATT CAGCAGTGCT 960

GCGGGATTTC GATATTCAAC CTTAAAGTCG ATAAGTCAAA ATTAATTCTG GCTGAAGAAA 1020

GCCCTGTTGA CGCCGGAAAG CAGGAGGTGT TTCCCGACAT AGTATCTTTG ACTAAATCAA 1080

TCAATGAAAG CAGCTCAGGC GTCAGGCATA ACGTCGGAGC ACCGGTATTG GCAGTACGTA 1140

AATACTGCAA ATCAGCCTTC CCCTTCCATA CATTATTAAC ATAAATATCA GAATAATACC 1200

TGCCCTCAGG CACAGGGTTA CCATGACTAA AGCGGCGGAT ATCAATAGCA TTTATCCCTT 1260

TATCCAAATG CAAAAACTCA GAATCAAACT CAGCCTCTTC AGCAGCAAAT GAATGGTTTG 1320

TTACTGTTAA CCCTAATGCA GCAAAAAGCA GAAGAGAACA ACGACAGTAA ATCAGGCATG 1380

ACAGATTATT AGCGTTCATT ATTACCTTAC TCCAGAACAG ATTCTCCTTG CTGATATCCT 1440

CCGTAATCAT TAACAATAAC CCAGGAAACT TTGCTGGTGG CGCAGTTCTG CCTTTAAGTG 1500

CAAATACTGT TGAAGAGAAA GGGGGAATCA TTCCACCATG TTCAACAGGC GTTAAGTGCT 1560

JSDOCID <WO__9822575A3_IA>

TATTCTGGTC AACTGCAATT TTGTTGTAGG TTATGTAATA AGGTGTTGGA TTAACTGCTT 1620

TAATTCGGCC TTCCTCCTGG TGCCAGGTAA CTTTCAGATA AGCATCATTT GGTGTTAACT 1680

TCAGGTGAGC AGGACGAAAG AAAAATTTTA TGCGACTACG AACAGCTAGT TGCAAATAAT 1740

TATTATTCCG CTGCTCTGAG TTATCGGAGT CTTTTTTTGC CCTGGGCTTT GCTGGAATAT 1800

CCAGAACATT TAGATAGAAA AGAGATTCTC GGTCTTTCGG TAGTGACTCG CCTGTATATA 1860

CAATTCTGAC TGTTTGTCCT GATTTAGAGT CCATACGAAA TATTGGCGGA GTAATGATAA 1920

AAGGACGTGG ACTGACTCAG GGGGAGCTGC TGCATCTCCA TCGYCAACCA GGACTGGACT 1980

AATGCCGAGA TTTCATTGTC ATTATTTNAA CGTATGCTAA TACTCTTTTG AGTCGCCGGA 2040

TAAACAACAC GGGTTCCCAT GATAACTACA CTACCCTGAA CAACTGCAGA TACAGATAGA 2100

GTAAAAAAAA ACAGCACAAA CCTTAGCATG GTATCTCCAG AAGAAAGCAG GGCAGTATTT 2160

CCTGCCCCAA AATACAAAAC CGTTTGTTAT TCGTAGGCGA TGGTATAATT GACTGTTGTT 2220

TTTACATTGC CTGGAGTTGA TGTCCCGGTC GCATAATATT GAGCCATATA ACGTAATGTG 2280

GCATTACCAT CCCCACCAAT AGTTTCAGAA T 2311

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TATTACCTGT GATTTTTCCG GGCGTAAATG GAGTCCCTAA AGTTATCGCA GTCCCAATAT 60

TTCCTGCATT ACTGTTATAA AGATAAACGA GTAACCCATC AGAAGATGTG TTTGATGTAT 120

TCTGAACTAA AATAGCATTG TNATAAGTGT TTGTTGCCGT TATCGTAACC TTCATTGTTC 180

CCAGATTATA GGGACACCGC ATATTCACAG TAAACTCTTT TTCGTGANTT CCATTTTGAC 240

TCAGGGTCTG AATCTCTACA NCCTGCCAGT CAACAGTTGT GTTGCTTACA GTACAGGCAG 300

GAATAATCAG TTTTCCTCTG AAGGTCAGAT TATCAACTGC ATGTACATGC TGAGACATTA 360

ACACTGCCCC CAGCATTACC GGAAGACACA AACCTCTTAT CTTTTTCATC TGAAATATCC 420

TGTACAAAAA TTTTGCTAAC GATATGTCAA TTCAAACGTG GCTGTTGCTT CATAATCACC 480

GGGTACCACA CTCTTCGTCC GCAGGGCTTC CGGCGTTGCC ACAACATACG CGCCGAAAGG 540

AAGCTCAAGA CTGTTTCCGG TAACCTTTTC CCCCTGGCCT TTGTTATGGG AGGTGCCGGG 600

TTTCAGCAGA CTGCTGCCAT CGGTGTCCAG CAGTGCAATG CCTAACCGGC CAGCATTCAC 660

TCCGGTTACC TTCAGATGGC CCGGGAGRCG CYNTCTTCCG TCCCCTTAAA GGTCAGGGTC 720

ACAATTTTGC CAACTGCTGT TGCATGGCAG TTTTCCAGCC TGATGACAAA CGACTCTGTC 780

NSDOCID: <WO 9822575A3 IA>

GGCGAACGTC CGGGCGGATA CCAGAAATCC CTGGACGCCC GGGTTTTGAA GACGACATGT 840

TTATTCAGAC TGTCACCGGA CACATGGCAG GGTCTGTCAA GCAGATTACC CCTGAATGCC 900

ACATCTGAGG CTATTGCCTG TCCGGCAGAC AGTGCGGCAA ACAGTAAAAG AGCGCCTGTG 960

CTTTTTATCA TCACATTCCC TTACTCATAT TTTATGCTCA GACGCAGCAT GGCCGGATTG 1020

CTCCTGGCAT CAGAATACTC AACCTCCTGT GGCGGCCTTT TCCTCCAGGC GGGCAAGCAT 1080

CTCCTCCTGG CGGCGGGTAA GGCGGGGACA GTAAAAAA 1118

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTCGTGGGTG AAATCGTAGG CCGCGCTTTT TTGCTGATCG GCCAGTTGAT GAATAGGGTG 60

GCCAKGATCG GGATAAAACG TACAGGCAGC GATAAACAGA CAGCCCGGAT AGCGGTTGTT 120

TTTAACGCAC TCCGATAACG CCTGATAACG TGCCAGCAAC TTTTGTTCGG CGGTTTGCGT 180

TTCGTCCAGC ATCAGCTGAC GACGCCAGAC ATCTATCTGT TGGCTAAGAT AACGCAGCGC 240

ATCGTAGAGG ATTGCCTCTT TGTCTGGCCA GAAGCGGCGT ACTCGTCCAG TGGATAATCC 300

ACACGTTCAG CAACCATCTC CAGCGTGGTG TTGGCAATCC CTTGTAATTC TAATAATTTC 360

AGGGCTTCTC CCAGTACATC TTCACGTTGC ACGCTATTTT CCTCCGKCTT TCCCACTGCA 420

ATGTTCGKTC ACGGTTGGCG ATCGCGCAAA TGTGCGCTGG AAGGTTTCAG CATCCATAAA 480

GCCCGTGACG CGTGCTTGTG GATGCTCCTG GCCTTGGTCC GGTCAAAAAA GAGAATTTGT 540

CCGGTAGGGC CAAGGATATT AA 562

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCATCGCTTT ACCCCAGAAA AGTTAAGCCA TATAATGTGA GGGATATAAG TCGTCGTATC 60

CGGTAAGTAC AGATAACCAC AACATAAGCT CATTCAGTAA ATTTTATCTC TGAACAAACG 120

ACTATGGCAT GCTCATTTAT ACTATTCATA AGAAAGTGTG ATTATCTGTA AGCATTAACC 180

ATCAAATCAT ATAACCATAC TAAACTGGCG GATCATCAGC ACCATTAGCA GGTAACTTAT 240

TGAAATTTTA TTATGTGTTT TTTGTTGATA ATTAATATGC AATATGAATT TGCTATTTTA 300

GAATCATGAA CACCATTTAA AATTACCATC ATTAACATCA TATAAAAATA TATTTTTACT 360

AAAACATGAA TTGTATATAT TTATTAGCTC AGGAAAATTA TCAGGGTTCA CCTTCAAATT 420

AACCTGAATG TTATGCTTAA TTTCACCCAG TAGTTCTTCA TGTGTAGATT TTATTATCCC 480

ATTATTATAA TCGATAAATG CACACATGTT TTTTATGAAT TCAAAACCTT TTCCTGTATA 540

CAGTTTAATG AATGCCACCA GAGCAAACAT TTCAAGATGT AGCCATAATG CTACGTTAGT 600

TTTTTGCAAA GTATAAAAAA TTGAATTCGC CACTTTTTTA CTTATTGCTC TTTTATACTG 660

TGATCGAGCA AGATTCAGTA GCGGAAGTCC TCGTTCAATA AATGAATGTG AAAAGACTGG 720

ATAAATTGAT GTCGGAAACC TTTCA 745

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCGTTNATGC ATTTCGASAT TTTCCACTTC GTTCTGACGT TGCACTGCTT TGGCGTCATC 60

ATTACGTAAC GTATCGAGGA AATCGAGGTA GCCCTGATCA ACATCTTTGG TGACGTAGAC 120

GCCGTTGAAC ACCGAGCATT CAAACTGCTG GATATCCGGA TTTTCAGCGC GAACGGCGTC 180

GATCAGATCG TTCAGATCCT GGAAAATCAA CCCGTCAGCA CCGATGATCT GGCGAATTTC 240

ATCAACTTCG CGACCGTGAG CGATCAGTTC CGTGGCGCTC GGCATATCAA TACCATAAAA 300

CGTTCGGGAA AGCGAATTTC CGGTGCCGCA GAAGCGAGGT ACACTTTCTT CGCTCCGGCT 360

TCGCGTGCCA TCTCGATAAT CTGTCAGAAG TGGTGCCACG 400

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGTCGACGAT GAGGCAGCCA GAGCATTAGA GCCGAAAAGA AGGGATGATG CCATGACTGC 60

TGTTGCTATA AAATGTTTCA TATATTCTCC ATCAGTTCTT CTGGGGATCT GTGGGCAGCA 120

TATAGCGCTC ATACTAGGGG TTTGAGGGCC AATGGAACGA AAACGTACGT TAAGGAGATA 180

ATTCGTTGTT TATATTTAAA TTTAGAGCTC TCAGTTCCCC TTTTAAAATA TCCTCTGGCA 240

ACGTGAATGT ATAATGGCCC AACATATTGA TATGCCCGTG CATCAGGGGA GATAGCCGAG 300

CGATATCTTC ATCTATAATT TCTTCGCCAT TACGGCGCAT CCAGCTCAAC GCTTCCTCCA 360

TATAGAGCGT GTTCCACAGA ACCACTGCAT TAGTAACCAG GCCCAGCGCC CCCAGTTGAT 420

CTTCCTGCCC TTCACGATAA CGCTTTCTGA TCTCTCCGCG TTGTCCGTAA CAAATCGCAC 480

GAGCCACAGC GTGCGKTCCT TCTCCTCGAT TAAGCTGCGT CAGGATCCGC CGACGATAAT 540

CTTCATCATC AATATAATTG AGGAGATATA GCGTTTTGTT TACACGCCCT ACTTCCATAA 600

TTGCCTGTGC CAGTCCTGAT GGGCGCGAGC TTTTCAGTAA AGAGCGAATG AGTTCTGACG 660

CATGAATTGT ACCCAACTTC AGGAACCAGC GGTTCGCATC ATCTCATCCC ACTGACTCTC 720

CGCTTTTGAC AGATCTGCAT ATCCTCGGGC CAACTTATCC AGTACTCCGT AGTTTGCCGA 780

TTTATTCACC CGCCAGAACA CCGCCTCACC TGCATCGGCA AGCC 824

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACAAATCAGA CCAGTTAACC AGTCAGTCGG TTTTATGATT TCACTCACTA TACTTTGTTT 60

CATAAGGATT TCAGGATCTG CCAGACTGCG CAGAAATGAT GCTTACGAAT ACACAGTAAA 120

GGCAATGTCA TTTCCGATAC AGAGCCTGAC ATTGCCATAA TGAGCTATTT ATCTGAAAAA 180

CGACAGAATA TGATGTTTTA TCGTAACGTA ATTTTAAGTT CTCAACTTAT TGAGACATAT 240

TGTCTTTTTT ACCCATGTGG TCATTTTTCA TCCCATCCGT TTTGCTCATG TGTTCTTTCT 300

CCATTTTCTC TTTATCCATT GCATTTTTGC ACATACCATC CTTGCACATT TTATCATGCG 360

CGCTGGACAT GCTGCCTTTT ACTTCATGTG TTTTATCCAT TGTGTCTGCT GCCTGAGCAT 420

TGAACATGAA CAGCGCGGAT AGTACAGTTG CAGAAATAAT ATTTTTCATG GTTCTTCCTC 480

ATTTTTAACA ATTGTATCAA CAACCACCAA ACCAGTTATA ACCCTGGTCT TCCCAGTACC 540

CCCCCGGAAA ATGATTAGTG ACCTCTATAA CCTGAACATG CTTGGGGTTT TTATATCCCA 600

GCTTAGTAGG GATACGTATC TTTATGGGAT AGCCATATTC TTTTGGCAAT ACCCTGTTAT 660

TCCATGTCAA TGTCAGCAAT GTTTGTGAAT GTAGTGCTGT CGCCATATCA ATACTGGTGT 720

AGTAACCATC GACGCAACGA AAACTGACGT ATTTTGCCCG CATATCGGCA CCAATCAGCG 780

TCAGGAAATG CCGGAATGGT ATCCCTCCGC ATTTTCCTAT TGCACTCCAT CCTTCAACAC 840

NGATATGACG GGTTATCTGA CTCACATGCT GCATGTTATA CAATTCAGAC CAAAAACCAG 900

TTACGGGTTA T 911

WSDOCID: <WO__9822575A3_IA>

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

NGGGGCAGGA TAATTGTATC CTGCCCNGTA TATAATTCTC AGCACAGGTG TTGACTAAAG 60

AGCGTGAAAC TTTGCTATTA TGTCTTCGTA AGATTCACGG ACGGTTATAC TTGAGCCTGA 120

TTCTGTGAAG TAAACAACAG CAGAAGCATC GTTGCCTTTT TCAATGTATG AAACATTCCA 180

GTCATGGATA GCCACTGCGG GCTGACCATT ATCCCGACGG TGCGTCTTAA TGAATCGCGG 240

AAGTAATTCT GCAATATCGT TAAAAACACC ATTTACGGTA TGAGTGATAC CACCAACGCA 300

ATGTAGATGA GTTGACTCCG GGGTATCATT GTCTGCTTCT GCAAAGAGTA TAGCTGTCTT 360

GCTAATTGTA ACAGGCGCCT GTGARCGGGA TAATTCGAGA GAAATAAACC CGGATTCTGC 420

CATAAAAACT CCAGTTTGTG ATGTTATATC ATTTCATATG TTT 463

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTCTAACCTC TGACCAAAAA CAGAATTACG GTTGTTATGC TGCAGAACCT AATGACGTGC 60

AACTGGCGCG CTATTTTCAT CTTGATGAAC GGGATCTGGC CTTCATTAAC CAACGACGGG 120

GCAAACATAA TAGGCTGGGC ATTGCGCTTC AGCTCACCAC AGCCCGTTTT CTGGGAACAT 180

TTCTGACGGA TTTAACTCAG GTTCTGCCTG GTGTTCAACA TTTTGTCGCG GTACAGCTTA 240

ATATCCACCG TCCAGAAGTT CTCTCCCGCT ATGCTGAACG GGACACTACC CTTAGAGAAC 300

ATACTGCATT AATTAAGGAA TATTACGGCT ATCATGAATT TGGTGATTTT CCATGGTCTT 360

TCCGCCTGAA GCGTCTGCTA TATACCCGGG CGTGGCTCAG TAATGACGAC CGGGTCTGAT 420

GTTTGATTTT GCCACTGCAT GGTTGCTTCA AAATAAGGTA TTACTGCCCG GAGCAACCAC 480

ACTAGTACGT CTCATCAGTG AAATTCGTGA AAGGGCAAAT CAGCGGCTGT GGAAAAAGCT 540

GGCCGCACTG CCGAACAAAT GGCAG 565

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

NSDOCID: <WO 9822575A3 IA>

(A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGATGGCGTC CGGGGTGAAC GCCGGATAAG TTTAATTTAT CCGGTCAGGC AAAAGGCATT 60

AATCTGCAGA TAGCTGATGT CAGGGGAAAT ATTGCCCGGG CAGGAAAAGT AATGCCTGCA 120

ATACCATTGA CGGGTAATGA AGAAGCGCTG GATTACACCC TCAGAATTGT GAGAAACGGA 180

AAAAAACTTG AAGCCGGAAA TTATTTTGCT GTGCTGGGAT TCCGGGTCGA TTATGAGTGA 240

GTCACTCCGG TGAGATGTCC GGTTATTTAT CTTTTTTGTG AATCTGGTGA TGCGTGGAAT 300

GAAAGACAGA ATACCTTTTG CAGTCAACAA TATTACCTGT GTGATATTGT TGTCTCTGTT 360

TTGTAACGCA GCCAGTGCCG TTGAGTTTAA TACAGATGTA CTTGACGCAG CGGACAAGAA 420

AAATATTGAC TTCACCCGTT TTTCAGAAGC CGGCTATGTT CTGCCGGGGG CAATATCTTC 480

TGGGATGTGG AATTGTTAAC GGGGCCAAAG TA 512

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGCCGGTGC GGTTANTAGT GGCAGTGGTG TCTTTTGGTG TAAATGCTGC TCCAACTATT 60

CCACAGGGGC AGGGTAAAGT AACTTTTAAC GGAACTGTTG TTGATGCTCC ATGCAGCATT 120

TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC TTTCAAAAAG CTTCCTTGAG 180

GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT TGGTTAATTG TGATATTACT 240

GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA AGCTGGCTTT TACTGGCCCG 300

ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG GTACGGGCAC AGCTATCGTA 360

NTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG AAGTGATGCT AATACCCTGA 420

AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTTAA GAAGTCGTCA GCCGTTGGTG 480

CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT CAACCTGACT TATCAGTAAT 540

ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATTCCGCTG TTTATTTCTC AGGGTATTTA 600

TCATGAGACT GCGATTCTCT GTTCCACTTT TCTTTTTTGG CTGTGTGTTT GTTCATGGTG 660

TTTTTGCCGG TCCGTTTCCT CCGCCCGGCA TGTCCCTTCC TGAATACTGG GGAGAAGAGC 720

VSDOCID <WO__9822575A3 IA>

ACGTATGGTG GGACGGCAGG GCTGCTTTTC ATGGTGAGGT TGTCAGACCT GCCTGTACTC 780

TGGCGATGGA AGACGCCTGG CAGATTATTG ATATGGGGGA ATACCCC 827

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CCAGGGGCCC AAAATCCGTG TATCCACCTT TAAAGAAGGC AAAGTTTTCC TCAATATTGG 60

GGATAAATTC CTGCTCGACG CCAACCTGGG TAAAGGTGAA GGCGACAAAG AAAAAGTCGG 120

TATCGACTAC AAAGGCCTGC CTGCTGACGT CGTGCCTGGT GACATCCTGC TGCTGGACGA 180

TGGTCGCGTC CAGTTAAAAG TACTGGAAGT TCAGGGCATG AAAGTGTTCA CCGAAGTNAC 240

CGTCGGTGGT CCCCTCTCCA ACAATAAAGG TATCAACAAA CTTGGCGGCG GTTTGTCGGC 300

TGAAGCGCTG ACCGAAAAAG ACAAAGCAGA CATTAAGACT GCGGCGTTGA TTGGCGTAGA 360

TTANCTGGCT GTCTCCTTCC CACNCTGTGG CGAAGATNTG 400

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 578 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CCGATTTTTT GCGAAACGTT CCGCCTGGCA TCAGGATAGT TTGTTCGTTA TCCAGTTCGG 60

ATAGCGCATT GACGATATGC AGGCTGTTGG TCATCACCGT GATGTNATTA AAGCGCGAGA 120

GCAGGGGAAC CATCTGCAAA ACGGTACTGC CAGCATCAAG AATGATCGAA TCGCCATCAT 180

GGATAAAACT AACGGCAGCT TCTGCAATCA GCTCTTTCTT GTGGGTGTTG ATGAGTGTTT 240

TATGATCGAT AGGCGGATCG GATTCCTCTT TATTCAACAC CACTCCGCCA TAAGTACGAA 300

TGACGGTTCC GGCATGTTCC AGAATGACCA GATCTTTGCG AATGGKTGTG CCTGTGGTGT 360

CAAATATTGC GCCATTCTTC AACCGAGCAT TTACCCTGCT TTGCAGATAC TCCAGAATGG 420

CGGCCTGACG CTGACGAGTT TCATGGGCGT GATACCTGAT TTAGGTTCAA ATGATAACTC 480

GCAAGCAGTA ACATCACACG NAATATCCAC GTTCAGTTAA GCGCCATGAT AGAGCATCCG 540

TGATAGGGNC AGGGGNAGTC ACACGGCGTA ATCACCGC 578

(2) INFORMATION FOR SEQ ID NO: 39:

NSDOCID <WO__9822575A3_IA>

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TGTTAGGTCA GGGCCCACAG TCAAGCTTAG GTTTTACTGA ATATACCTCA AATGTTAACA 60

GTGCASATGC AGCAAGCAGA CGACACTTTC TGGTAGTTAT AAAAGTGCRC GTAAAATATA 120

TCACCAATAA TAATGTTTCA TATGTTAATC ATTGGGCAAT TCCTGATGAA GCCCCGGTTG 180

AAGTACTGGC TGTGGTTGAC AGGMGATTTA ATTTTCCTGA GCCATCAACG CCTCCTGATA 240

TATCAACCAT ACGTAAATTG TTATCTCTAC GATATTTTAA AGAAAGTATC GAAAGCACCT 300

CCAAATCTAA CTTTCAGAAA TTAAGTCGCG GTAAATATTG GATGTGCTTA AAGGACGGGG 360

AAGATTTCAT CGACACGTCN GCGTGCAATC TATCCGTAT 399

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CAGCCTCCGT TACCGGACAG CAAGGAGGCT GAATGGAGTT TACAGGATTT GCTTTTTTAT 60

AATGTCTGGC CATGCAGTMA AACCGGACAG GTTTTATTAT CATGTGAGGT ATTCTGACAT 120

AAAATGCTGG ATTTTTATTT TGTGACGAAT GCTGCAAAAT TGCATCTGCA CTCTGATGTA 180

GCTTTTATCT GTTTCAGTGA AGCATGCCCA CAAACTGAGT TATTAAGTTG TGGAAGAACA 240

GTTTTGTCCC GCCTGCATAT CTCCTTTCAA AAACCAGTAT GTCGCCATGC CTCGCCTTAA 300

TGGAGAGCGC TGAACCATAC CTTCTTT 327

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGAGATGGGC ATGGAACTCA CTTCATAATA ATGCCTACCG AAGAAATATT AATAGATGAC 60

ATTTCCACGA GNGATAGCAA TAAAACATCA GAGCAGTCTT CTCGCTTAGA AAAAGCTTTA 120

JSDOCID: <WO 9822575A3 IA>

TTAGGTTTTA CAAACACAAT GTACAGTGAT TCAAACCCTC CTATTATAGC TCGTTTTAGA 180

GACTATCTGG AAGATGGTGA GTGCATTGAC AGAATTAGCG AATCAATTTT TTTTACACCG 240

CAAGAATTCA ATCTTGCAGA TCACCACATT GAAGGATGGT TCAATGAATT TGGTCAATTC 300

AGTGGAACTG TTTC 314

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TCCCAAGATC TTTTTGGCCG CAAATCCACA AAACCCGTCG TTANTGTCGC GCAGCCANTT 60

GCAGGCCGAA TTTGCACCGT TTTAGAAAGC GGCGTTTTGT AGAGCAGCAC GCAGTGAGAA 120

GCCACCGCGC CACGACCTAC GNGCNCGCGC AGCTGGTGTA ATTGCGCCAG ACCCAGACGC 180

TCCGGGTTTT CGATAATCAT CAGACTGGCG TTAGGCACAT CAACGCCGAC TTCAATAACG 240

GTTGTGGCAA CCAGCAGGTG TAGCTCACCT TGTTTAAACG ACGCCATCAC CGCCTGTTTC 300

TCGGCAGGTT TCATCCGCCC GTGTACCAGG CCAACGTTCA ACTCTGGTAG CGCCAGTTTC 360

AACTCTTCCC AGGTAGTTCC GMCGCCTGCG CTTCCAGCAA TTCCGACTCT TCAATCAACG 420

TACAAACCCA GTATGCCTGA CGACCTTCAG TTATGCAGGC GTGGTGCACC GGGTGCAATG 480

GATGTCGGTA NNGCGGGTAT CAGGAATAGC GACCGTAGTC ACTGGGCGTG CGGCCTGGGC 540

GGCACTCCAT CTATCACCGA GGGTATCGAG ATCGGGCATA CGCNTGCATT 590

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT 60

CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT 120

TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGGATA AATGCTTCAA 180

TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCCTTT 240

TTTGCGGCAT TTTGCCTTGC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA 300

TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGGATCTG CAACAGCGGT 360

AAGATCCTTG AGAGTTTTTC GCCCCGAAGG AACGTTTTTC 400

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATTCGGAAAG ATGCTTCTAN TTTTTTTAAG CACGTATAAA CTGTTAATTC AGGTTCAATG 60

CTACGAAATG CACTAGTTAT AACCTGTATT GAAGGAAAGA TCTTCTGATA CTCTTTCCAG 120

AGATCTTCAA GTCTGGCCAT GGAAATTGAC TTGGCTGCAT ATTCTAGGTC AGTGTTTATG 180

ATAGTTTCTC TATTCTCTCT GAATGCGGAA AAAAAAGCTT CATTCAACAA TGATAGTAAA 240

TCCCTGGGCC GGTAAAGGGT AAATTGCAAA CATCGCTTAA AACCATTCCT CCCTTTAAGA 300

TCATCCGCTG TGCATCTATC CCAAACTCGT TGATCTTTCT CAATATCTAG CTTAAATGCT 360

ACTTTCATTC TTTTAGCTGA CAGCATTAGG AGTTGTGCCC 400

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TAATGTTGAA GACAGAGATA TAATNTACAG CATCATCCCA CAAGGCAGAT ATAACAATAC 60

TTGACTGGGA TATGCAAAGC GATAGTGGGC AATTTGCTAT TGAAATAATA AAATCGATAA 120

TCGTTTCAGA TATAAATTCT GGAGGACGTT TACGTCTTCT TTCTATTTAT ACTGGTGNAC 180

ATGTTACTGC TGTTATAACT AAGTTGAACA ATGAGTTAAA GAAAACATAC CGTAGCGTAA 240

TAAAAAATGA TGATAGTATT TTTATTGAAG ATAACTATGC ACTCGAACAA TGGTGTATAG 300

TTGTTATTAG TAAAGACGTT TATGAAAAAG ATCTTCCAAA TGTGTTAATA AAAAAATTCA 360

CTAACCTTAC AGCTGGGTTG CTATCCAACG CCGCACTCTC TTGCATTTCT GAAATAAGAG 420

AWAAAACCCA TGGGATATTA ACAAAATATA ATAATAAATT AGACACTGCA TATGTTTCCC 480

ACATCTTAAA TTTAATAAAA TCCAAGGRGT CAAGGGCATA TGCTTATGAA AATGCTCATG 540

ATTATGCAGT AGATTTAATT TCTGAAGAAA TAAGATCAAT ATTGC 585

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ANTCATCCAA CTGGCCGATC AGCAAAAAAG CGCGGCCTAC GATTTCACCC ACGAACTGTT 60

AACCACGCTG GAAGTTGACG ATCCGGCGAT GGTAGCAAAG CAGATGGAAC TGGTGCTGGA 120

AGGCTGTTTA AGCCGAATGC TGGTGAATCG TAGCCAGGCG GATGTCGACA CCGCACATCG 180

GCTGGCGGAA GATANTCNTT GCGTTCGCCC GCTGCCGTCA GGGTGGTGCA CTGACCTGAC 240

AGAAACACAG AAAAGAAGCG ATTTGCCGCA ATCTTAAGCA GTTGAATCGC TTTTACTGAA 300

ATTAGGTTGA CGAGATGTGC AGATTACGGT TTAATGCGCC CCGTTGCCCG GATAGCTCAG 360

TCGTAGAGCA GGGGATTGAA AATCCGTTGT 390

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGATGCCAGT GTCAGCGACT GGTTAAAGTG GTCGATATCG ATGAGCAAAT TTACGCGCGC 60

CTGCGCAATA ACAGTCGGGA AAAATTAGTC GGTGTAAGAA AGACGCCGCG TATTCCTGCC 120

GTTCCGCTCA CGGAACTTAA CCGCGAGCAG AAGTGGCAGA TGATGTTGTC AAAGAGTATG 180

CGTCGTTAAT TTTATCTCGT TGATACCGGG CGTCCTGCTT GCCAGATGCG ATGTTGTAGC 240

ATCTTATCCA GCAACCAGGT CGCATCCGGC AAGATCACCG TTTAGGCGTC ACATCCGTCG 300

TCCCCTGGCA AACGGGGGCG ATTTTCCTCC ATTTGCCTCA GTGGCTGGCG TTTCATGTAA 360

CGATACATGA CAGCGCCCGA CAAGATCCTG ATACTCTTTG GGTATTCAAC CGTTTCCAGT 420

GTAATTCGTC GTTCACNAAC ATTGGCGTTA CAGGCGGGGC TGGCNGTNAC CCA 473

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

INSDOCID: <WO 9822575A3 IA>

GAAGTGACGG ATGGCTGTGG TTTCTCCATC GGTCACCAGC AGCAGTTNGC ATCATGGATT 60

GCCTATAAAG TCGCGCCGTT CCTCGGNAAA AAAGAGGAGA GCGTTGAAGA CCTCAAATTG 120

CCGGGCTGGC TGAACATTTT CCACGACAAC ATCGTCTCCA CGCGATTGTG ATGACCATCT 180

TCTTTGGTGC CATTCTGCTC TCTTCGGTAT CGACACCGTG CAGCGATGGC AGGCAAAGTG 240

CACTGGACGG TGTACATCCT GCAAACTGGT TCTCCTTTGC GGTGGCGATC TTCATCATCA 300

CGCAGGGTGT GCGCATGTTT GTGGCGGAAC TCTCTGAAGC ATTTAACGGC ATTTCCCAGC 360

GCCTGATCCC AGGTGCGGTT CTGGCGATTG ACTGTGCAGC TATCTATAGT TCGCGCCGAA 420

CGCCGTGGTC TGGGGCTTTA TGTGGGGCAC CATCGGTCAG CTGATTGCGG TTGGCATCCT 480

AG 482

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GACGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA 60

AAACCCTGGC GTTACCCAAC TTAATCGSCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG 120

TAATAGCGAA GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCANCT GAATGGCGAA 180

TGGCG 185

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAACGCTTCA ATACGCGCGA CCAGCTGGCG GCGCTCATAC GGCGTAATTT TGGCGTCGGC 60

GAGCAAAATC CCTTGTTTAA AGGTATTTTG CCAGCTGCCG TCGTCATATT GGCGAGCTTG 120

CTGACGCGAC TGCGCAGGCA TTAAACGATC AGCACAATCC ATCGCCCGCA GCCAGTAAAG 180

CGGATTGGTT TCGGTTGATT TACCTTGCAG CGCCCAGATG TCGCTACATT CAGTAGAAAG 240

ATAGTCAGCC AGTTGATAAA CCGGAATTTT TTCTTCTGCT GGCGTATCAA TGGCTGGCTT 300

ATTGTGATTC TGCACGCAAC CCAGCAATGC CAGACATGGA GACCCTGCCA GCCACAGCCG 360

TCGGGGCAAT AATCGTTGAA AAATGTGTCG CATATTCACC AGACTTAAAG CCTATCCCAG 420

TGGGCGTAAT TGTTGCAGAC AGTCTGGACA TGGACAGCGC GGAGAAACCG GNAGCGTACA 480

TATCGTACGT G 491

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACTTGAACGG CAATTATTAT TTATCCATGC AACTTCAAGT TGCAGTATCG GAACATTAAC 60

TTTTCTGGGG TGAATATCAC TCTGATATCG TTTTTTGTAT GCGTNT 106

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TTTATGTGCG GTATTGATGG CTGAAGCCTG TAATATCGGA CTGGAACCGC TGATAAAGCA 60

CAATATACCA GCACTGACCC GCCATCGGCT CAGTTGGGTG AAACAGAATT ACCTTCGTGC 120

AGAAACGCTG GTCAGCGCCA ATGCCCGCCT GGTTGATTTT CAGTCCACAC TGGAGCTTGC 180

TGGTCGTTGG GGAGGTGGAG AAGTGGCATC AGCTGACGGC ATGCGCTTTG TCACACCAGT 240

GAAGACCATC AACTCAGGAT CTAACAGAAA ATATTTTGGT TCTGGGACGA GGCATCACCT 300

GGTATAACTT CGTATCTGGA TCAGTACTCT GGGTTCCATG GCATTGTGGT ACCCGGTACA 360

TTACGGGRCT CGATTTTGTA CTGGAAGGAC TTCTTGAGCA GCAGACAGGG CTGAATCCAG 420

TTGAAATCAT GACAGACANT GCGGGTAGCA GCGATATTAT TTTCGGTCTG TTCTGGCTAC 480

T 481

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGGNCCGTAA TTCCCAACCA TTTGCCGAGG TCCAGNTTTT TCACCATGTT ACTCGGGATA 60

INSDOCID: <WO 9822575A3 IA>

GCCAAAACNG ATACCGATGT TGCCGCCGTC CCGGTGCGAG GATCGCGGTG TTGATACCGA 120

TCAGTTCGCC GTTCAGGTTA ACCAGCGCAC CACCGGAGTT ACCACGGTTG ATCGCTGCAT 180

CGGTCTGGAT GAAGTTTTCG TAGTTTTCGG CATTCAGGCC GTACGCCCCA GCGCAGAGAC 240

AATCCCGGAA GTTACCGTCT CGCCCAGACC AAACGGGTTA CCAATCGCTA CGGTGTAATC 300

ACCCACGCGC AGTGCATCAG AATCCGCCAT CTTAATTGCG GTCAGGTTTT TCGGGTTCTG 360

GATTTGGATC AGCGCGATAT CAGAGCGCGG ATCTTTGCCA ACCATCTTCG CGTCGAACTT 420

ACGGCCATCG CTCAGTTGAA CTTTAATGAC CGTCGNGTTA TNAACAACGT GGTTGTTGGT 480

GACGACATAG CCTTTATCGG CATCAATGAT GACGCCGGAA CCCAGCGCCA TGAATTCTGT 540

TGCTGGCCGC CACCATTA 558

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CACCTGCGTG ACGTGACCGA CCTTTTCTCC TCGCTGNTTG TTTCCCCTAT CGTCGGCCTG 60

GTCATTGCGG GAGGCCTGAT ATTCCTGCTG CGACGCTACT GGCGCGGGAC GAAAAAAGCG 120

TGACCGTATT CGCCGCATTC CGGAAGATCG CAAAAAGAAA AAACGGCAAA CGTCAACCGN 180

CATTCTGGAC GCGTATTGCG CTGATTGTTT CCGCTGCGGG CGTGGCGTTT TCGCACGGCG 240

CGAACGACGG ACCAAAAGGG ATC 263

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTAACGCGTC TGGAAGATGG CCTGCCAGTG GGCGTCGTCG ATGTGGTCGA GGGGCTGGAC 60

GGTTGCCATT CCGCCAATAT CTCACCGGAC AACCGTACGC TGTGGGTTCC GGCATTAAAG 120

CAGGATCGCA TTTGCCTGTT TACGGTCAGC GATGATGGTC ATCTCGTGGC GCAGGACCCT 180

GCGGAAGTGA CCACCGTTGA AGGGGCCGGC CCGCGTCATA TGGTATTCCA TCCAAACGAA 240

CAATATGCGT ATTGCGTCAA TGAGTTAAAC AGCTCAGTGG ATGTCTGGGA ACTGAAAGAT 300

CCGCACGGTA ATAATCGAAT GTGTCCAGAC GCTGGATATG ATGCCGGAAA ATTCTCCGAC 360

VSDOCID <WO___9822575A3 IA>

ACCCGTTGGG CGGCKGATAT TCATATCACC CCGGATGGTC GCCATTTATA CGCCTGCGAC 420

CGTACCGCCA GCCTGATTAC CGTTTTCAGC GTTTCGGAAG ATGGCAGCGT GTTGAGTAAA 480

GAAGGCTTCC AGCCAACGGA AACCCAGCCG CGCGGCNTCA ATGTTGATCA CAGCGGCAAG 540

TATCTGATTG CCGCCGGGCA AAAATCTCAC CACATCTCGG TATACGAAAT TGTTGGCGAN 600

CAGGGGCTAC TGCATGAAAA AGGCCGCTAT GCGGTCGGGC AGGGACCAAT GTGGGTGGTG 660

GTTAACGCAC ACTAACCGCT GAT 683

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGATGCAGG GAAAAACATT GATATTACCG GGGCAACGTG CTCGTCCGGT GGAGACCTTG 60

GAATGTCTGC GGGTAATRAC ATCAACATTG CCGTAAACCT GATAAGCGGG ACAAAAGTCA 120

GTCCGGTTTC TGGCACACTG ATGACAACAG TTCATCATCC ACCACCTCAC AGGGCAGCAG 180

CATCAGCGCC GGCGATAACC TGGGCGATGG CTGCAGGCAG AGATKCTGGG NTGTCACAGC 240

ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTTCTGCA GT 282

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATGAACGGCC CCCCCCACAG CCCGTTAACA AACGGNTGCC CCGGCGATAA TCGTACTGAT 60

AAGTTAACTC CAGCAGGCGG TTAATTGAAA GCGAACGGGA GGCTGATGCA TGGTAATAAT 120

CCCTTAAAAC GCGACGGCAA CGCGCCAGTA AACCGTGAGA TGGTCAGGGG CAAGCCAGTC 180

CGGGTAAACC AGAGGCAGTC CGGCAGTGAA CGAACCGGAA ACATGACCAC TGGTGGTGCT 240

GAGCCCGGCA GCAGCACCCC ACAGCGTGCC GGACGAGTAC GGGTCATCTC TGTCAGAGTG 300

CAGCCAGCCG CCCTCCAGTG CAGTCACTGC ACGGACTGTC CCCACATATG GCAGGGAGAA 360

CAGAGACCAG GACAGCTCAT TTCGCAGATA ACCGCCGTTA TTACCGGAGA TATACTGCTC 420

CTTAAAGCCA CGCACTGAAC TCTCACCCCC GAGGCTCAGT TGTTCCACAC CATGAAGACG 480

GTCCGGTGAC CACTGGGCAT AAGCGCTGGT CAGCCACCAC ACCCTGTCCG TGACGGGGCG 540

CTGAAAACTG GCACTCACCG ACCATTTCCG GAACTGATTT ACGGGCAGGT CTCCCCTTTT 600

CCCGTGGTCG CTTTCTGCGC CGAACCAGGG CATCCCCCGT GTGAATACCG GATTCAGTGT 660

TCCGACACCA CCCAGAAACT TGTGTGTGTG ATTCANC 697

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TTCGACTGAG CACCACAAAT ACTGGGTATC TCCCCAGATA GTTCATTGCG GTACAAGCAA 60

TATAGGTGCA GAAAGTCAAC CTGCTGCACC CTATTGGATA ATTATATATG GCCTTCAATA 120

AAGTTTGCGG TTGTCGACGT TGGCTATATC AGCCATTTCC AATGCATAGT TCTTTGGTTT 180

AGCACCATCA AGTTATAGAT TTGGGAATAG TTTCAACTGG TATTGATTGA ATTGGGTTTC 240

ATCGTCGATG ATTAATACTA TTTGTAAAGA CTTTATTGTT GATTTCTTAT TATACCACAA 300

ACCCAAACTG GTCTAGGTCA TCATTTGGTG TTGATAACGG GCTCTGATAA TTTCTGCTCT 360

TCTGCTATAC TGGGGATTAT GAAGAATATT AAGGCTGAGT GTATTGAGGT AGTGTTCTTT 420

GAACCGACCA TTCATGACAA TATATTCTTC AATTCGTGAG TGATCCAGCA ACTGGTTGAA 480

TTTAAAACAC TGAGTGATGT TATCCTCTGT AATCGTATGG TTGCTGAACT AGTTGATGTA 540

GCCGATAAGG TTTATACCAG ATATCTTTTG GGGGGATTAG ATAACGTAGC CGCGGATAGC 600

AAACGAGATA GTTGAATTTT ATTACCGTAA TTTCTTCCAT TGAGAAAAGC TTATTTTTCT 660

TGGTGGTATT CGCAGTTATG TATCTTCCAT AAAGACTTGG GAATATCTTG CTTGAAARGC 720

TATCTGGAGA TAGCCTTAGT TATTTGATAA ATATTTCAAA TAGGAGGAGC CGTATGGCTG 780

TCATTTATAC CCTCACTAAA TCGTCACTTG TCAAGTCTGG TGGTCAATTA CATTGGAATA 840

TTGATTCGCC ATCAGAACAA CAGCCACAAA AGATCGTCAA TGGTCGGGTT GCGCTTCGGG 900

GATGGTTACT GGCAGATGTG GAAAAAGATC TCCGTGTTGC GGTTAAAATT GAACATTTGA 960

CATACAGTTT TCCCTTCAAT ATAAAGCGCC CTGATGTTAT TTCAGCTATA CTGAAACAGC 1020

CACCTGAAAA ACATCAAAGA CTTCATTGTG GATTTGATAT CAATGTCCCA TTTTCTACTA 1080

AAATAATTAT TGGCCTTGAG TCTGATGGGT TGATTACCTG GTTGGAAGAG TTATTATTTC 1140

TCCTGCCTGA TAATTGAATT AAGTATCTAT ACCGATAGTA TCGCGATAGA TATATTTTTT 1200

TACAGGATGA TAATTTGAGA ATCTATATAG CCGCTATTAT CAAGGATGAG TATTCAAGTT 1260

TACTTGAATG GATTGCCTAC CATCGAGTAT TAGGTGTTGA TGGGTTTAKT ATTGCAGATA 1320

ATGGCAGTCG TGAWGGTAGC CGAGAATTAC TATTTTCCCT CGCTCGCCTA GGTATTGTGA 1380

WSDOCID <WO__9822575A3 IA>

CGATGTTCGA ACAACCGACT TTGGTGAATC AAAAGCCACA ATTACCTGCA TATGAACATA 1440

TTTTACGTAG CTGTCCCAGA GACATAGACC TGCTTGCATT TATAGATGCT GATGAATTTT 1500

TATTGCCACT TGAATCGGAT ACCAATTTGT CAGATTTTTT TTCTGAAAAG TTTCAGGATG 1560

AGAGTGTCAG CGCTATTGCA TTGAATTGGG CAAATTTTGG TTCTAGTGGT GAATGGTTTG 1620

CTGAAGAGGG GTTGGTTATT GAACGTTTTA CCTATCGTGC CCCGCAATCC TTTAACGTTC 1680

ATCATAACTT CAAAAGCGTG GTCAAACCCG AACGAGTTAA CCGCTTTCAT AATCCGCATT 1740

ATGCTGATTT GCGTTATGGT CGATATATCG ATGCATTGGG TCGTGATTTG ATTCTGCACC 1800

CGAGGCATGG TAATGGGGTT AGTGCTGAAG TGACTTGGAG CGGTGTCAGG GTAAATCACT 1860

ATGCAGTTAA ATCACTTGAG GAATTCTTGT TGGGCAAGCA TCTGCGTGGT AGTGCTGCCA 1920

CTGCTAATCG AGTAAAGCAT AAAGATTATT TCAAGGCACA TGATCGTAAT GATGAAGAGT 1980

GCCTTCTCGC TGCCGCATTC TCAGAACAAG TAAAAGCTGA AATGGAACGA TTAAGTGTGA 2040

AGTTGACTGA GTTACCAGCA GTTGAACCTA TTCCTACTGG TTCTTGGTTC AAAAAAAAAA 2100

TGAAGAAATG GATGGTTTGA ATATATTGAG CAAGCACTTT GGTATTTATT TCTGCTCTTA 2160

TCTACAGGTC TGCTAATAAG GATCTGTATC CCCCAGGTGT TACCTTGGAC TGTAAGTTAT 2220

ATTATGTGTA GCTATTGCGA TTGGCAGCCT CTGACATTGC CAGACTCGTT TTCTCTTCAT 2280

TCTGGTTGGC TTCTGATTCG GGGGCGCGTG TTGACGACTC AAACTCGAGG TGAAACTCGT 2340

CTGCGCTGGC AATGCGGACA AGGAATATGG CATGAACAGA AGTTGCCGGT CACTCGTCGA 2400

GGCACGTTGC TGGAGCTGGT TTATCTACCY TCGGGAGCTA GTCATTKGTC TTTGCTGGCA 2460

AGTAATAAGG GCGCTGAGTG TAATGTTGAA ATTACTCAGC TTTGTTGTGT ATCCCGTGCC 2520

GAGAGTCTCT GGCGTCGATT GCGCCGGGTT GTACCTTTTT ACCGACGCTT AACGAAGTCC 2580

AGACGCAAAA GGTTAGGCCT TTCATGGCAT TTGTGGCTCA CGGACTTGCA GCAAGCTTAC 2640

CAACTTGTCA GCAGAGTTCG CGATGATAAA CCACTCAATA GCTATGATGA GTGGCTAGCA 2700

GACTTCGACA CCCTTGAACC CGCCGAATAC AAGCTGATTA AGCGCCAGCT GGCTCGCTGG 2760

GGCACATTAC CACGTTTCTG TTTGCATCTT GTTGGCGTTG GGGATGAACA GAGCCGCCAC 2820

AAGACCCTGG AGAGTATTCA GGCACTCTGT TATCCGGCAA GCAATATAAA CCTGCAGGAG 2880

CATGGTGCAT ATCCAGAAAT CTCCAGTCAG TCAAGCGGCG AATGGCAGTG GGTGTTGCCT 2940

GTAGGGGCAG TGGTTTCGCC AAGCGCCTTA TTTTGGGTTG CCCACCAGTT ACGCCAGAAT 3000

CCTGATTGTT TATGGATATA CGGTGATCAC GATCTGCTTG ACGAGAGAGG TGAACGTCAC 3060

TCTCCCAACT TCAAACCTGA TTGGAATGAA ACGCTGCTAC AGAGCCAAAA CTATATTAGT 3120

TGGTGTGGTT TGTGGCGTGA ACAAGGTGCT GGCCGTGTTC CCTTTGATGC GGCGACATGC 3180

CATCAGTGGT GGCTACAGTT GGCAAAGATG TGTGAACCGA AACAGATAGT CCATATTCCA 3240

TCATTGATGA TGCATTTGCC TGCAAGAGCG TTGATTTCGG ATGATTTTGA GTCGCTGAAA 3300

INSDOCID: <WO 9822575A3 IA>

GATAAAGAAG ATTTACTGCC ATCAGGAGTG AGCATTGAGG CAGCACCTCA TGGTGTATGT 3360

CGTTGGCGCT GGCCGTTGCC AGCGCAATTG CCATTGGTTT CAGTGATTAT CCCTACTAGA 3420

AATGGTATTG CTCATTTACG CCCTTGTATC GAAAGCCTGA TACAAAAGAC GCAATATGCC 3480

AATATGGAAG TCATAGTGAT GGATAATCAG AGCGATGAGG AGGAGACGCT TGCTTATCTT 3540

GCTCATATCG AACAGGTTTA TGGCGTTAGG GTGATTTCTT ATGATCAACC GTTTAACTAT 3600

TCAGCCATCA ACAATCTGGC AGTGAGAAAC GCACATGGAG ATATGATATG TTTGCTGAAT 3660

AATGATACTC AGGTAATCAG TATTGACTGG CTGGATGAAA TGGTTTCTCA TTTATTACGC 3720

CCCGGCGTGG GTGTGGTAGG AGCAAAGCTG TATTACGGAA ATGGCTTGAT TCAGCATGCA 3780

GGCGATGCTG TCGGCCCTGG CGGTTGTGCA GATCATTTTC ATAATGGTTT GTCAGCTAAC 3840

GATCCTGGAT ATCAGCGTAG GGCTGTTAGT GCCCAAGAGC TGTCAGCTGT GACTGCAGCT 3900

TGTTTATTGA CTCATAAAGA GTTATATCTG GCGCTCGGAG GACTTGATGA AACGAATTTG 3960

CCGATAGCTT TTAATGACGT RGATTATTGT CTCAGAGTTC GAGATGCTGG CTGGAGAGTA 4020

ATCTGGACTC CCTTCGCTGA ATTGTATCAT CATGAGTCTA TTTCCCGTGG TAAAGATGTA 4080

TCAAAACAAC AGCAGATACG AGCGAAATCT GAGTTGCGCT ATATGAAAAA ACGATGGGCA 4140

TGTGCACTTA AACACGATCC AGCCTACAAC CAAAATTTGA GTTATGAACG TCCTGATTTC 4200

TCTTTAAGTA GAGCTCCTAA TATAGTATTG CCATGGATGA ATTAATTCGC AGGAAACTAT 4260

TTAAGCCTTA TCGTAAATTA AATAAACAGA GTTATAGAAG TCCGCAAAGC TCTGAGATTA 4320

ACTTTGAACG ATTGTTTATA TTACATGAGG GAAAATCACC TACATTAGCC TATTTTGAAT 4380

CGGCTATTAT AAGTCGGTTT CCTGATGCAG AATGTCATTT TATCGACACA TTAGCATCCA 4440

CTGATATATT TATTCCTAGA GGATCTGCCC TTGTCGTCAT TAGATTCATC TCCCCAAAAT 4500

GGCAACAGCA CATAGAAAGA TATAACGACA GGTTTTCTCG AATTGTTTAT TTTATGGATG 4560

ACGACCTGTT TGACCCGACT GCACTATCTA CGTTACCAAA AGAGTATCGT ACCAAGATAA 4620

TAAGGAGGTC GGCGGCTCAG CATCGATGGA TTACGCAATA TTGTGATAAC ATTTGGGTTT 4680

CAACTGCCTA TTTGGCTAAT AAATATGCAC ATCTTAACCC GGAGATTGTT TCTGCTAAAC 4740

CGTCACTGGC ACTCATTGAA ACACATCGAT CAGTAAAAAT CGCTTATCAT GGCTCAAGTT 4800

CTCATCGGGA AGAAAAATAT TGGTTGAGAC AAATC 4835

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1746 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

WSDOCID: <WO 9822575A3 IA>

GAAAAATGNC ATAACCGCAT TCCATCAAGC CCGTNAATAT CCCGGACTTT CATTTATTTC 60

TGAGGCGTAC AGGGAAGCAA TAACTGCTGG TCAGATATTG CTGTCTCCGG TACATTTACC 120

TGACACTGTA TTTTTCCATC CCAGTTTACC GACAGGGTTT CCCCCGGCGT CACGCCACTC 180

AGCCAGGCAA GGCCTTCGTC GGCCACCATG CCCAGTTCCC GGCCTTTTTC ACTGGTTACA 240

CTGGCACCAA ACGGGGGCTG AGAGCCATCA GCAAGACGCA GTATTGCAAA CAGACGTTTC 300

CCTTTAAGCA CGCTGAATTT CCGGTAACCA ATGGCACCTT CTGTCAGCGC CGATTCCACA 360

ACAGAACGGG TTGCTTCCAC ATCATCCGGT AAGCGCTTCA GGTCAACAGA GGTTGTATTC 420

CGGTAATAAC TGCTGATGTC AGTCACCACG CCCGTTCCCC AGCGATTTGT CACCACCTGC 480

CCGCCATCAA CCGGTACACC TCCCACACCA TCCGTGTCAA CAAGAAGACG TGTTCCACCG 540

GACATTCCCC CTGCATGTAA CGCCGCACCT TTTCCGGTAA TTGTTGCCCC ACCGGAAGCA 600

CTGACGCCGA AAGACGTATA TCCTTTCTGC AGGGATGCAA TATTCGCGGA CAAATTTGCC 660

AGCGGACTAC GATGACTGTA ATAGGCATTA ATCTGACGTT GCGATGTCAG TCCACCGCCA 720

CTGTTAAGGC CGGCGTTCAG GCTGTAGCTG TCCAGACCGT CATTGAACGT GWCAGTGTAG 780

CCGGCCATAT TCACATAACG GTCATTACTC ATACTGCCAC TGTAGCTCGC TGTCCCCGTC 840

CCCCAGCGGC ACGGATATAC GCAGGTAAGC AGAATCNTTA TCACGCCCCA GATATTTAGA 900

CCTTGAGGCT GACAATCCAA CCGCCACACC CTGCAGTCCG AAAACATTAA AGTAGCGGTT 960

GACGCTCACC GTATAATAGT CCGTTTTCCG TATGTCCCAG TATGTCTGAC GGCTGTACTG 1020

CAGGTTAAAA GAGGTGTTCC AGTCCGCCAC GTTTTTATTC AGCGTAACGG TATACATCTC 1080

TTTTTCCCGA CTGCTGTAAT CATTACGGTA GCGGGCGTTC AGGTACTGCT CCATGGTCAT 1140

ATAGTTTCGC TCTGAGAAAC GATACCCGGC GAACGTAATG TCGGCATCCG CATTATCAAA 1200

CCGTTTGGAG TAGCTCAGAC GCCAGGATTT TCCCTGAAAC GTTCTCTCTC CCTCAATACG 1260

GGCTACTGAC TGCGTGATAT CAGCGGAAAG GGTCCCCGGC ACACCCAGGT CCCAGCCGGC 1320

ACCGGCTGCC AGTGCATTAT AATCACCGGC AAGCACAGCC CCGCCATACA GCGACCACTG 1380

GTTACTGAGC CCCCAGGATG CCTCTCCGGT CGCAAATACA GGCCCTTCGG TCTCATGCCC 1440

GTATCCACGG GAACGACCGG AGACAAGTTT GTACCGGACC TGTCCCGGAC GCGTCAGATA 1500

AGGAACCGAG GCCGTATCGA CCTGAAAGTT TTCTTCCGTC CGTTCTGTTC AATAACCTCA 1560

ACATCAAGAC GTCCGCGAAC TGAACTGTCC AGGTCCTGAA TACTGAATGG CCCTGCGGGG 1620

ACCATCGAGT CGTACAGCAC CCGTCCCTGC TGCGACACCA CAACACGGGC ATTAGTCTCC 1680

GCAATCCCGG TAATCTGCGG TGCATAAGCC TTCGCATTCT TGGGGCGGCA CATTCCGGGT 1740

CAGCGN 1746

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

3NSDOCID <WO___9822575A3 IA>

(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TGTACTGAGC ACGGCGAATA TCCAGTGTTC AAATTCCACT TTGCAGCGAC TGCATGATGT 60

CTGCGGCGCG GTAACAATCA GGGCATTACT GTGTTTGCTG GCGGCGATGG AGACAACCTC 120

ACGCCCGCTA CCGACCGTGC CTTCCGCCTC TTCTTTAGCC GCCGTGAGCG TGCCGCTGAC 180

CTGCTTCAGC ACATCGACCA GATCTTCGGC TTTGCTGTAT TTGAGATAGA AAACCTGGCT 240

GTTGCCGCTG CGTTCCATTT CTGAGTCCAG CCGACGGATC AGGCGGCGCA TTTTGTCCCG 300

CGTGGCCGGG TCACCACTGA CAATCACACT GTTGGTGCGT TCGTCGGCGA CAATTTGAGA 360

TTTCAGCGTC GCAGGCTGGT TCTCGCCGCT GTTTTTAGTC AGGCTTTCCA GCACGCGGGC 420

GATTTCCGAA GCAGAGGCGT TATCCAGCGG GATCACCTCT TCAGTGCGAT TANCCGCGTG 480

ATCCACACGC TGGATCACTT CCGTCAGCCG CTCCACGACG GAGGCGCGCC CGGTGAGCAT 540

AATCACGTTG GAGGGATCGT AATTAACAAC GTTGCCTGAG CCTGCGCTGT CGATCATCTG 600

GCGCAGAATC GGTGCCAGTT CGCGTACCGA AACATNACGT ACCGGCACGA CTTTGGTGAC 660

CATTTCATCG CCCGCGTATT GTCGCTGCCT TCACCAACCA GCGGCAGGGC TCGACTTTCG 720

CGG 723

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TAGAGGATCC CCGGCGTTGC GATCGTCACG AACATAGACC CACAKCCGTC CGGTAGGTAT 60

TTACCCTGAC CCGGYTCCAG TACATTTACC GGCGTGTCAT CGGCATGCAC TTTACCCGGC 120

ATCAGCACAT AGTGCTTCAG TTCATCATAC AGCGGGCGAA GCTGCTCTCC CATGATGTCA 180

ACCCAGCGCC CCATCGTATT GCAGTGCAGC TCCACGCCCT GGCGGGCATA GATTTCCGAC 240

TGACGGTACA GCGGCAGATG CTCGGCGAAC TTAGCCATGA TTATGCGGGC CAGCAGAGCC 300

GGACTGGCGT AACTGCGCTC GATGGGTTTT GGTGGCTGCG GAGCCTGAAC TATACAGTCG 360

CACCGGCTGC AGGCCAGTTT TGGGCGAACC GTTTCGATTA CCCTGAACGC GGTGTTGATG 420

ATATCCAGTT GTTCAGAGAT GCTTTCTCCC AGCGGTTTCA GTTTGCCGCT GCAGACGGGG 480

JSDOCID: <WO__9822575A3_IA>

CATTCGGTTT CTGCCGGGGA GATAACCTGC CTGTCACGGG GAAGTGTTGC CGGAAGTGCT 540

TTGCGGACGG GAGAGTCTGA TGTTTTCGGC GCTGTCTCTC CGGCCATTGA GGTGAGTTGC 600

AACTGCGCCT CACCAAGCCT GTTCTGGAGC TCGGTTATAC GCGTTTCTGC CCGTGCGATC 660

TTCTTTTCTA TCTTCTCGCG GCTTTTCTCG CTGCTGCGAC CGAACAACAT TCTCTGTAGT 720

TTAGCGACCA GCGCTCTGAG TGAGCTGATC TCGCGGCATA GCCGGTTATT TCACCAGACA 780

GACGGACGAT AACAGCCTGC TGTGCGATCA GCAGGGCCTT CAGTTGCTCG ATGTCGTCGG 840

GGAGTGTGTT GTTCATTCCC CTGTTTTATC ACGGGTTATA TCCGGATGCC AGGCCGTTCT 900

GTCCGTTTGG GATGTTGCCA CGCGATCCCC TCCAGTAGCA TGGATAACTG AGCTGGCGTC 960

AGGTGCACTT TCCCTTCCCG GGTTACCGGC CAGACGAAGC GGCCCCGTTC CAGGCGTTTG 1020

GCGAACAGGC ATAACCCGTC ACGATCGGCC CACAGTATTT TCACCATTTT GCCACTGCGG 1080

CCCCGGAAGA CGAAGATATG CCCGGAGAAC GGGTCATCTT TCAGCGTGTT CTGCACCTTC 1140

GAAGCCAGGC CGTTGAAGCC ACAACGCATA TCTGTGATGC CAGCGATGAT CCAGATTCTG 1200

GTACCGGTTG GCAGCGTTAT CATCGGGTAC CTCCTTTTAT TTCGCGGATT AGCGCCCGTA 1260

ACATTTCCGG AGTGAGAGGG TCAAACAGTT TTACCACACC TGATTTAAGA TGCAGCTCGC 1320

ACCGTGGGAC GTTTCCGGGA TCACACTCAG GGCACTCATC AGGCTTGTTA CGCCAGAAGG 1380

GATTTGTAAC TGGTCTGGTC GGCTCTGGCG TATCAGTCAG AGCCACCGGG ACAGGCATGC 1440

ATTCCTGTAT GTCATCATCG CTCAGTAAGC CGTCCTCGTA CTGGCTTTTC CATTTAAACA 1500

GCAGGTTATC ATTGATACCG TGCTCTCTGG CGATCCGGGC AACAACAGCA CCGGGCTGTA 1560

ATGCCTGCTT AGCCAGACGG ACCTTAAATT CACGGCTGTA GCTGGCTCGC CGTTCTTTTC 1620

GCCATGTGCC TTCGCTGATT TGAGGCTCTG TTAATTCCTT CTTTCTGTTG GCATAAAGGA 1680

TGGCGTCAAG CTGAGCTAAT GAAACTGAAT CGGGCAATGG CCATGCGATA CCGGATGCAA 1740

TAAATCGCTG AAAAAGCGTA TGTATTGTGG AATGACTGAG ACCTAGACGC TGAGCGATGG 1800

CCCGGATGGT CAGTTTATCT TCAAATCTTA AACGCAGAGC ATCAGGCAAA TAAGAACGGA 1860

AGCAGGGAAT ATCTTTTTTT GTCTGGGAAT TCATCGTTCG TGTCCATCTA TATAGATGGG 1920

CGCGATTGTT GCCAGACAGG ACAATTTTCA CAAGACGTCG CAGATGGGGC GCTTACCAGA 1980

AATGCGCGGG TACGACAGTG ACTCGTCAAA TCTCAGTTGT AGCACACGCG GGATCAATTC 2040

CGGATTGTCT GCCAGTACCG CCTTTCGTGC ATTCATCTTA AATGTCCCTT TACTGCAAAA 2100

ATGGACATTA GTATCGGAAA CAGGAAAGGG AGGCGAAAGA CGGTTTAAAT GAGACGGTTA 2160

CCATTGTGTC GGGCTGTGTA CGTTCTCCCC GGACAGACAG CCTCAGTTCG TAGAATCTAT 2220

AAATTACTGC TACTGATGCT GCCGGGGAAA GGCGTAACGA AAAAACAGCC TCCGTTACCG 2280

GACAGCAAGG AGGCTGAATG GAGTTTACAG GATTTGCTTT TTTATAATGT CTGGCCATGC 2340

AGTAAAACCG GACAGGTTTT ATTATCATGT GAGGTATTCT GACATAAAAT GCTGGATTTT 2400

NSDOCID <WO_ 9822575A2 IA>

TATTTTGTGA CGAATGCTGC AAAATTGCAT CTGCACTCTG ATGTAGCTTT TATCTGTTTC 2460

AGTGAAGCAT GCCCACAAAC TGAGTTATTA AGTTGTGGAA GAACAGTTTT GTCCCGCCTG 2520

CATCTCTCCT TTCAAAAACC AGTATGTCGC CATGCC 2556

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CAGTTAGTGT TAAAAAATNT CCTCTGCTNC AGAAATTACA CCCACCAATA TACAATNATT 60

AATAAATTTT CGGTTGGGTT AGGTAATGGC TGGGATTCGA TAATATCTCT TGATGGGGTT 120

GAACAGAGTG AGGAAATATT ACGCTGGTAC ACAGCCGGCT CAAAAACAGT AAAGATTGAG 180

AGCAGGTTGT ATGGTGAAGA GGGAAAGAGA AAACCCGGGG AGCTATCTGG TTCTATGACT 240

ATGGTTCTGA GTTTCCCCTG AATAAGATGA TGGATTATCT GACTGGCTGT TCATCAGTCG 300

GATAATGATG AAAACTGATG AGCAACAGGT TGTGCGGGCA ATGTGCAGGA TCCGTCACCA 360

AAGGGTGGAA GTTGCGGGCG ACTCAGATAA ACGGGTTACA TGAGCTATTT CTGGAGTTTG 420

ACGAAGCCGT CTGGAAGGGA GAAGAGGCGA TTCCATTGAT GTCTCTGGAA AACATCTGTC 480

AGTCGTGCTG CTGGAAATAT TGATAGAGCA ATGGGAATGG TTATCCAACA TTGATGAACA 540

TATTGTATAT TTACAGAAAT TTTTAAAAAC AGGACTCAGC AGGTTAAATC GTGTAAAAAT 600

TACTCATGAA TACCATTATG GGCTTACAAA GCGATGTGGT TAAGCAGATC TTATTCAGGC 660

CTGTGCAGCG TAGGATTACA ATAGGATCGA ATAACGCCAT ACAGGGGAAT GGGAGATAGG 720

CTGATTCATC CTGTGGCTAT AACCAGGAGC ATATCGGGAA TCMANTATGT TACCCCAGAT 780

GGAACACCAT 790

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCGGCCGCAG TACTGGATCT CTTTGCGGCA TGACGATGAG GGGGAGAGAA ATAAACTTAA 60

CCCAGTCATG GCAGATGAAG AACAGGCTTA CGTAAAAGGG TTATATGAAG GGATTATGCT 120

GATTGGTAAT ATAATCAATA AGCCTGAAGA AGCTAAAGCG TTAATCAAGG CAACTGAAAA 180

TGGCTGCAGA ATGGTGAGTA ACCGGCTGCA ACTTCTACCC GAAGAGCAGC GTGTTCGTGC 240

CTATATGGCG AATCCTGAAT TGACCACTTA TGGTTCCGGA AAATATACAG GATTAATGAT 300

GAAACATGcT GGCGCAGTAA ACGTCGCCGC TTCCACCATT AAAGGTTTCA AACAGGTCTC 360

GATAGAGCAA GTCATTGAAT GGAATCCTCA GGTAATTTTT GTGCAGAATC GTTATCCTGC 420

TGTAGTGAAT GAAATACAGT CAAGCCCACA GTGGCAGGTA ATAGATGCTG TCAAAAATCA 480

TCGTGTTTAT TTGATGCCAG AGTATGCCAA AGCATGGGGC TATCCGATGC CCGAGGCTAT 540

GGGGaTTGGG GAATTGTGGA TGGCGAAAAA GCTGTATCCA GAAAAATTCA ATGATGTTGA 600

TATGCATAAA ATAGTCAATG ACTGGTATAG AACGTTTTAC CGTACTGATT ATCAGGGTGA 660

AGACTAATGC GAGTGCTTGC TGCGGGCAGT TTACGCCGGG TATGGAAATC ACTTGTGTCA 720

GAGTATCAGG CCGATAATAT ACAGTGTGAT TTTGGACCAG CGGGTATATT AAGGGAGCGT 780

ATTGAGGTGG GTGAGGCATG CGATTTTTTT GCATCAGCCA ATATGACTCA CCCACAGATA 840

TTAATGtCCG CAGGanGAGC ATTGTGTATT AAACCTTTTG CCAGAAATCG TTTGTGTTTG 900

TATGTTCGGG CGAATAAATT CAATGAGAAT GACGACTGGT ATTCTTTATT AAATCGGGAA 960

ACATTGCGAA TCGGAACATC AACGGCGGGA TGTGATCCAT CTGGTGATTA CACTCAGGAA 1020

CTGTTTGAAA ATATGGGGAG TGTCGGTGAA AAAATAAGGC AACGGGCTGT AGCATTAGTT 1080

GGGcgGGAGG CATTCGTTTC CTCTTCCAGG AAATGCGATA gcAGCGCAGT GGTTAATTGA 1140

AAATGATTAT ACTGATCTGT TCATCGGTTA TGCCAATTAC GCTCCTGGCT TGCAATCAAT 1200

TGATTCAGTA AAAGTTATAG AAATACCGGA ACCTTATAAT CCGATTGCTA TCTATGGATT 1260

TGCCTGTCTG ACCGATAATG CCCTGCCACT TGCCGACTTT TTAGTTTCAC CTGTTGCCAG 1320

AGGTATACTT GAACAGCATG GGTTTATGCC TCCAGGTACG TTATAGCCCC CTGTCTTACA 1380

GCTGtCTCTT gATCAGATCT CCTGATCAAG AGACTTCATC ACCAGGTAAC CCTCAACCAT 1440

ATCCTGCATA TCCTGAAGTC TGAACCAGCC ATCCCACATA ACTACCCAAC CGGGGCGGCC 1500

TGTGCGTTTG CTGTCATGCC ATCGCCCCAG TTTCGCCAGT TTCAGACAGG CCCATTTCAG 1560

TGTCGGCGTC TGTGACGGAA GCGGTTTTCC TTCCAGCTTA ACCCACAGCA GTTTCCACTC 1620

TGTCGGCGTC AGTATTTTCT TACAGCTGTC ATTTTGTGTT TCTTCACTGA TACCTCCCTG 1680

CCGCAGGCCa GCACCCGTAC CGCGATAAAC GCCTTGATAA CCACCATGCG CTCAAGGTTA 1740

TCCCGGGTCT GCATTCGCAG CGATTCCACA CATGTACCAC CACTTTTCCA CGCCTTGTGG 1800

TATTCCTCTA TCAGCCaGCG TCGCTCGTAA TGGCTGACGA TACGTCGCGC ATCGGCGGCA 1860

CTCGCCACTT TTTCTGACGT CAGCAGATGC CAGCAGGCAC CGTCCTCTGC CTGCTCCCGC 1920

CAACAGACAT ACGTGAGCGG GAGCGCCTGG CCGCTGTTGT CGGGATTTTT TATGCTGAcT 1980

TCGTTGTAAC TGATGAACAT CCGGGCCtgg CGGGCTGCCC GCCCGCCTTT TTGCATCACA 2040-

TTCAGCGTGT GGCTTCCCGC GGTTGCCAGG ACTTCCGGCA GTTCGAAGAG CTTGCCGGGT 2100

)NSDOCID: <WO _ 9822575A3_IA>

GCTTCTTCCA GCCGGCGATT CTGTGCAGCA CGCACCACGA AGCGCTGTCC GTGGCTGACT 2160

TTATAATGCA GGTAATGCTA GATATCCGCT TCCCGGTCAC AGACAGTGAT TACCCGTTTC 2220

TGTATCTCCC CCAGCCGTTC GGCCATACGC TCCGAAGCCT GCTGCCAGCG GTAACTTTCT 2280

TTTTCTTCAT AGGGACGTTC TTTTCGCTGG TGCTTAACAC CATAGGTgtC CGTGACCCGA 2340

CTCCAGCGCT GCTGTTCGAT AAGACCGACT GGCAGGGCGC TGTCGGGGGC GTACATCAGG 2400

ACAGAGTGAG CCAGCAGCCC GCGCGTCTTC GGGTTAGTGG TGGTATTCCC CAGGTCATCA 2460

GATGCCGTAC TGTGGCTGAA GTTAATGGTG GTGGTGTCTT CCAGTGCGAG GAGCAGCGGA 2520

TGAGCCTCAC ATGCCCTTAC AGTGGCGGTA AATCCGGCTT CGGCAATGGC TTGCGGGGAC 2580

ACAGACGGGT TACGTATCAG GCGGTACGCA CCTTCAACCT GAGCAGTGGA CTGGGATGAT 2640

TTCACAATAG AAAGACCTGC ATGCTGAGCG AGAGAAGAGG TCAGTGACAC AAGGCGTCGT 2700

GTACGACGCG GATCACCGAG ACGGGCATGT CCAAACTGCT CGTTAGCCCA TGAATAACAA 2760

TCAGAAAGTA CCATAACAGA GTCGAATAAA ATGAAATATA AGAGAAGATC AACGGGTGAA 2820

GAAAAAGTTC AAAAAATGGC TACCGGGGAG GAAGGAAAGT ACCGGATGGA AAGAGCCCCC 2880

CTAAAGCAGA CTGACAGACA TCACAAATCC CCGGGGGGGA CTTGTGTATA AGAGACAGGT 2940

CTTACAGGGG GAGCGTCCGT CTTTTTATCA ACATCAGGCA ATGACATAAC ATTATGAACA 3000

AGCTCACAAG TCTGATGGTT AAATTTTATA ATGCTCCTTA CTAAGACCGT ATTTTTTCAT 3060

TCTGAGATAG AGTTTTTTCC GCGGGATTTG TAAATATTCA GCAACCTCAT TGATACGCCC 3120

CTGATGGATA TTAAGTGCCT CTGTGATTAT CTGTCGCTCA GCGTCCTCCA CTCGTCTGTC 3180

AAGCGGTGTC GGGGTTCCGA CGTGCATCAA CGGATTTGCT GTTTCTGCCA GCGGTAATAC 3240

TCCTACAGTA AATAGTTCTG CTGCATTGGC CAGCTCTCGC ACATTATTTG GCCACATGCG 3300

GCGCATCATC TCTTTGAGCA TCTCTTTTCC CACTTCCGGA ACAGGATGGT TAAGCCGTTG 3360

ACATGCTTTA CAAAGGTAAT GGCGAAACAG TGGTTCAATA TCATCGGGGC GTTGAGTTAA 3420

TGGCAGGCAA GCGATTTGTG TCATTGCAAA GCAGTAATAG AGCTCCGCGA TGATATGGTT 3480

GCTGGCGGCC AGCTCGACCA GCGAAGTGTC TCCAATACCA ATCAGGCGAA AAGGTCGGTG 3540

TTCCTGGCTT TGTAACTGAA CCAGATGGTA CTGCTGTTCA CGCGTCAGGT GTTCAGGATG 3600

GCTGAGCACT AATGTTCCCC CCTGAGCCAG CGCAATGAAA TCATTAAGCT GTGGTGCATT 3660

GTCTGGTGTC AGCTCGCGGT AGATAAATTC GCCTTGTGCA TTACGTCCAA ATTGGTGCAG 3720

ATAACGTGCA CCGGTCATCC GTCCTGTGCC TGGGGCACCG TAGAGCCAGA CGGCAATATC 3780

TGTTTCAGAC AACTGCTGTA AACGTCGCCG ATACTGATTT ATCCATTCAC TTCTCCCTAT 3840

CAACTCCACC TGCAACGTCT GTTGGCAATA CTGACGACGC GCAATGATTG ATTGACGCTG 3900

GCGTAgcGCC TCTTCAACCA GAGAAAGCAA TTTGCCGGGA TCAACCGGTT TTTGCAAAAA 3960

ATCCCACGCG CCTTTTTTTA CCGCATCAAC TGCCATTGGC ACGTCGCCGT GCCCGGTaAT 4020

AAGCAGAATG GGGATCTGTT GATCATCCTG GTGAAATAAC ATCATCAAAT CGATACCAGA 4080

GCAGCCAGGC ATACACACAT CACTTAGCAC AATACCTGGC CAGTCTGGTT GTATCCACGT 4140

CTGCGCCTCA AAAGGATTGT TACAGGCAAA AACCCGATAG CCTGACTGTT CAAGTAACTG 4200

TGTGTAGGCG TCCAGCACGT CAGCATCATC ATCAATCAGC AGAATCGAAT ATTCACTACT 4260

TAGCATCTTC CACATCCGTT AGTCTGAATT GCAGTACCAC ACAGGCATTC CTGGTCATCG 4320

TTGATGCCAG CCGTAATTCA CCTTTCATTT GCTCCATCAA CGACACACAA ATTGAAAGAC 4380

CAATACCCAG TCCTACTTCT TTACTGGTGG TAAACGGCTT CAATAACGAA GGCAACAATG 4440

CCTCAGGCCA GCCCGGGCCA TTATCGCCAA TGAATACGTT CAGCGTTTTA CCCTGCATTT 4500

GCCAGTTAAC GGTAATGACA GCGCCTTGCC CACAAACATC AAGCGCATTC GCCAGTACGT 4560

TAACCAGTAC CTGCTGGGTT CTGACCTCAT CGCCTGAAAC TGTGGCTGTA CCTTGCGGCA 4620

GAACAAGCGT AGCTTGCAAA GGGCGATGAC GCATGGCCAG AAGTTCCCAG GCCGCACTGA 4680

ACATCTGTGC TAAATCAACG GAATGGAGTG ATATTTCCAG TTCGGCGCGC CGGGTAAACT 4740

GCCGTAGTGA ACGGATAATG GCGTCAATGC GACCAATCAC CCcTTCGGCT TTACCAAGCA 4800

TCATGCTGGC CTGTTCTGTC TGGGTCTGTT cAaTGcCTGC GGGCTGTAAA CAGATACATC 4860

GACAGCGCAT TTAGCGGCTG ATTGATCTCG TGGGCCAGCG TGGTCATCGT TTGCCCGACT 4920

AnCCGCaGct TCGCTGTCTG AATCAGTTCG TCCTGGGTGG CTCGCAGATC GGCTTCTATC 4980

ACCTTTCGAT CGGTAATTTC TTGTTCAAGT TGCTGTTTTT GCACATTGAG CTGCCCGAGA 5040

GTATGGCGTA ATAATCCTGC AATTCTCCCC AGTTCATCAT TCCCATAAAC AGGAATAGCC 5100

GTTTCCGTGC CTCCCAGACC AATTTGCACA ACGGCCTGAT TCAGTAGGGT AAAGCGTTTC 5160

ACCAACCGTG AGCGGATAAA ATAATGGTTG AATACCCATG CCAGCAGTAA CGCCAGTGcT 5220

GTCGCCACCA GGATCAGCCC ACCgctAACG CGAACAATTT GTTCCATTCG TTGATTAAAC 5280

ATCTGCATTT GTTGATGAGT ACTGCcAAGT GCGCTTCCAG TAACGTTCTG AAGCGACCCA 5340

GTGTCGCTTc CCTGGTGCGA CTGGCATCCT CTAAGGCTTT TTGGGCGGTG ACATATTCAC 5400

GCATCGTAGC CGGCATTTTG TTTTTTACGA TTCCCATATC CAGCAATTCA TCGATAGTCT 5460

GCCTCAGGGT AATGGTGCCA GGCCAGTCAT CCAGCATACG TATATTTTCA TCTGCCGTTT 5520

TTTTCAGATT TTCAAAATAA CGGAGATGAG TTTCCACCTG TGTGTCGTCA TCACGTCCTG 5580

ATTTGAGTTC ATTGAGTCTG TCACGCAGAT CGTCAACAAT CTGATTTTCA ATGCGTGCCA 5640

GGGTATAAAC CTGCTGCTGT TCATTTTGCA CTTCACGAGA TCGCTTCAGG TATTGCGCCG 5700

TATCGCCyTG TCGGGAGGCG ATTTGATCCA GCAGCGTTCC CTGCTGCCAG GTGAAATCCT 5760

GCACTAAAGA ATTAAGCTCG GTAGTAAAAT CATCGTGTAA CCAGTCAATC CTCGCTGATA 5820

GCTCACTCAC CTTTTCCCGT AGTAAAAACA TGTTGTAAAG CGCACGATCC AACTCGGATA 5880

ACAGTGATCG ACTGTCCTGC AAAAtGACCG TCAGTTGTTG GCGTTCCCGG GATGACAGCC 5940

3NSDOCID <WO 9822575A3 IA>

CCCGACTAAG CCGTTCTATG GTGTCGAGAT GCTGAATAAT CTGGGTACGA AGTTGCAATC 6000

GCACCGTGGT GTTGGGAGCC TGCAAAAATT CATTTAGCTG GTCTACCACC AGATTCAGGT 6060

TCCCTTCAAT AAGGAAAGCA GAGTGAATAC GGGGAAAATA CTCATCCAGC GAGTAACGAA 6120

TTTGTGAGCT TTGTTCATGC CATGAATACA GACTGACACT ACTGACAATC AGGGTCAGAA 6180

GTGCCCCCAT CAGAAATGCG CAACGTAAGC TGGTACTGAT ACTGACCTGT CTTAAACGCT 6240

GCCACAGCGT TATGTTTTTC ATTTCAGCTC TTCCAGTTTT TTTATCGCCA GGCGCTGGTT 6300

ATTCAGAAAC CAGAGTTGCC ATTCCATCAT TTGCTGCTCG GCAAAGCTTT TGTTATCGAA 6360

CTGTGCCAGC CAGACGGGAT CTTCACTGCT GGCCGCTGCA ACGGGCACTT GTGTTAACAG 6420

TGCACGTATT TCTGGTAATG GTTTCTTCAG ACGTGCCTCG GTACTGTGCA GCGCTCGCCA 6480

GGCATCTTTT AGCTGTGCTA ACCGAAAGCT AATTGCCGTA TCAAACAAGC GCTGCACCAG 6540

ACGCTGACGT TTCAGGATAA GGTGATAATT CAGCGGGGGT TGATTCATCA GGAGCTGTTG 6600

TTGCGTTGCC CGCGGATTGT CTGCGGCAAG TGGTGTCACC GGATATTTTC CTGTATTGGC 6660

ATCGGCCAGA ATACGCTGTC CTTTCGGACT TAACAGGTAG TGAATAAAGC GACGGGCTGC 6720

ATCGACGTGT GGGCTTTTCC TGAGAATTGC AACGTAGGTG GGGGATACCG CAGACCGGGG 6780

GAAATAGGTA AAAGAGAGAT GGGGGTCATT TAACAGTAAA TTAGCATAGT TATCGATAAC 6840

GGGGCCGGCA ACGCCGAGTC CGCTTTTTAT TTTAnTCGcT ACGCCAAAAC TGCGGGAGGA 6900

GATTGTCACC AGGTTTCCTG CACTTGTCAG CAACGTTTCC CATCCTTTCA CCCAGCCTTT 6960

TTGCTGTAGT AATGACTCAA CCATTAAATG GTTAGTATCT GAACGCGACG GACTACTCAT 7020

CAATAAAGCG TCCTGATAGA TCGGCAAAGC AAGATCGTCC CAGTCAGCAG GGGCAGGAAG 7080

GTGTTTTACA GAAAGCGCCG GACGATTAAT GAGCAGACCA AAACCTGATA TTGCTACTGC 7140

AACGGAGGTT GCACGGATCG ACTCCGGCAC CAGGTTTTGG CTTTCTGCGG GTGCATCATC 7200

AAACGGGGCC AGTTTCTGGT GCTCCTGAAG GTGCTGGAGC AGCATTGGTG ATGAAGTCAG 7260

GATAAGATCG ACGTTTTCTA CGTTGGCCGT ATCAAGCAAc TGTTCCAGTG AGGCACTGGT 7320

GCGGTTAAGC GTACGGATCA TTACCGACTC AGGCTCTGTT TGCCAGCGCT GTATTATCCA 7380

CGCGGTAGCT CCGGGTGAGA ATGTGGTGGC CATCACCAGT TCATTTCGTT GAGCCcTGAC 7440

GGCCCCGGCG TCCATCAGCA ACAGTAAAAG AATCATGGTT TTGATGCCGA TTTCGCACCA 7500

GCTAAAAAAT CGGTTTGTGA TCCAGGTCAT AAATATTAAT ACACCGCAAA AATCGCATTG 7560

AGACAAAAAT TACCCGTTTC AGACATTCGT CTGATAACAC GTCTGCTCAA AGAGACCGTT 7620

AATATATTAA TCAGAGATTA CCCGATAATC AGCATGAGAT TTGTTAATAT CCGCACATGC 7680

TAACAACAAA CCAGATAAAG CATAAATCTA CCTTGTCTAT GCATCAATAA AATGGGTCAA 7740

AAACAGGCTT TGATTTTATT ATTTTGTGTC AATTGTGACA CATTTTTTCA GTTTGATGTT 7800

TCATYTCAAT TATATGACTC TCATTGTCAG AATACTCCTG ATGTTCATAT CAATATAAAA 7860

JSDOCID <WO 9822575A3 IA>

TACAGGTGAA GACATGTTAT CAATATTTAA AACGGGGCAA TCGGCGGATA GTGTTCCGGT 7920

GGAGAAAATT CAGGTGACAT ATCGTCGCTA TCGTATGCAG GCGTTACTTA GCGTATTTCT 7980

GGGGTATCTT GCATACTATA TCGTGCGTAA TAATTTCACT TTATCGACGC CTTATCTTAA 8040

AGAGCAATTA GATCTCAGCG CCACACAAAT TGGCGTACTG AGTAGCTGTA TGCNTATCGC 8100

CTATGGTATC AGCAAAGGAG TGATGAGTAG CCTTGCCGAT AAAGCCAGTC CGAAAGTCTT 8160

TATGGCGTGT GGGCTGGTGT TATGTGCCAT CGTTAACGTT GGCCTGGGAT TCAGCACTGC 8220

ATTCTGGATT TTTGCGGCAT TGGTTGTTCT GAATGGTCTT TTCCAGGGAA TGGGCGTTGG 8280

TCCTTCTTTC ATCACTATTG CTAACTGGTT CCCTCGCCGG GAGCGTGGTC GGGTTGGTGC 8340

TTTCTGGAAT ATCTCTCATA ACGTCGGTGG TGGTATTGTT GCCCCTATTG TTGGTGCCGC 8400

TTTTGCCCTA CTCGGCAGCG AGCACTGGCA AGGTGCGAGC TATATCGTTC CGGCCTGCGT 8460

GGCTATCGTT TTTGCGGTAA TTGTGCTGAT TCTCGGTAAA GGTTCCCCAC GTCAGGAAGG 8520

TCTACCCTCT CTGGAAGAGA TGATGCCGGA AGAAAAAGTC GTCCTGAATA CCCGACAGAC 8580

GGTAAAAGCA CCAGAAAACA TGAGCGCCTT TCAGATTTTC TGCACTTATG TATTACGCAA 8640

CAAAAATGCC TGGTATGTCT CACTGGTTGA CGTATTTGTA TACATGGTGC GCTTCGGGAT 8700

GATTAGCTGG TTGCCTATTT ACCTGCTGAC GGTGAAACAT TTTTCTAAAG AACAAATGAG 8760

CGTCGCGTTT TTATTTTTTG AATGGGCCGC AATCCCTTCC ACGCTACTTG CCGGTTGGTT 8820

GTCAGACAAA CTGTTTAAAG GGCGTCGTAT GCCATTGGCG ATGATTTGTA TGGCGCTGAT 8880

TTTCATTTGC CTGATTGGCT ACTGGAAAAG TGAATCGCTG TTTATGGTGA CAATTTTTGC 8940

TGCCATTGTT GGTTGCCTGA TTTACGTTCC ACAATTTCTG GCTTCCGTTC AGACTATGGA 9000

GATCGTTCCC AGCTTTGCTG TTGGTTCTGC AGTAGGCTTA CGCGGTTTTA TGAGCTATAT 9060

CTTCGGTGCG TCTCTGGGCA CCAGCCTGTT TGGTATTATG GTCGATCATA TTGGCTGGCA 9120

TGGCGGATTT TATCTTCTTG GCTGCGGTAT TATTTGTTGC ATCATTTTCT GCTGGTTATC 9180

ACATCGTGGT GCAATTGAAC TTGAACGTCA CAGAGCCGCA TATATAAAAG AACACTGATT 9240

ACCTTCCCCA GGGCCGTCTC CCTGGGGAGT GGAGTATATT ATGATTTATA AGATATCTGG 9300

AAATCAGAGA TTAATATGGA AATTTTATAA GACTGATTAC AATAAATGGA GATGGTATTG 9360

TCATGAGAAA AATGGATATC TTTTGTCTCA ATCAGATAAC GCATATAATT CGCAATTGTT 9420

ATGCATTGAA AATGCTAAAA AACAGGGATA CTCAGACGAA TCGGTCTTGC CACTTTTTCT 9480

ACATATTTCC TATATTCAGG AAAAAGGCTG GAAATGGTAT CAATGTTATG ATTGTGGATA 9540

TATTGTAAAA GAAACCTCTG TTTTTTTTTC GACATACCAG GAATGTGTCA ATGATGTTAA 9600

AAGGAATATA CTAGCATCTA TGTGTAGTGG TTGTAGTGGC ACAGTAAATT TGGCCACCTG 9660

ATTAAAGGTG ATATTCTCAC CACAACATAA AACAACAAGA AAACAAAGCG TACCTTCTCT 9720

CCTGAGTTTA AACTGGAATG CGCCCAACTT ATCGTTGATA ACGGTTACTC ATACCGGGAA 9780

GCTACTGAAG CTATGAATGT TGGTTTCTCT ACTCTGGAGG CATGGGTACG TCAGCTCAGA 9840

CGGGAACGTC AGGAGATCAC GCCTTCTGCT GCAGCACCAC TCACATCAGA GCAGCAACGT 9900

ATTCGTGAGC TGGAAAAGCA GGTGCGTCGT CTGGAGGAAC AAAATACGAT ATTAAAAAAG 9960

GCTACCGCGC TCTTGATATC AGACTTCCTG AATAGTTACC GATAATCGGG AAACTCAGAG 10020

CGCATTATCC GGTGGTCACA CTCTGCCATG TGTTCAGGGT TCATCGCAGT AGCTACAGAT 10080

ACTGGAAAAA CCGTCCTGAA AAACCAGATG GGCTGTATTA CACAGTCAGG TACTTGAGCT 10140

ACATGGCATC AGCCACGGTT CGGCCGGAGC AAGAAGCATC GCCACAATGG CAACCCGGAG 10200

AGGCTACCAG ATGGGACGCT GGCTTGCTGG CAGGCTCATG AAAGAGCTGG GGTTGGTCAG 10260

CTGTCAGCAG CCGACTCACC GGTATAAACG TGGTGGTCAT GAACATGTTG CTATCCCTAA 10320

AAGCAACAGC AAACAGCGAC CACTGGGGAG CCCTGCATTG CGGGATTGTA TTGTTCAGCG 10380

GGCCATGCTG ATGGCGATGG GGCCGAGGAG AGTGATTTTC ATACGCTCTC ATATGGTTTT 10440

CGACTTGTGC GAAATGTCCA CTACGCGATC CGCACGGTGA AACTGCAACT CACCGACTTC 10500

AGGGGAAACT CGGGGCCGCT GGGTAATCTC ACATAAAAGT TCTTCGGTGT CATAAACAAC 10560

GAGAGTATTT GATTCCTTTA TGGTGGCCTG GTGCAGAGCT GCCCTTTCCC AGGACCTCCA 10620

TATAATTTTT GTAGCGGCAG TCAGTGGCAC ACTCAGTTAA CTACTTTCAC TTCAGTGACT 10680

TTGAATGAGT CAGGGCTGCC GTTAAAGGTG TTAATGAAGG CTTGTATTTT CCACTTCTGG 10740

CCTGGTTCAA GATTGGATGC TGTGTCGATT GTTTGACCGA TAACGACTCC ATCTTTTAAN 10800

AGATTAAATT TTACATAAGC ATTTTTGACA ACAGAGTTTG ATTTATTTNC AGCATAACCC 10860

ACAATTGCCT TCGTCCCACT TGGGGTGTTT TCCACATGAA GGTTAG 10906

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ATGGTTATTT TTATTTCCTG CACCTTGCTT CATTTGAAAT AAAAACATAT GCATACGACG 60

CTGCCATTGA GCAGAAAAAT ACAGGAATTA ATGTTATGAG TTAACCATAA TACCTGTGTT 120

ATGAATATCT GACATAAACA AGAACAATTC ATATCTTCTG TATTCAGCAG AATAATAAAA 180

GTTCGTCTGC CATTCTCAAA CTTATTCTTC GGAATACGTT GTTTCATGAA AGAAGGGGCC 240

GGAATAAAAG CTGGTCACCG TAATGCTAAT ATTAATGCAG ACTACCGCCT TCTGGAATTA 300

ACAGTCATCA ACCAGCACAA ACCATTAGCA ATCAAACAAA TTTTAATTAA CAAAATTTTA 360

GCTAATACAA TTACTGCATT AACCACTCTG CAGTTTGCCT TCTCAATAAG TTACAGATGC 420

NSDOCID <WO__9822575A3 IA>

CAAACAATAC TCTTTTATAT GTTATAACAT AACACAAACA ATAAATAAAG AACAGACGGC 480

ACTCCATTTC TCCACGTAAG TGAGCCATCA GAATCGCTTA TGAATGTGTA CGGCAGACGT 540

ATACTCGTGT TTTACTGCAG CAACCGGAGC AAAAGTTGCA CTTCCACAGC CTGGGTTAAG 600

TTTTTCATGC TTGTGGGCTC GTCCTCCCTC CATTTCCACC GCGGGCAAAC AAGGCCATCT 660

TTTGTCTGGC CACACAGCAG ATGGAGAGTC GAATTATGCT GTCTGACGAC ACCGGGAACA 720

AATATGCCAT GCCTTCGCAC AATGAACCCG GGCATCATCG TTTTATCTTT ATAATCGAGA 780

CAGGTATGAG GGAAAGTCGG ATGATAAGCA GATAGTGAGT GAGGCGCTGG AACATGGCGC 840

TCTGGCAAGA GAAGTGTCAC AGGTTACCTG ATGATATGGG GCAACCTGAT ATCTACTTAC 900

TTTTTTGCCT ACTCTCTTAC TTCATGCCAG CAGCGAGGGT ATCGACATTG TGTTTGAACG 960

CTGCCGTGTA GGTAGCAGCG AGGCCGCTAC TGTCGGTAAG TGCTTCCGGA TAAAGCTCTC 1020

CTCCCGCTTG TGCACCACTG GCATTGGCGA TTTGTTTCAC CAAACGGGGA TCTGTCTGGT 1080

TTTCGATAAA GTACAATTTT ACGTGCTCTC TCTTAATTTG ATTAATCAGT TTCGCCACAT 1140

TTTTACTGCT AGCTTCCGAC TCAGTGGAGT ACCCCACTGG CGACAGAAAG CGAACCCCGT 1200

AGGCGGCAGC GAAATACCCA AACGCATCAT GACTGGTCAG TACTTTACGT TTTTCTCTTG 1260

GAATAGCAGC AAACGTCTGC GTGGCGTAAT TATCCAGTTG CTTCAACTGC TGGATATAGC 1320

TGTCACCCTG TTTTCGATAA TCGCTGGCGT GCTCCGGGTC TGCTTTGCTC AGGCCATTGA 1380

CAATGTTGTG AGCATAGACA ATACCGTTTT TCATGCTGTT CCAGGCGTGC GGATCAGTGA 1440

TGGTGATCCC ATCCTCTTTC ATTTTCAGTG TATCTATTCC GTTAGACGCG GTAATTACCT 1500

CACCTCTGTA GCCAGAGGCT TTCACCAGAC GGTCCAGCCA TCCCTCCAGT CCCAATCCAT 1560

TGACAAAGAC AACATCCGCC TGTGCCAGCG TTTTGCTGTC TTTCGKCGAC GGTTCAAATT 1620

CATGTGGATC ACCATCCGGT TGCACCAGAT CAGTGACATG AACGTATGGG CCGCCAATCT 1680

GGCTGACCAT ATCGCCCAGT ACCGAGAAAC TTGCCACCAC ATTCAACTCT TTTGCAATCA 1740

CCAGTGGGCT CACTAGTAGG CTGGACAGTG CCACAACCAA AATGGACCGT TTCATCTTTC 1800

CTCCTTCATC TCGTTGCTAT GTGTAAAAAC ACTTCTTGTC AGCGACATCT GCATAACATG 1860

CCGCCATTAG AGCCAAACAG AACTGAAAAG CAGAAAAACA GAGTGCTCGT GAGGATGACT 1920

GCAGGACCTG CAGGCAAATC AGCGTAATAA GACCAGATCA GTCCAACCAG ACTGGCGCAG 1980

GTACCAATAC CCACTGCAGC TAACAACATG ATGGACAGAC GTTGACTCCA GAAACGCGCG 2040

CTGGCAGCCG GTAACATCAT AATACCGACT GTCATCAGGG TGCCAAGTAG CTGGAAACCT 2100

GCCACCAGAT TGAGTACCAC CATTGACAAA AACAGGCAGT GGATCAGCGC CCGCGACCGA 2160

CGTGACAGAA CTTTCAGGAA AGTGACATCA AACGACTCAA TCACCAGCAC CCGGTAGATC 2220

AACGCCAGTA CCAGAACCGA ACCGGAACTA ATTATGCCGA TAGTGATCAG AGCATTGGCG 2280

TCAATAGCCA GAATGGAACC GAACAGCACA TGCAGCAGGT CGACACTGGA GCCACGCAAA 2340

GAGACCAGGG TGACGCCAAG TGCCAGCGAG CCGAGGTAAA ACCCGGCGAA ACTGGCGTCT 2400

TCTCTCAATC CAGTGCGGCG GCTGACCACA CCAGACAACA TCGCCACAGA CAGCCCGGCA 2460

ATGAAGCCAC CGACTCCCAT CGCAACCAGC GACATGCCCG ATACCAGGTA GCCAATTGCT 2520

ACTCCCGGCA ACACCGCATG GGACAGTGCA TCACCGATCA GGCTCATACG GCGCAGTAGC 2580

AAAAAACAGC CAAGTGGCGC GGCGCTCAGG GTCAACGCCA GACATCCGAC CAGCGCCCGA 2640

CGCATAAAAC CGAAATCGCC AAATGGCTCG CACAACAGGT GCAGTAACAT CATGGCAGCA 2700

GCCCCTGCTG CGGTGGCGTG GCTGCAGCCG TGAGGGAATG GAGTATATCG GCACTTCTCC 2760

CCCATCGGTG GCCTTCCGCA CTGAGCATCA GTACATGAGG AAAGTATTTT TCTACCTGTT 2820

CCATGTCATG CAACACCGCA AGAATTGTAC GTCCTTCCAG ATGTAGCTGC CGAATAACAA 2880

CCAGCAGAGT ACGGATAGTC TGAATATCAA TGCCAGTAAA TGGTTCATCC AGCAGAATAA 2940

CCGACGGCTG CATCACCAGC AGTCGTGCGA ACAGTACGCG CTGTAACTGA CCACCGGAAA 3000

GTGTGCCGAT GTGCATCGGC GAAAATTCTG TCATACCGAC GGTATCCAGC GCTTCGATAG 3060

CTTTTTTTCG CCATAGACCG GAAATACGAC CGAACATCCC GCTGTGTGGA ATACATCCCA 3120

TCAGCACCAG ATCGTTAACA CTCAGTGGAA ACTGGCGATC AAATTCAGTC AATTGGGGCA 3180

AATAACCTAA CTGGCGTTGC CCCTGCGGTG CCATGCAGAA GCAACCACCC AGAGGTGGCA 3240

GCAGACCGGC CAACGTTTTA AGCAAGGTGG ATTTACCTGT GCCATTCGCT CCGATAATGG 3300

CAGTCAGTGA ACCGGTGTCA AAACATCCAT TCAGCGTACC CAGCGGGTGC TGTCCCGAAT 3360

AGCCAAATGC CAGTGAATGT AATGCGATCA TGTCAGTACC ACCGCCCAGG AAATAAGAGT 3420

CCATAACAGT ACCAGCAGCA CACCGACGAT ACCCAGTCGG GCTATTGCGG AAAAAGCATA 3480

AAGACTGACC ACAGTATCCC CCATCAAAAT TGTTATAGTA TAACATTATT GCTTTATGGG 3540

TGCCGATGAT AGGTAAGAAA ATGTGTCATG GCTTCTGCAG CGTAAGCATA CAGCGAGAGC 3600

AGTATTGACA GGGATGCGTT AGTCATTTAG CAGTGTAATG CGCTAAATAG NTGCGCGGAA 3660

TAGTAGATCA CTTTGAGGGT ACTCAGCCCG GATTGTGCGC TCTGATCAAT CGCCAAATCA 3720

AAACAAATCA CCAACCGAAC TGAGCAATGC CGATCATAGC ACCAATTTCC CGTGACGAAC 3780

GACACCGGAT GCAGAAAGCC ATCCATAAAA CACACGATAA AAATTATGCC CGCAGACTGA 3840

CTGCCATGCT GATGCTGCAC CGGGGCAACC GTATCAACGA CGTTGCCAGA ACGCTCTGCT 3900

GCACCCGTTC ATCTGTTGGA TGCTGGATTA ACTGGTTACT AAAATCATTC CCTGCCGGGC 3960

GTGCCCATCG CTGGCCATTT GAGCATATCT GCACACTGTT ACGTGAGCTG GTAAAACATT 4020

CTCCCGACGA CTTTGGCTAC AAGCGTTCAC GCTGGAATAC AGAACTGCTG GCAATAAAAA 4080

ATCAATGAGA TAACCGGTTG CCTGTTAAAT GCCGGAACCG TTCGCCGTTG GTTGCCGTCT 4140

GCGGGGATAG TGTGGCTAAG GGTTGTGCCA GCTCTGCGTA TCCGTGACCC GCATAAAGAT 4200

GAAAAGATGG CAGCAATCCA TAAGGCACTG GACGAATGCA GCACAGAGCA TCCGGTCTTT 4260

TATGAAGATG AAGTGGATAT CCATCTTAAT CCCAAAATCG GCGCTGACTG GCAGTTACGC 4320

GGACAGCAAA ACGGGTGATC ACGCCGGGAC AGAATGAAAA ATATTATCTG GCCGGAGCGC 4380

TGCACTGCAG GACAGGTTAA AGTCAGCCAT GTGGGCGGCA ACCGCAAAAA TTCGGTGCTG 4440

TTCATCAGTC TGCTGAAGCG GCTTAAAGCG ACATACTGTC GAGCGAAAAC CAGCACGCTG 4500

ATCGTGGGCA ACAACATTAT CCACAAAAGC CGGGAAACAC AGCGCTGGCT GAAGGAGAAC 4560

CCGAAGTTCA GGGGCATTTA TCAGCCGGTT TACTCGCCAT GSGTGAACCA TGTTGAACGG 4620

CTATGGCAGA CACTTCTCGA CACAATAATG TGTAATCATC AGTACCGCTC AATGTGGCAA 4680

CTGGTGAAAA AAGTTCGCCA TTTTATGGAA ACCGTCAGCC CATTCCCGTA GGGGAACATG 4740

GGCTGGCAAA AGTGTAGCGG TATTAGGAGC AGCTATTTAG GAGAACAGCT CGCTGACCCG 4800

GTTGACTATG ACTCAAGCCC ATGACGAAGA TAGCTTTCTG GATCAACATC GTTCAGTCTG 4860

CACGTCCCAA TCCAGCCACC AGCCACCAGC CACCAGCCAC CAGCCACCAG CCACCAGCCA 4920

CCAGCCAGGC TACAGTGCCA TCCCGACCTC CCCACGTAAA CCCAGGGACA GGCTAAAGGC 4980

AGAAAATGGG GAAGGCAGTA TGACTCTCCG TGACACAGAT GCGGGTACCT GATGGGAGTG 5040

AGATCATCTT CCCCTCCCGG TCAGTTCCCG GATCAACACC GTGAGCAGCT CTGGCGAAGG 5100

TTTTTCCAGC GTCATTTTAC CGTAACGAAA TTCAACCTTA CAGGAACTGG CACAGACTGT 5160

GCACTAAGTG GCAGTGGATA AAAGCGGAGT AAGAGCCGCC ACAGGCTCTT TCTGCTCATC 5220

AGGCATTATC TCAACAGGTA ATAATTCAAC GCCAGCGCCA GAAGAGGTTG TTACCGGAAG 5280

ACGCCGCGCC CCCCTTCGTT CAGCCAGAGC CTGAGCCATT TGACCAGGAG GTTATCATTG 5340

ATATCGTGTT CCTGGTCAAT ACGGGCAACA GAGGTGCCTA CGACGTTTTT TCAGTTCGGT 5400

TATCTATTGA CTTAACTCTT TGGCCAGTAA TGCTGCAGCC CCCGTGCCAT GAATAAACGA 5460

GTGGTCGCAG ACCACGCAAC ATGCAACATC ATTCAGATCC CCCGCTAATA TTACAGGTAA 5520

TTCAGAATCA GCAATACTTT TCCCGACCAT TAAAAGTTCT GAGTCACGAT CAGTTGACTC 5580

ATCACTTTCA GTCGGGCTCG GTGGAACAGG ATGAAGACAA TGTAATCTTA TTCTCAAACC 5640

TTCTGGCATA TGAACTATCA TATTCATGGA GGGAATTTCC TTGTCCACTA AATACTGTAT 5700

TTCTGCATCA CTTAAAATCA TCCAGGAATA TACATGCATG CCATATAAAT TTTCTTTCGG 5760

GCATTTCAGG GAGTATGGAA ACACTTCATC CAGAGGTGAT AGTTTCTGTT CCCACCATAA 5820

GTTTGTTTCA AGAAGAACAA GTATATCAGG TTTTTCTTTA TTTATAAGTT CAAGAATGGG 5880

TATATATTTT TTATTGGTCA TAAGAACATT GAATACCAGT ATACTTAAAC CCAGAAATCC 5940

ATCAGAGTCC TTTATTTCCT TTACCTGCTT CTTGCCAATT ACTGTATAAG GAATTATCCA 6000

TACCAACTGG TAAGCGACAC AAATTAAACT TATTATCCCA ACAAACAACT CTGTAAATAA 6060

GTCAAGAAAA ACAACAGACA GAAAAACATT CAAAGTACAC AGCAAAAGTA TCTGTAGTCG 6120

GGGAAAATCC CATCCCCCGA CAACCCATGA TGTATTACCG GAAACAGGGA TAAAAGTTAT 6180

3NSDOCID <WO__9822575A3 IA>

GACTGCCAGA AGGATAGCAG TAAAAATAAA AACACAAGTT ATCACAAATC GCTCCTTGTT 6240

CTGAACCGGA ACACAAAACT GTCATATACG TTTCAAAAGT AAAAATACAC TGCTGCCACA 6300

AGATTTACAG CGTAACCGGA CAGCATATCC TGATTACGGA CAATCCATGA AACCGCCTCA 6360

CCAGAAGCGT CCATCACATC CGTTTTTTCC CTGTTTTATA TTCCCCGAAA CATTTTATTT 6420

TCAGGAATCT CCGGGCCTTT ATCCCGCATC ATTGCAAAAT GGCATCTGAA TCGATCATGA 6480

TTTGGCATCC ATCTCCGATC ACAGTTTGGC ATCACAATCG ATCACGATTT GGCATGCTTC 6540

CGATCATTGA TTAGCATCCT GCCAGTCACT CCGGGAATTA ACTCTTTTCG CCACAGTCTT 6600

CATTGCCGTG TTTAAACCAA TGGAGACGGC AATGTCCAAA AAGAGAATAT CCAGGAGCAC 6660

TATGGATACC TGTTTTAAGA TCCTTCAGCT CAAGTTCGAC CAGAAGCTGG CTAACCGTTG 6720

TATCGGACTT GCAAAACACC AATGGGGATT GATCTCTATT TTGCGACACA GACGCATTAT 6780

CAATACATCG ATGGTGCGAT CAAATACCTC AGTGGTCTCA CCGTGGATCA AATCCAGCAA 6840

TTGCTCACAG ATTAAGACTC GTCGGGAGTT TTGAGCCAAC ACCAGCAGTA ACCCATATTC 6900

ACCTTGAGTG AAATCTACAG GCTGTTGATG AGCATCAACC AGCACGTAAC GGTCCGGGAT 6960

CAAGTGTCCA GCCGTTAAAA AAACCACTCT ACTACCCTGC TCGACCTAAG CCTCGGCGTT 7020

CAGCCGCCTG AACGGGTATG GCAAGGGTGA AAAGAAACAG CATCCCCACA GTACCGACCA 7080

GACGACAGGA TGATGCTGGA ACAGAAAGCA TTCGCACCTC TCTTAGAATT AGACAGTGCG 7140

TACAGGATAC GTAAGACAGG GTGACGGGGC GGCGATAAAC TCTATTTACA AAGCTGAAAA 7200

TTTTCTGACG ATGAAAAACT ATTCAACAAG GTTATCTGAG GCGTTAAAAT AACCAGCTCG 7260

ATTAACGACT AACTTGAGGT GAATATGAAT TTAAAAAATA TAATTTTAAG TACTGTTTTA 7320

TCAATCGCTA GTTGTCATGC CCTGGCTGTA GGTAATTCTC CAAATAGCGC TATCTAACCT 7380

TCATGTGGGR AAACACCCCC AGTGGGGACS AAGGSCAATT GGTGGGGTTA 7430

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGATTATTCT GGCTCAGATT CATTTTTCAT CAGTCGCTTT CCCCTATAAA CCGTAAGGTT 60

CCATAGTGTC GACGCTCTCG CTTAATTCCC ATATCGTCGA TAGTCTTATT AGCCGCTTCT 120

GTCAGGTCAG AAAAAGTATC ACGCTTCTTT GGGAGTTCAA GTCAGATTTC TCGCCGTCGG 180

GCGATGCGCT CAAAATGTTT GTCTGTATGG GGTCGCTTCA TCACGTCAAG CCATCGCGCT 240

GCCGCTCTCC GCCAGAGTAC AAGCTCTTCC AGTTGTTCTG CTTTTTATCT TATCTGTGGC 300

GATGCAGTAT CCTCCTCCGT TTGTGTAAAT CGTTGAGTGG TGAATCACGC AAAGGGGCTT 360

CTTTTTTCTG ATCTATCCCC ATATTCTTTA GCGTTCTGGT CGCAGCATCT CTGATGTCGC 420

AGACACTGAA CCTTTGTATT TTCCATGATC TTGTGGAGTT TTCGATACAT CTGCTCCGAT 480

GCTGGGTTAT AAAGATCCGC TCTTTATCAT CCTTGGCTTG TGTAAGCAAT TCTCCCCAAC 540

GTTCTGCTGC ACGCCGCCAT AACTCTCTTC TTTCCAGTTC CTCAGCTTTT TCATCATGTA 600

CCATTCGTGT ATCCCCGTTT ATCCAGTCTG AACCGCACCG GGTTTCCTGG AGAATGTTTT 660

CTCTGTGAAC TCAGGCTGCC AGATCATCGT TTCCGATGGA AGCATAATAA GCTTTTTCTG 720

CTTCTGCCGG ARGAATATGG CCCAGCTTTT CCAGCAATCG TCGATTGTCA TACCAGTCCA 780

CCCACGTTAG TGTGGCCAGC TCCACTTCTG TCCGTTTTTT CCAGCTCTTA CGGTTATTAC 840

CTCCGTTTTG TAAAGACCAT TGATGCTCTC CGCCATTGCG TCGTCATACG AGTCGCCTGT 900

ACTCCCTGTT GATGCCAGTA ATCCGGCTTC CTTAAGCCGT TGCGGACACA TAATGAGAGC 960

CTTTATCGCT GTAATTGTCA ACGACGGATG AAAAGTGATC CACTTATATC TCCACCAACG 1020

GCCCAATATT GATCCACCGT TTTACTCAGG ATTAGCTTCT GCTATAACCC CGGCCTTTCG 1080

TTTCTGTCTG AGTCGATAGC TTTCTCCTTT GATTTGAACG ACATGTGAGT GGTGTAAGAT 1140

ACGGTCCAGC ATCGCTGAGG TCAGTGCTGC ATCACCGGCG AACGTTTGAT CCCACTGCCC 1200

GAACGGCAGA TTGGATGTCA GGATCATTGC GCTCTTTTCG TAACGTTTAG CGATGACCTG 1260

GAAGAACAGC TTTGCTTCTT CCTGACTGAA CGGCAGATAG CCTATTTCAT CAATGATGAG 1320

CAGGCGGGGG GCCATTACTC CACGCTGAAG CGTCGTTTTA TAACGGCCCT GACGTTGTGC 1380

CGTAGATAAC TGAAGTAACA GATCTGCTGC TGTTGTGAAG CGAACTTTGA TACCTGCACG 1440

GACTGCTTCA TAGCCCATCG CTATTGCCAG ATGGGTTTTC CCCACACCTG ATGGCCCCAG 1500

TAATACGATA TTTTCATTAC GTTCTATGAA GCTGAGTGAG CGTAACGACT GGAGTTGCTT 1560

CTGCGGTGCT CCGGTGGCGA ATGTGAAGTC ATACTCTTCG AACGTTTTCA CCGCCGGGAA 1620

GGCTGCCATT CGGGTATACA TCGCCTGTTT ACGTTGATGA CGTGCCAGTT TTTCTTCATG 1680

AAGCAGATGC TCCAGGAAGT CCATATAACT CCATTCCTGG TCTACTGCCT GTTGTGACAG 1740

CGCAGGCGCT GCGCTTATAA GGCTTTCCAG TTGCAACTGC CCGGCGAGCG CCATCAGTCG 1800

TTGATGTTGC AGTTCCATCA TCACGCCACT CCTCTGCAGA ATGAGTCGTA GATGGAGAGT 1860

GGATGATGCA GGGGGTGTTT GTCGAAGTTC ACCAGATTTT CATCAAGATG CACGTCATAC 1920

TCTTTTTTCT CCGGAGCAGT GCCAGCATGG ACTGCTGTCT TCGAGCCAGC GATCGCAGGG 1980

ACGGGCCTGG ATTGTTTCAT GCTTTCGTTG GTTAGCGACA TCGTGCAGCC AGCGCAGACC 2040

GTGGCGGTTG GCTGTTTCAA CATCGACAGT GATCCCCATC GGGCGCAGGC GAGTCATTAG 2100

TGGGATGTAA AAACTGTTAC GGGTGTACTG CACCATCCGT TCCACCTTAC CTTTAGTCTG 2160

TGCCCTGAAG GGGCGACACA GTCGGGGAGA GAAGCCCATC TCCTTGCCGA ACTGCCACAG 2220

3NSDOCID: <WO _ 9822575A3_IA>

CGAAGGATGG AACCGGTGCT GACCGGTCTG ATATGCGTCA CGTTGCAGAA CCACAGTTTT 2280

CATATTGTCA TACAACACTT CGCGCGGCAC ACCACCAAAG AAGCGGAACG CATTACGATG 2340

GCAGGTCTCC AGCGTGTCAT AACGCATATT GTCAGTGAAT TCGATGTACA GCATTCGGCT 2400

GTATCCGAGA ACAGCAACGA ACACGTGAAG CGGTGAGCGA CCATTACGCA TAGTGCCCCA 2460

GTCAACCTGC ATCTGTCGTC CGGGTTCAGT TTCGAACCGA ACGGCAGGCT CCTGCTCCTG 2520

AGGAACCGAG AGAGAACGAA TGAATGCCCT GAGAATGGTC ATTCCGCCAC GATATCCCTG 2580

GTCTCTGATC TCGCGAGCGA TTACCGTTGC CGGGATTTTG TAAGGATGAG CATCGGCGAT 2640

GCGTTGACGA ATATAATCCC GGTATTCATC CAGGAGTGAA GCAACAGCAG GTCGCGGCGT 2700

ATATTTTGGC GGCTCAGATT TTGCCTGCAA ATAACGTTTA ACCGTATTGC GGGAGATCCC 2760

CAGTTCTCTG GCAATCGCCC GGCTACTCAT TCCCTGCTTG TGCAGGATTT TAATTTCCAT 2820

AACTGTCTCA AAAGTGACCA TAAACTCTCC TGAATCAGGA GAGCAGATTA CCCCCTGGAT 2880

CTGATTTCAG GCGTTGGGTG TGGATCACTA TTGCACCGTT CGTGACAGTA ATGGATTGTG 2940

TCAGACGGAC GACGGGCCCA TAACGCCTGC TCCAGTGCAT CCAGCACGAA TGTTGTTTCC 3000

ATGGACGATG AGACTCGCCA TCCCACGATG TATCCGGCGA ACACATCAAT GATGAACGCC 3060

ACATAAACAA AGCCCCGCCA TGTGCTTATC CCGGTAAAAT CAGCTACCCA CAACTGGTCC 3120

GGGCGTTCTG CGATGAACTG ACGGTTTACA CCGTTGCATG CGGCAACAGC TTTCCGGCTG 3180

ATTGTCATGC GAACCTTTTG CAAACCCCAT ATATTTCAGA CGATACCGTT CAACGGTAGT 3240

GAACCCACCA TCACCGCTCC CGGTATCCCG CTCATGCTGG TATACCCAGA CATGCAGGGG 3300

TTCCAGCGTA CAGCCAATCT TTGGGGCAAT GGAACAAATT GACGCCCACT ACGAGTCATA 3360

CGACTTTCCA GAACAATACG GAGCGCCCGC TGACGGACCA CCAAAGAGCC GCCATTATTC 3420

TTATTACCTT TAACTAATAA TGCCAATTCA GACCCAAACA CGGCATCATT CGCTTCAGCC 3480

TCTGCGCCAT TAATTAATGC CAGGACTTGG TCAAGAAAGC GTTGCGCTTC GTTTACATCT 3540

GTTGCTTGTC GCAGGTAATA AGGTATTCGT TCAACAAACT CGGAACGTGA TAAAGGCTGA 3600

TGCTCCAGCA AAACCTCAAG CATTGCGGGC CGCAACAAAC GACGCTCAGC ATCAACATTG 3660

GGAAACTTAA CCTCAATGGC ATATGTGGCA AAATACTTAA GTTGCTCCTT AAGCCCCAAA 3720

TTAGGCATAA GAGAATCAAT TGAGCCAGAC GCCACTGCAG CGCTTGATTC AATTGTTTCT 3780

ACATACTCGT AGGAAGGTAC AACAACATCT GGAGCCAATG TTTTAAGCTC ATGGAGTTGA 3840

CGGATAATCG GGGATAGAAC CTCATCAGGA TTACTGAACC AATCAGTGGA CCAAATACGG 3900

CTAATTCTCC ACCCCAAACG CTCCAAAACC TCTTGACGCA AACGATCACG GGCAGATTTA 3960

GCTGAATGAT AAGCCGCACC ATCGCACTCT ATACCCATTA AGTAACAACC CGGATCTTCT 4020

ACCGACAGAT CAATAAAGAA TCCTGCAACC CCACCTGAGG TTCACACTCA AACCCAGCGT 4080

GATTGAGTGC TTCCATTATA GCAACCTCAA AGTCACTATC CGGAGCCCTG CCCGTATACG 4140

TCGTGAGGGA ATCTAATTTG CCACTTTCGG CAAACTGTAA AAAACCTTTC AACGAAATAA 4200

CACCAAATTT ACTGGTTTCA CTCGTCAATA CATCTTCAGA ACGCATTGAA CTAAACACAT 4260

GCATCCGTTT CTTTGATCGA GTTAAAAGCA CATTCAAGCG GCGCCAGCMA ACATCGGAAT 4320

TGACAGGCCC AAAGCGTTAA TAAACCTTTC CACCATGCTC AGAAGGTCCA CAGGTAAAGG 4380

AAATAAAGAT TACATCACGC TCATCACCTT GAACGTTCTC AAGTTTTTTC ACAAAAAGTG 4440

GCTCTTCCAT GGCATATAAG CCATCAATTG CATCGTTAAA TTCAGTGCGA TTTCGGCGCA 4500

ATTCATCAAT AGCGCGCTCA ATCTGATCGC GTTGCCTGGA ACTCATGGCC ACTACCCCAA 4560

GAGATTCATC CAGCCGGTGT TGCGCATGAT GAAGTACAGC CTCAGCAACT GCTTGGGCTT 4620

CTTCAATATT GTGTTGATTA GAGCAACGAC CTTTTGATAC ATAAGTAAAT TTGATTCCAT 4680

ACTCTGGAGA CTCAGCATTT GGAGAAGGGA ATATCACCAA ATCACTGTTA TAAAAATGGC 4740

GGTTAGAGTA TGCAATTAAC TTTTCGTGTC GTGAACGATA GTGCCAATGC AAACGTCTCA 4800

TAGGAAACAG TGGCAAAGCA GCATCCAAAA TGCCGTCAGT ATCACTTAAA GCCGCGACAT 4860

CATCGTCATC TTCTCCGGCG GAACTTCGAT CTGAAGTGGC ACACTGAATT TGGCCACCTG 4920

AACAGAGGTG ATATGCTCAC CTCAGAACAA CACAGGTGCT CCAATGAAAA AAAGGAATTT 4980

CAGCGCAGAG TTTAAACGCG AATCCGCTCA ACTGGTTGTT GACCAGAACT ACACGGTGGC 5040

AGATGCCGCC AAAGCTATGG ATATCGGCCT TTCCACAATG ACAAGATGGG TCAAACAACT 5100

GCGTGATGAG CGTCAGGGCA AAACACCAAA AGCCTCTCCG ATAACACCAG AACAAATCGA 5160

AATACGTGAG CTGAGGAAAA AGCTACAACG CATTGAAATG GAGAATGAAA TATTAAAAAA 5220

GGCTACCGCG CTCTTGATGT CAGACTCCCT GAACAGTTCT CGATAATCGG GAAACTCAGA 5280

GCGCATTATC CTGTGGTCAC ACTCTGCCAT GTGTTCGGGG TTCATCGCAG CAGCTACAGA 5340

TACTGGAAAA ACCGTCCTGA AAAACCAGAC GGCAGACGGG CTGTATTACG CAGTCAGGTA 5400

CTTGAGTTGC ATAACATCAG CCATGGTTCT GCCGGGGCAA GAAGCATCGC CACAATGGCA 5460

ACCCGGAGAG GCTACCAGAT GGGGCGCTGG CTTGCCGGCA GGCTCATGAA AGAACTGGGA 5520

CTGGTCAGTT GCCAGCAGCC TGCGCACCGT TATAAACGAG GTGGTCGTGA ACATGTCACT 5580

ATCCCGAATC ACCTTGGGCG GCAGTTCGCA GTGACAGAGC CAAATCAGGT ATGGTGCGGC 5640

GACGTGACGT ACATCTGGAC GGGGAAACGT TGGGCATACC TTGCCGTTGT TCTCGACCTG 5700

TTTGCAAGGA AACCGGTAGG TTGGGCAATG TCGTTCTCTC CGGACAGCAG ACTGACCATC 5760

AAAGCGCTGA AAATGGCCTA GGAAATCCGC AGTAAACCAG CCGGGGTAAT GTTCCACAGC 5820

GATAGTAATA ATGCCGGTAT CAGTTTTTAT CATCACTCTG TTTGCTGTTT AACCAGACTG 5880

GTGTGATTAC TGATGCAGTG AAGACCTTCC CGCATCCTGA CTCACACAGC GATCGACCCT 5940

TTGTGTCCTG CCCTGGACCT GTCGGTTGCC GGAAGCGCCT TCATGCGAGG CGTCTCCTCA 6000

CCGATGCGCG TGACTCAAGA AGGGCCTGAC GGTTTGTCTC GTTACTGTCC TGTCCGGGTT 6060

3NSDOCID <WO 9822575A3 IA>

ATCTGTCTGG AGATTCAACT CTGTTTCCTC ACAGGAGCTC TGTTATGGCA GGTAAAGTTA 6120

CGGAAACCGC TGTTGTGGGT GGCGTGGATA CACATAAAGA TCTGCACGTT GCCGCTGTCG 6180

TAGATCAGAA CAATAAAGTT CTGGGGACCC AGTTTTTCTC CACAATACGG CAAGGTTACC 6240

GGCAGATGCT GGCATGGATG ACTTCGTTTG GGGCATTAAA GCGAATTGGT GTTGAGTGTA 6300

CTGGCACCTA TGGATCAGGT CTGCTTCGCT ATTTACAGAA TGCCGGGTTA GACGTTCTTG 6360

AGGTGACTGC GCCAGATCGG ATGGAGCGAC GCAAACGGGG TAAAAGTGAC ACGATTGATG 6420

CTGAATGTGC CGCTCACGCC GCATTCTCCC GAATAAGAAC CGTCACACCC AAAACGCGCA 6480

ATGGCATGAT TGAGTCTCTG CGGGTATTAA AAACTTGCCG AAAAACAGCA ATATCAGCCC 6540

GCAGAGTCGC TCTCCAGATT ATCCATTCCA ATATTATCTC TGCCCCGGAT GAATTACGTG 6600

AACAGCTCAG AAATATGACG CGCATGCAGC TCATCAGGAC TCTGGGATCC TGGCGGCCTG 6660

ATGCCAGTGA ATACCGCAAT G 6681

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TATTCGCGCA TACGCGTTGC ACATGTTCTT TTGGCGAACG ATCATCGGCA ATACAGAGTT 60

CCCAATGGGG ATAGCTTTGA GCCAGGACAG AATCCAGACA GGCACGCAMG TAGATCTCCG 120

CTGGATTATA AACAGGAATC ACAATAGATA TAACTGGAGG GTGAGTCATA CTGGCAAGCA 180

TCAGACTCAC CWCTTCKTTG CCAGGCAACG AAGGTAATTC CACCGTTTCT ATCCATTCCT 240

CATAACCGAC AGAAGACGGG GTAACGCTGA ACGTYTCGTT ATAGAATGCT TGCAGGCGCT 300

CTATTGACAT ATCGCCATTG TSCATCAATA TGGATTTTWT GATTTTTTCT AGCGGCATGT 360

CACGATAGCT TTGGTGTTCT TTTTGAATGC GAGCCAATAG TGCAGACTCG ACTACTTTCA 420

CATCAACAGC CGCTATTTCA AACTGATTAA TTGCAAATTT TGCTGCCTGT TCTAATGGAT 480

CAAATCGTAA TGCACAAGAG GCGATTCCAG ATAGAACAAC GACTGACGCT GACCGCTCGT 540

TTATATGGCA ACGTTACTGT TTCAAACTCA TTGAACCCTT TACCTGTATC CAAATRTAAC 600

TTAGCTAATC CTTGCTTTGG TTGGGCAATT AATAGAGATA TTAAATTGAT ACCATCCCTT 660

GCTAATATTT GAGAGCTGCT CCAAATCAAT AATGAAAAAT GGATCATTTC CCTCTGCAAC 720

CCAACTTTGT GAATTATCTA TATCTATCGA GAGCTGATTT GTTGCCAGAT AGGGCAGCAC 780

AACTGTATTT TGCATTTTAC TCACTGCAGG AGAAACGTCC CATGCTTCGC ATGGTTTCCT 840

ACCAAGTAAC ATCCCATAAC GCTTAAAATG TTCTCTTGCT GACAACCCGG TCTGTTTCAC 900

ATCCAAATAG TTATGCAGAT ACCAATGTTC ATCAAAGTGA GCTAGCAACT CGTCTTGGTG 960

ATTTTTAACC ATCACTTTTA TTCTCCCTTA TTGACAGGCA GGCAACTGCG CTGCTCAAAC 1020

TTCCCATACA TAATGTAATG AAGCAGCGGA TTAATGCCTC CTTGGGCCAC ATCCGGATAG 1080

GTTTGCAAAT ACCAGCGAGT ATCAAACTGC TCACTAGGGC TATAACCTTT ATCCGCCCCC 1140

ACGCTAATAA AATGCTCAAG AGCTGAGAGC CCAGTGTCTG CAACCTCTGG GTAGCGATGT 1200

TGATACCAGA GTTCATCAAA CAATCCTGAA GCGGCAANTA CTCCGCGGCA CTCTCTGTAG 1260

CTGTTGTTCT GGATGGAGTC TCCTCCTTAA ATGTTCTGCC AAGAGCACGA ACTGGGGCTG 1320

TAATCTTCCA AGAGACGGTT CT 1342

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CGAAGGAAGC AGTNTGCNGC CTGCGCTGGC GGAGTTGCGC CTGTTCCCAC CGATGATGCT 60

GTACATGAAT CCTCCGGCGA ACAGAGCGGT GAACTGGAAA CCATGCTTGA ACAGGCCGCG 120

GTCAATCAGG AACGGGAATT TGATACCCAG GTGGGGCTGG CGTTAGGGCT GTTTGAGCCG 180

GCGCTGGTGG TGATGATGGC GGGCGTGGTG CTGTTTATCG TCATCGCCAT CCTCGAGCCG 240

ATGCTGCAAC TGAACAATAT GGTTGGAATG TAATTTACGG AGTTATCACA TGAATTCGTT 300

ATCCCGCACA CAAAAACCAC GGGCAGGTTT TACCCTGCTG GAAGTGATGG TGGTGATTGT 360

TATTCTTGGC GTCCTGGCAA GTCTGGTGGT GCCTAACCTG TTGGGCAACA AAGAGAAARC 420

CGATCGGCAA AAAGCCATCA GCGATATCGT GGCGCTGGAG AATGCGCTGG ATATGTACCG 480

ACTGGATAAC GGGCGTTATC CGACCACTGA GCAGGGGCTT GAGGCGCTGA TCCAGCAACC 540

GGCCAATATG GCGGATTCCC GTAACTACCG TACCGGTGGA TACATTAAAC GACTGCCAAA 600

GGATCCGTGG GGCAATGATT ATCAGTATCT CAGCCCGGGT GAAAAAGGGC TGTTTGATGT 660

TTATACCCTG GGGGCAGATG GTCAGGAAAA TGGGGAGGGC GCTGGCGCAG ATATCGGTAA 720

CTGGAATTTG CAGGAGTTTC AGTAATCAGT GCCTGAACGC GGATTCACAC TTCTGGAAAT 780

CATGCTGGTG ATTTTCCTTA TCGGCCTTGC CAGTGCGGGC GTGATACAGA CGTTTGCGAC 840

CGCTTCAGAG CCGCCTGCGA AAAAAGCGGC GCAGGATTTT CTGACTCGCT TTGCGCAGTT 900

TAAGGACAGG GCAGTGATCG AAGGGCAAAC ACTCGGTGTG CTAATCGACC CGCCTGGCTA 960

TCAGTTTATG CAGCGTCGTC ACGGACAGTG GCTACCCGTT TCTGCGACCC GCTTATCGAC 1020

ACAGGTTACG GTGCCAAAAC AGGTGCAGAT GCTGTTACAA CCCGGCAGTG ATATCTGGCA 1080

GAAGGAGTAT GCGCTGGAGC TGCAACGTCG TCGCCTGACG CTGCACGATA TTGAACTGGA 1140

GTTGCAAAAA GAGGCGAAAA AGAAGACGCC ACAGATCCGT TTTTCGCCTT TTGAACCCGC 1200

CACGCCGTTT ACGCTGCGCT TCTACTCAGC GGCGCAAAAC GCATGTTGGG CGGTAAAACT 1260

GGCACACGAT GGCGCGTTAT CCCTCAGTCA ATGTGATGAG AGGATGCCAT GAAGCGTGGA 1320

TTTACCTTGC TGGAAGTGAT GCTCGCGCTG GCGATTTTTG CGCTGGCTGC CACGGCGGTG 1380

TTACAGATTG CCAGCGGCGC GCTGAGTAAT CAGCACGTTC TTGAGGAAAA AACGGTAGCG 1440

GGCTGGGTAG CTGAAAACCA GACCGCACTG CTCTACCTGA TGACCCGCGA ACAACGGGCG 1500

GTCAGGCACC AGGGCGAGAG CGATATGGCA GGAAGCCGCT GGKTCTGGCG AACCACACCA 1560

CTGAATACCG GTAATGCGCT 1580

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTTAACCATT ACCCAGCATT TGGTAGTTAA ATAGTCGTTA AAAGCATAAA ACATGGACAT 60

TGTGCCATCC CAGCTAAAGC ATCCATTACC GCCTGACAGG GATAAAAATA AAAAAGCAGG 120

GAACCATTTT TTCATCAGAA ATCACTTCCG TAATTACAGT TATTCATTTA GGTATGACTC 180

AGTTATAAAT CATGCTCATA CTGGCCGTGG TCTGGRAATC CCCGCCATTC AGTATCCCGC 240

TGCCATTACG AAAGGGCACT GAAGTAAAGG TGAACGTTGA ACGTGCTGTG TCCAGACCTG 300

CTGTCACTCC GTAACCATTT CCTGAACCAT TACCTAATAT AAGAGGTGTT GACATTCCTT 360

TTCCCTGATA CAGCGCTATA CCAAAATGAG TTATATTTGT TGCCAGTACA TTATTCTGAC 420

CTCCTCCCAT AGTATTTCCC GTAACTTTTA TCCAGAGAGA GCCACTCTTA TACGGACAGG 480

ATATGCTTAT GGTTTTTGTG ACTTCACCAC GTGAGTTGTC CACGTGCTCA GGATTAATAT 540

TCCCAAAATC AACAACAATA TTCTGCCCGT TATTAATGGT GCATGGGGGG ATATAAACAT 600

TCCCCCTGAT GTTAATCTGC ACATCAGCCA GTACAGCGAC CGATGTCAGA AGCAACGATA 660

TAAATAATGA TAAACGAATC ATTCCCCTCC GGAGAGCGGT ACAGAAAACA TTTTATTTTA 720

CGAGATATAA AATTAACGTA TTTTAGTTGA TACTATTACG AATATGATGC AACCAGCGTT 780

GCTGTTGCAG AGAAAGGACC GGCTATCAAA TTCTGCATAT TCCCTTTATA TCCAAGTTTG 840

GCATGAAGTG ATATAGTTTT ATCTGCATTA TTACCTGTGA TTTTTCCGGG CGTAAATGGA 900

GTCCCTAAAG TTATCGCAGT CCCAATATTT CCTGCATTAC TGTTATAAAG ATAAACGAGT 960

AACCCATCAG AAGATGTGTT TGATGTATTC TGAACTAAAA TAGCATTGTT ATAAGTGTTT 1020

JSDOCID <WO__ 9822575A3 IA>

GTTGCCGTTA TCGTAACCTT CATTGTTCCC AGATTATAGG GACACCGCAT ATTCACAGTA 1080

AACTCTTTTT CGTGATTTCC ATTTTGACTC AGGGTCTGAA TCTCTACATC CTGCCAGTCA 1140

ACAGTTGTGT TGCTTACAGT ACAGGCAGGA ATAATCAGTT TTCCTCTGAA GGTCAGATTA 1200

TCAACTGCAT GTACATGCTG AGACATTAAC ACTGCCCCCA GCATTACCGG AAGACACAAA 1260

CCTCTTATCT TTTTCATCTG AAATATCCTG TACAAAAATT TTGCTAACGA TATGTCAATT 1320

CAAACGTGGC TGTTGCTTCA TAATCACCGG GTACCACACT CTTCGTCCGC AGGCTTCCGG 1380

CGTTGCCACA ACATACGCGC CGAAAGGAAG CTCAAGACTG TTTCCGGTAA CCTTTTCCCC 1440

CTGGCCTTTG TTATGGGAGG TGCCGGGTTT CAGCAGACTG CTGCCATCGG TGTCCAGCAG 1500

TGCAATGCCT AACCGGCCAG CATTCACTCC GGTTACCTTC AGATGGCCCG GGAGGGCGCC 1560

TCTTCCGTCC CCTTAAAGGT CAGGGTCACA ATTTTGCCAA CTGCTGTTGC ATGGCAGTTT 1620

TCCAGCCTGA TGACAAACGA CTCTGTCGGC GAACGTCCGG GCGGATACCA GAAATCCCTG 1680

GACGCCCGGG TTTTGAAGAC GACATGTTTA TTCAGACTGT CACCGGACAC ATGGCAGGGT 1740

CTGTCAAGCA GATTACCCCT GAATGCCACA TCTGAGGCTA TTGCCTGTCC GGCAGACAGT 1800

GCGGCAAACA GTAAAAGAGC GCCTGTGCTT TTTATCATCA CATTCCCTTA CTCATATTTT 1860

ATGCTCAGAC GCAGCATGGC CGGATTGCTC CTGGCATCAG AATACTCACC CTCCTGTGTC 1920

GCCCTTTTCC TCCAGGCGGC CAGCATCTCC TCCTGCCGCC GGTCAGGCCG GCACAGTAAA 1980

AAGGTATCAC CATCGTGTAT AACAAGATGG TCACAGCCGG ATAGCTTACG GTCAGGAAGT 2040

AAAGCACTTC CGCTTCCGGG ACCGGTTACC AGTGAGCCGG AGACTGTCAT CGCAACGCCC 2100

CGTTTTCCGG GCTGAAGTGC ACCACCGTCC CCACATCCTG CCAGCCTCAG CATCAGAGGT 2160

GCTCCGGCTG CCGCAGAGTG ATTTTCCGGC CGGAGGYTTA ACGGCACCTC ATTACTCACC 2220

AGCGTGCAGG GTGAGGACAG CAGTGCACCA CTGACGGTCA GGCTTCCGGT GCGTCCCCCC 2280

CGTTCATTTA TCCGGTAATG ACGCAACTCA TCTGCAGTAA AGACGTCATC GTATATACCC 2340

CGCTCTTCAG CCCGCAGGAA AGTATGGATG AAACCACTCA GCGACAGTGC AATAAGATAC 2400

AGTACTGCTG TTGTTTTATT CACAACCATA ATATCCCACC CGCATTTAAC CGTTATTGCG 2460

GTACATTATT TCTCTTTTTT CACAGAGCAA CGGCTACCAT TACAGATAAA CGACAGTACC 2520

GGGCGACCAC CATAGTCATT AATATAAGAC AGATAAGGGG TATTATAATT TGCCGATTTT 2580

ACTGTCTGCT CTGAACGGGG AGACAGCATC ACGGTTTCAA ACTCACCTTC CTCTGCCTGC 2640

TTTTCACTTC CTCCCAGACC AATAACAGTG ACATAATAGG GCGTTGGGTT TTCAATACGA 2700

TACCCACCGC TGACTTTGTT CAGAATTAAC TGGTCCTGCC ATACTTCATT TGGTCTGGTT 2760

TTAATTGCTG CCGGGCGATA AAAAAGCTTT ATTTTGGTCT GTAAGGCTAT CTGCAGTACA 2820

TTGGCCTTTT CACTCCTCGG CGGTATTTCC CTGAGATTAA AATAAAACAG TGATTCCCTG 2880

TCCTGAGGAA GTTTACTGAT ATCCGGTGTG GTACTCAGCC TGACCATGCT TTTCGCACCC 2940

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

GGCTCAAGGC GCTGAACCGG AGGGGTGGCA ATAACCGGCC CTGTAATAAT TTTTTCCTGA 3000

TTTTCATTTT CTATCCATGC CTGAGCAAGA TAGGGCAGTT GTTTGTTATC ATTGGAGATA 3060

TCAAGCGTCA TTGACTTCTC ACTCCCGTCA AACACCGCGC GGGTTCTGTC CAGCGAAACA 3120

GCAGCGTCTG CCCCGGATAT AACAAACAGG GGGATGGCAG CCATCAGAAT CTTTTTTCGA 3180

ATCATACTTA ATTTCCACAT TCTGTAATTT CACCTGGTCC GGAAAATGGC ATAACCGCAT 3240

T 3241

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AACGTGGATC TCCAGCTGAT CGGTGCCGTA TTCCAGGTCG TAAGTTTCAC TGATGGTTTC 60

ACGCGGCAGT TTGCCCGGTT TACGGACCGG TACAAAGCCA ACGCCCAGAC CCAGAGCTAC 120

CGGAGCGCCA AACAAGAAGC CACGCGCTTC GGTGCCGACA ACTTTGGTAA TGCCCGCATT 180

TTTGTAACGC TCAACCAGCA AGTCGATGCT GAGAGCGTAA TTTTCGGGTC TTCCAGTAAG 240

CTGGTGACAT CGCGGAAAAG AATGCCGGGT TTTGGGTAGT CCTGAATGCT TTTGATGCTA 300

TTTTTGAGAT ACTCAAGCTG CTGTGCATCG CGGGKCATAA GTGTATGCCT GCTTGTTACG 360

GTGGTACTCA CGGCGCGTTT TTAAACGTAT CAAAAGTT 398

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17710 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CAGTTNCNGT TCTCATAGAC AGATTGATAA AATCGTAAAC AGCCCCTAGC ATTCCCGTTT 60

CCTTTGCACA CATATTCAGG CACGGGGATA AAGTATAAAG AATGTCGTAC TGCTGCTACC 120

AGAGCAATAT TCCCCCCTGA TGGCCGTATC AGAGATAGTA TGCCGGTATT TTGCGGGTGG 180

TTCCCGTCAG GTTATCGTGT ACCTCCACGG TCGTAGTCAC CACCGGCATT CCGGCYTTTC 240

TCAGCCTCAA AACATCAGCT GCAATACGCT GACTGCCGAA CCAGAACAGG CCGTCCAGTG 300

CAGTCACCAG CAACCCCGCC TCCAGCGCAT GCTTCAGCCG TTCACGGGGC GCTTTCACTT 360

CCCGGGCAAT CTGCTGGTAT GGCGATGATG TGTTTTCATT CCCAATCACC CGGCGAATAC 420

GATGAGACAG ATGATACCGG TATGTATCCG GCACACCGGA AAGGCTGGCC TTCAGGCTGT 480

ACACGCAGCC AAATCGTTTA TCATTGAACA CCACATTTTT CTGGCTGATG CCCCATTCTT 540

CACGCAGCGC GGCAATCAGT TGTGGTGTAC GGGTAAGCAA CAAGCGAAAA GGCAGTTCAA 600

AACTGGTGAC ATAATCCACA TTCAACAGGG CAATGCGAAG TCGTTCTTCT GGTCCGGCTT 660

CTGTCTGCCG GCACTCCTCC AGGACATCCT GCCACTGCAG GCGAAGACGG GAAGACTCAT 720

TCAGTTCTGT AAAGCAGTAT TTATCCGCCA GATAGTCAAT TCGTGTATGC ATACTGAAGA 780

GTATTCCGTA TAAAGATTCA GCTGGCAAAA CTTTATCAGT CTGTAAAAAC TAACGGAAGA 840

GTCGATATTT CTCCCGACAA TCACCGGATG ATTGTTGCAA TACCTCGTGG CATCAGAGAC 900

TGAACAGCAG TTTTTAACGC AACGTATTGC TCTGATGTAT CAGGCCGGAC AACCCGAAAA 960

CAGCCTTCCA CCCGGCATTG TCCGCCAGCG CTTATCACCG GCCAGGTCTG TTGCAGTAAA 1020

TCCGCCACTT GCGAACATGC TTCATCAACT GTGACACTGG CCCGCGGATG GCAAATGCTC 1080

GTCTGGCTGA GCAGCAACAG GCATCGCATT GTTGCTCCTC TATGTTGTTC CCGCAACCAG 1140

CGTAATACCA CCGGCGAGGA TGGACAGGCA GTGTGATTAC GCTCCGTAAT ACGTTCGTGC 1200

ACCCGTCGGT GAAAGGAACT ACAGAATGTC TGAATCTGTT GCCCGTTGAT GTATCCTTCT 1260

GTCGAATGAA GTGTGAAGTG GATTGCCAGC AGATGCGGCC AGTGATCCAC CGCCTGCTGA 1320

ACAAAACGCC GGATTTCCCC CGGCTCTGAA AGTAAGGCTT CGGTTATTTG CACTATTTTA 1380

TCTCTGTTGA ATTTGGTTAA GTCGGTGCAG ACGCATCAAC ACAAGTACGG TTCGATGCAA 1440

ACAGCTGTGA CTGGCAATAT GAAAGGAATG ATGAATCAGT CAGGATGACA AAGTGCCGGC 1500

TGACCGGAGG GGACGCAGGA AGATTCACGG GGGGACCAGC ACCAGGGAAC AGCGCCACAA 1560

TACCAGCGGT GACACGTTGA ACATTGCCAG CGTACCGGTA TCACAACACG TTTCATACTT 1620

CTGCCCCCGT GATTCTTCGA TTCGTTACTG TATCTACTGT GACACTTCGC TTTTATACCT 1680

GCGGCTGGAT CGGCCCGGCT TGATGAATCT TCACTGATCA GCTTATAAAA CCCTCTGTCG 1740

GTCATACCGG TGAAACTGGT GATATAGTTC ATGTCAATCA GGGAATTATC GGCACGCAGA 1800

AATACGCTGT CGTGGCTTGT TGTAGTCAAC ATGGTCAGAA TGTCCTCTGT GAGATTTATG 1860

AAGATTGTGC GAATGCGGGG AATCTACTGA GCTGTGCTTT CAGAACTGGC CTGTTACGGG 1920

AKRSCAGGGA TTACCGGCGG GGTAACGGGC TTCCGGATCA TACACACCAC GATTATCGCG 1980

GACAAAATCA CTGAACGCCC ATATCACCTC TTTAAGTATG TCTTCGCAGC CCGGTACATG 2040

ACGATCCAGC GCCACATCCC GAGTGGTACT ACTTTGATGC GCCCGGTGAC ACAAAGCCCG 2100

GATTGTTCCA GACATCCTGA ATCAAACGCC CCAGATTAGG GGCGTCGAAA TATGCCTCTC 2160

TGACCATTAT ATTCCGGTGT ACAGGTAGCA GGTCAGAAGT GACAATGCGT CACCTGACGT 2220

TAAAAGTCAC TACACCCAAG ATGACGTTCA ACAGCACCAT GCGATTCAAT GTAAGCCCGG 2280

GCTGTCTGTT CCAGTACACC AGGCTCAGCG TTGTATGTGT TAGCTGCATC AAATACCAAC 2340

NSDOCID: <WO__9822575A3 IA>

GACAGCACTT CAGGATACAC AACCAGATGT GTAATGGAGT TATCTTCACC CAATACTTTT 2400

CCCCACGCCT GCTCAATCAG ATTTCTGAGA ACCACCACCT CACGACTCTT ACACCAGACA 2460

TCGTTATTAA GTAGCAGCAC CATAAGATAA GGAGTGGTAT CGTTAGTCAC AGCCTCCCTA 2520

CTCCAGAGAT AATATAAAGG GGTGGGCTCA ACAGATTTAT CTTTACGTCG CTTACACTGC 2580

AAATATTCAG AAATGAGTCT ATGCAGTTCA CCAGTAAAAT CCGCCATCAG AGAGGGAATG 2640

GCCTTATTAA TACCAGGGCA AGGTATTAAT TTAAATTGTA ATAATTTAAT TTCAGGATGT 2700

GTGGCTGCAG CCCGATACAG AGTTGCAAGG ACACACTTTT GCCAGAGGGC GTTACTGGAA 2760

AGCTTAACGT TTGATTCTGT ATACATAATA AATCACCTTA CAGTTACAAC AGGTCAAAAA 2820

CCGCTGTAGC CAGAGTTACG CTGGCCTGAT GCTTTAGTAC CGGGCTTCGT CAGATAATCC 2880

AGACGCTCCA ATAAGCGCTG ATACTGCTCA GGGAAATCAG GATCATGAAT ATCCTGGATG 2940

TCACGTCCAT TAGCAGGGAA ATGAATAACG CAGCCCCCTG GATTAACAAT GCAGAAATCG 3000

TCCTGAGGTA CTGATCAATA CGGAGAGGAC TCTCGCGTGT GGTTTATTGA CACCACAGTG 3060

CAGATTCGGC GAATCCGCGA TCACGGTGCG ATTTCGTTCC ACAGCACACA ATCATGACCC 3120

CGGGTTTTAT TCAGGTAAGC AGGATTGCGG ATATCCGGTG TCGCGCCTTT CTGTCACGAA 3180

CGGGGTAGGT GCGAAACACC GGATAAAATG CAGGCTGGCA ATACCTCTGA ACGCCCTGCG 3240

CAGAGCGGAT ATTTTGGATT AAGTACTCGC ACCTCCGCAG TCCTGAAACA AGTCTGGCTG 3300

GTAGCTGTAA ACAGACTTCG TACATGTTGC TCTGGAATAG ATCCCCGTGC CACAGGCTTC 3360

GCAGAACTTT TTCCCGGGAA AATGCTGCCC GCACATCACA CAATGCCACT CCAGCACGAC 3420

CGGTAATGGC GATAGAAACA TCGCCATATC CTCAATGTAA GGGTGGGACT TTTCCGGATT 3480

CAGCACCACG CAGGCCGCCT TCTGTTGCGC GCTCAGGGCA TGTAAATCGT GCTCAAACCA 3540

CGCCCCCTGA GCATCTGTCT GCAAAATCAA CCGACCACGA CAGGAAAGGC AGAAACAATG 3600

CCTGATATTT CTGCTAAGGC TGAGGCCGCA CTGATAATGT GTTCACCCGG CGTGATCCCC 3660

AGCCCCGTTT TTATACCGTT CATTCAGCCA CTCCCTCCTC ACTGAAGTGC CCTGTATGGC 3720

AGTGAGTGCA GTACCGCTCC CCATAATAAT CGTGGTGACA TTGTCTGCAG TGCCAGCTGG 3780

CTTTACGCAC CACGGGTAAG GCATCCGGTA CGAATTTCTG CAGACGCTTA ATCAGTTGTA 3840

TTTCTCTGCG CTCCGGTCTG ACATAAGGGC ACTGTTGACC GTGCTCCGTC AGCCCGTCGT 3900

CAGTGTGTTC AAACCAGGGA AGTTCAGTGT CGTATTGCGG ATGGTATCTG AGCGCACTGC 3960

CGCAAAGGTG GCAGGTGTAG CGGTCGTAAG GTGCAGTCTG TGCGGTACGG GCAGCGGTCA 4020

GACGTCCGTT GCCATCAAAT GCGAGAAAAG ATTTTGCGTA CATAGTATAT GTTCCTTACC 4080

GCCAGACGAC ACGCAGGCGT CAGCGTCCCT TTACGGGCAG CGTGGGCAGG GTGTGAATGG 4140

CGGTACAGTT AAGGGGGGGG TGGAAAATGG GCGGGCTGTT GTTACAGCAC TGTGGATGTC 4200

ACATCATGGC GTACCAACGT AAAAAATAAT CAGCAGGCCC GGATACATCG TTGTCGCCGG 4260

ACATCAGCCC GTCCTGCTGG TTTTGCCGGG CTCAGCCCCG ACTGCAGCCG AAATTACGCT 4320

CACCAGTGGC GTGAGCTTTG GTATGTTCCT TCGCCAGATA GTCAGCACGT TCCAGCACCT 4380

GCTGAAAGCC AGTGTCATCA CCGCGTTCCA GCCACACCGC CGGCGTGTCA GGAAAATGCG 4440

CCAACGTGGC ATAAGGCCCG GCATCCACCC CCAGGGCACT GCACCAGGCN TGWTTAATCA 4500

TCCCGGCCAG TGACCCCGGA TCGCGGTAAT CGCCGGCACG ACACCAGGTA TCCCGGTTGA 4560

CCAGCAGCAG GAGGTGATAG TGTTTTTTGC CCCTGAGTAC CCCGAACTCC CGGGCCCAGG 4620

CGTAATGCAG GGTGGTGGGA TGCACGCGTT TACCTTCACG NCGTTACGCT TCTGGTAAGC 4680

GTCGATTCGG GCTTTCAGGG CATTGATGAA GCGGGATATC ACAGCCGCGT CCGTAGCTGC 4740

CGGTACATCC GGGAGACGCA GATCAACCCG AAGTGCCGTC AGGCGGGGAT GAACATTCAG 4800

TGCGTGCCGC ACCGTCTCAC GAATACGTTG CTGCCAGAAG GGGTTGTATT TGTAGGTCAT 4860

GGTTAAATCT CCGTATGGTT CATACGGAAT AGCCACGTCG TAAAAAATGC GCAGAGCCCC 4920

TGACGTGGCC ACCGACAGAA CACGGCCTCA GGCGCGTTGT GATAACCCAG CTATCGTTTC 4980

CGGACTGACG GTTGAATTTC CTGCGTTGTT TTCTTAATGT AAAAAACCTG CTACGGGTAA 5040

GGCTGTGAGG AGGAAGTGAT GGTGATACGC AAAAAGAAGT GCAGGGACTG CGGAGAAGCG 5100

ACAGAGCATA ACACGGTATG TTGCCCACAC TGCGGTTCTG TCGATCCCTT CGGCTATTAC 5160

CGCAATACAG ACAGAATATT CACCCTCCTG ATGGTCCTGC TGGTTGTGGT TCTGCTGATG 5220

ACGGCTGCGG TCAGCGTGTA TGTGCTGTGG TAGTCGGAGG GGCAGGGAGC AGACGATGAC 5280

GTAAAATATC TCCGGTGCTC AGATATCACG GCCGGTCAGA CCGCAAACCA ACGGTTAATC 5340

GTAACCGGAT CAGGCAAATG TGTGATTAGC CCCCTGGCGC TCATACCCGC ACCGCAGACC 5400

ACCTTAAGTA CTTCCCGCCC GACACCATTC CCTGCTCCCG GATAATTTGT TGTCGCTATA 5460

CCGCTTAACA TCACCGATAC CACACCGGCG CAGATAGCAC CGGATTCATT GTAGAGATGA 5520

CTTAAGGTTC AGGTAACATA TTTCCAGACA GAAGCGGGAA CACGATCGTA AAGTTTGTTC 5580

ATGGTCAGTT CTGCCAGCCG GTGATCAACC GCAGAGTTGA AATTTTCCAG CTCCGCCGGG 5640

GTGAGTTTAT ACCGTGCGTG GGAAATCACT TTTTCCAGTG TCTCCCGGGA TGAACAACGA 5700

CGGAACTGAT ACAGCCAGTC TTCTTTGGTT TTTACTTCCA TTCGTCTCTC GTTACTTTAT 5760

GCTGCGGTTA ACAGGATGCC GTCAGTATAC CGCATGCAGA CACTCTCCCG CTCCCCCGCT 5820

TGCTGCGATA CAACTTAACG TTTCAGGAAT CCAGTCATCG CACCGGGAAA GGCTTTCTGG 5880

TGACAGGAAA CGTCAGGAAC AGGAGTTTCT CAGACTCCCA CTCATCGGAT CAGGCTCAGA 5940

CAGGATTATT AATACGCTCA GTTCATGTGT CATATACAGG GCATCGGGGA TGAATATATG 6000

GGTATAACTC AGAGCCTGTA CTACAGCTTT CACTGCTGAC TGATTTTACG TATCAGCGTT 6060

CATGTATCTG CACTCTGATA TAGAATACTT CTACCGGAGC TACTCTTACG TTAGCTCACT 6120

CTCACATCAG GCAACATCAC TTATTCAGCT CACTTACCTC TTACCACTCA CTACTTCTTT 6180

3NSDOCID <WO_ 9822575A3 IA>

ATATTTATAA TATCAATCAG ACAGCCTTAT CCCCCCGGTA ATATCTGTTG CCTTCCCGCC 6240

AGCCACAGGC TTATTCACCA CAACCACCTC CGATAACAAC TCTGCAATTA TCAGAACGCC 6300

TGCTTCTCTC CCTGTCCTCA CGAAAACTAT CCCCTCTTTA TCGCGCGTGC GTGCGGAAGC 6360

ATCTTTTCGC AACAACCACC CGGGATTCCG CTACGGCTCT GCCATCGCAA TCCCCCCGTT 6420

TATCTCCGGA CAGCCACATT CCCGATTATT TTTTACGTTT CTCCCCGGTT GTTATGCCGG 6480

TGAAGGTGGT GCGTCGTTTT CATCACCACA CCGGTTGCGA TTAACAACAT CCGGAGGAAC 6540

ATTCTCATGA CCACACCCTT TTCACTGATG GATGACCAGA TGGTCGACAT GGCGTTTATC 6600

ACTCAACTGA CCGGCCTGAG CGATAAGTGG TTTTACAAAC TCATCCAGGA CGGAGCCTTT 6660

CCGGCCCCCA TCAAACTGGG CCGCAGCTCC CGCTGGCTGA AAAGTGAAGT GGAAGCCTGG 6720

CTGCAGGCGC GTATTACACA GTCCCGTCCG TAATTTCTGC CCCTTATCCG TTCACCCGCA 6780

GCAGACGCCT CCCCGGCCTG CCGTTGACAT TCTGCTGCCT GTTTTATCCC CGTGAGGAAT 6840

ATGAAAATGA AACAACAGTA CCAGACCCGC TACGAATGGC TCCACGAAAG CTACCAGAAA 6900

TGGCTGACCG GCTTCAMCCG GCACGCCGTA TCCTGGGGCG TGTGTCATCC GAATATCTAC 6960

TATTTCCATA ATCTGACGCC CGGGTGGGTG TCATTCAACG GCGAACAGTC GGAGATTGCC 7020

ATTGTTCCCG GCAGTCTGCA CCGGCTGATT TATGGTCATG ACAAACGGGC CATGCCGCCC 7080

CTGGATGATG ATCTGGTGGT GAATTTATGC ACCAGTGAGA ATCTGCTGGT TCATCATCCG 7140

ATGCTGGAAG GCATTCTGCT GTCTGAGTGC ACGCGCCTGC ATAAAAAATC ACTGGCGAAC 7200

AAACTGATCA GTATATTCCG TCAGTTTGAC GGCACGGAGC TGCGTCTCAA ACTGGTCTGG 7260

CTTTGCTGGT TTGATTTAAT GACCGGAAAC TGCCTTGACG ACTGGACGGA GAACCTGNAA 7320

CGGAAATCAG AAAAAGAGCT GGAGAAATGG ATCATTGAGC GCCAGAACCG GAACGCACCG 7380

CTGACGAATC TGATGGATCA GTACGTGCTC CTGGCATTCC GCACAACGGT TGACGATAGC 7440

CGCAACTGAT GTCTGCATGC TGCCSGCTGA AGCCATATTC ACGGGGCAGG GACGCCCCTG 7500

CTTCCGCAAC AATCCGGGGT AATGGCGACG TACGCCTGCA GAGTGTGTTC ATCGTTGTCA 7560

CAGCCGGACA AGGTGAATAC CGTTGATGAT GCGGGGATGA ACCTGCTGGT CCACCGCGCT 7620

GTCACTCAGA CGCGTCAGCG TGTATGGACG CCCCGATCGA ATGGTTCTTC CGCCAGAGTG 7680

CACAGAAATG AGGCACGGAA CGTTACCTGA AGGGTGACCG GCACGGACTG CAACTTGTTG 7740

CCATTGATGG CGCACAAGTC ACATACAGCA GAATGTCGTG ACCGCACCTT ACCGGTGAAG 7800

CGAAACGGTG CTGCCCCACT CCACCACCAT CCCGGATAAC GCCATTACGC TGTCTGATAA 7860

GCGCTTTTAC AGCGCAAATC TGGTGCAGAA AAGCGTAAAG CTGACCTGCC GGAGCAGGAT 7920

GTGGGCATGT TGCGGGCTTA CAACCTGATA CGGCATGAGG CACTAAAAGC AGCATCAGAA 7980

ATCAGCCTGA GTTCGCGTTC CGGTTTATCC CGACAGAGAG GACAGTGCCG GGCAACACGG 8040

TGTCACCGGG GAGCATCCCG AAACGACCGG AGCATCTGCG GGATGCTCTG TAAGTGGTGT 8100

TAAGGTGGGC GGTTAAGGTA TCAAAAAAAT CGTTATCCTG TGAAAGACAG TGCGCTCTGC 8160

TGAAGTGAAC GTCACTGCCG GGAAGCATCG GGTTTCGCTA CCGGACAGTC GCGGTAACGC 8220

GTTTACCGGC ATCTGTCTGT GTGGCAGGGA TGGCTGATAT TGTCGGTTAT ACCAGCGGCA 8280

GGTGCGTCCT GTTATCTGTA AAATCAGGGC GTGCCGGTAC ACAACGCCTC GTTGATGCCG 8340

GTCACTGAAC GAATCATCCT CTGACGAAAA CAACCGTCGA TACAACGCCG GCGTAAAAAG 8400

AAAACCGGAA ACCATCTTGT GCACGACAGG TACTCAGGGG GGTATAACGC CTGCGCACCA 8460

TCACATCCGG GAACAGGGCT GCTCCTCAGT GTCTTCGTGT GGCGAAGCAT CTGCAACCGG 8520

ACGGTACTGC CCTCAGAGCA ATCTCCCTGC TGCAGTGCAC AGAGTAAGCC GGAAAGCTGG 8580

TGAATGCCGC CATGACACAC TGCGACGTGG AGAAACAAAC GACACACTCC GTCCGCAGTA 8640

ACACTGAAGG TAGTCCCGCA AACCTCAGAC TTCTTCCTGC ACGTTATCAG CGGACTGAAC 8700

CCCGGTCAGC CACTTAAACC TGCTAATCGT GTTGCTGCAT ACCCGCCCGG CCGGAAGGTG 8760

TTATGAAGCC CGCCACCGGA GCGCTTCTGC AAATATCCGG GGAGATAAAA TTTTCGTGAC 8820

AGGATGACGG TCGTGCTGCA GACGTAAAGC CGCAGGAGCG GACACGACAG ACAGTGTTCA 8880

CTGTGGCGTC CTTTGCCGTC GGTATCGTGC TCACGCTGAG GTCCCGGGGG TACACCTGAC 8940

GACAAATACC TGCGATTCCC GGGACGGTCT GTTCTCCGTA AAATAAAGAA AATGCGGGAT 9000

GCCTCCCGGA CTGCAGAGAA GAGGGATTGA CAGACAGTGT ATATTGCGTA CGATTACAGG 9060

GGAAAAACAC AGTAAATATG GAGGTCAGGT CCGAAAACAA CCTACGAAAT TTCTATGAAA 9120

AACGATTGAA AAAATCATCA AATTCAGTTC GTTTTTCTAT GGTAATTTTT AAACACTCCC 9180

GATGATAACC TGTTGTATGT GCATGTGGGG AACGCACCGA AAACATCAGA ATCATCTGAA 9240

AAAAACAACG AACACACCAG AAAAACAGGA GCAACCATAA CGAAGCAACA TATTGATTTT 9300

AAACAGAATT TAAGGTTAAC AGACAAAAAA CACTTTCAAC TGAAGGAGAA ATATACACTG 9360

GCGACAGTGC AGGGTTTTTC ATGCAAAAAA AATGAGCTTT TATCTCCGGC GCATACTGAC 9420

CGGGATGCAG CCATGACAGA GCAAAAACCA TTAAATATCA GGAGGTTAAA CACACAAAAA 9480

GCTGACATGC ATCAGGGAGC AATCCCTCAC AACAGAGGCT GAGCGGCAAC GCTTCCTCAC 9540

AGGACGGCAT TCCTGAAAGG ACAGGCAGCC ACGGCTTTTT ACTGCCCGTA TCCGGTATAT 9600

TTATCTGCCG TGACGTGCAG AGGATTTTGT GTTTCCGGAA ATCAGGAAAA CAGGAGAACC 9660

GCGGGAGATA TGATGGAAAA AGAACCGGAT GATATCTGCG CAGACTGTCC GAATATTGAT 9720

GCAATAAAAC GGCACAAACA ACAGGCCGGA GCCATCAGGG AATACACTGA GTGGTTAAAA 9780

AAACAACCGC GTGCTTCTTA CTTTTTTCTC TTCCGGTTGT ACGCATACCT TCAGAATGAA 9840

GTGATATCCC GAAAACAAAA ACATTCGCTC ACCAGCGATA ACAGCCATCC CCCGGAATCT 9900

GATGTCACCC CTCCGGATTT AACCCTTCCC CGTCGCTACT ACTGTGATTA CGGTTACACG 9960

CCCTACCCCA TGATGGGCGG ACAGATGTCT GTTTTTGCCA CAACGTCAGA AACCACCAGT 10020

3NSDOCID <WO 9822575A3 IA>

TCGACGAATG CAGTCCCCGG AAACGCAGTT ACCGGGAATG AGACTGAAAA GCATGAAAAC 10080

GCGGTACCGG CGACATTCCC CGTCAGCCGT TCTGCAATGC CCCCGGAACC TCTGCGGTTT 10140

GCCACGGGTT TTCCATCGCA ACCACTGCTT GCCGGTCCCC GGGAAAAGCC GATGCGCACC 10200

GTGCATCCTG ACATCCACAG CGAAATTATA TGGTTCTGCT CCACTTACCT GCTGAAATCC 10260

GGACCACAGA TTACGAAGAC GATTATCAAC TCAGTATTCT CTGAATGGGC CCGCATCAGC 10320

AATGATTACC CCTCCCCCTT TTCGTGGGTG GACAGCAGGG ACAGTGAACA GTGTGACTGG 10380

TTATGGAACG CCATGCAGCT CCGGTGTGTG GGAACCCCGC TGAATCCCCT TACCCCGGAG 10440

CAGAAATACT GGTTTGCCTG CGCCACGTTT GATAACTGGG AGGGCTGGAA TGAGCAACAG 10500

ATACAGTTTT TACTGAAAAG TAATCCCAGA CGAAACAGAG CGAAGTTTAC GGTCACCTTC 10560

GGCCCTCCCT GGATTCAGCA TAAAGCCATT CTTCTTGATG AGCTGAAGAG TGCCCGGGAG 10620

CAACAAAAAA GGCGCGATGA ACGCGCTGAT GGTTCCGTCC CGCTGAAACT GTCCGGAAAA 10680

ATCCACAAAC ACCTTGAAAG TATTGCCCGG AGTCGTGGTA TCCCCCCAAA AAAACTGCTG 10740

AATGAAATGA TTGAGCAGGC GTACCAGGAC TCAGTGGTGA ACAGCCGGAA TAAACCACTG 10800

ATTTAAAATA ATTTCAGACA GATATTATCT CCGTGAATCC CCCGCCACCT TTCCGGTGCG 10860

CGGGGTTTTG TCTTTTTTCA CCGGGAATAC ATGTATGAAT CCGTCTGATG CCATTGAGGC 10920

AATTGAAAAA CCGCTCTCCT CCCTGCCTTA CTCGCTTTCC CGTCACATCC TGGAACATCT 10980

GCGCAAACTC ACCCGTCACG AACCCGTGAT TGGCATTATG GGTAAAAGCG GGGCCGGTAA 11040

ATCCTCACTC TGTAATGCAC TGTTTCAGGG GGAGGTCACC CCGGTCAGTG ATGTTCACGC 11100

CGGCACCCGG GAAGTGCGGC GCTTCCGTCT GAGTGGCCAT GGTCACAACA TGGTTATCAC 11160

TGACCTGCCC GGGGTGGGCG AGAGCNGGGA CAGGGATGCA GAGTATGAAG CCCTGTACCG 11220

TGACATTCTG CCTGAACTGG ACCTGGTACT GTGGCTGATT AAAGCCGATG ACCGTGCCCT 11280

GTCTGTGGAT GAGTATTTCT GGCGACACAT CCTGCAACGC GGACATCAGC AGGTGCTGTT 11340

TGTGGTGACG CAGGCCGACA AAACGGAGCC CTGCCATGAA TGGGATATGG CCGGCATTCA 11400

GCCCTCTCCC GCACAGGCAC AGAACATTCG CGAAAAAACG GAGGCGGTAT TCCGTCTGTT 11460

CCGGCCTGTA CATCCGGTTG TGGCCGTATC GGCCCGCACC GGCTGGGAAC TGGATACGCT 11520

GGTCAGTGCA CTCATGACAG CGCTTCCCGA CCATGCCGCC AGTCCCCTGA TGACCCGACT 11580

GCAGGACGAG CTGCGCACGG AGTCTGTCCG CGCTCAGGCC CGTGAACAGT TTACCGGTGC 11640

GGTGGACCGG ATATTTGACA CAGCGGAGAG CGTCTGTGTT GCCTCTGTTG TCCGTACGGC 11700

CCTGCGCGCT GTTCGTGACA CCGTGGTCTC TGTTGCCCGC GCGGTATGGA ACTGGATCTT 11760

CTTCTGAACC TGTTGTGGAT GATGTCCTCC CTGCCTCTGA GTCTGCTCAC AAAAGCGCTG 11820

TTTTCGTTAC TGTCTCTCTT GTCCGTGCAA TAGCTCAATA ATAGAATAAA GCGATCGATA 11880

ACTATTTCAT CGATCGTTTA TATCGATCGA TATGCTAATA ATAACCTTTA TTACCAACAT 11940

GCGCAGATAC GCACAGACAG ACATTCAGGG GACGACAGAA CAACACTTCA GAAACTCCCG 12000

TCAGCCGGAC CTCCGGCACT GTAACCCTTT ACCTGCCGGT ATCCACATCT GTGGATACCG 12060

GCTTTTTTAT TCACCCTCAC TCTGATTAAG GAAATGCTGA TGAAACGACA TCTGAATACC 12120

TGCTACAGGC TGGTATGGAA TCACATTACG GGCGCTTTCG TGGTTGCCTC CGAACTGGCC 12180

CGCGCACGGG GTAAACGTGG CGGTGTGGCG GTTGCACTGT CTCTTGCCGC GGTCACGTCA 12240

CTCCCGGTGC TGGCTGCTGA CATCGTTGTG CACCCGGGTG AAACAGTGAA TGGCGGAACA 12300

CTGGTAAACC ATGACAACCA GTTTGTATCC GGAACAGCTG ATGGCGTGAC TGTCAGTACC 12360

GGGCTTGAGC TGGGGCCGGA CAGTGACGAA AACACCGGCG GGCAATGGAT AAAAGCGGGT 12420

GGCACAGGCA GAAACACCAC TGTCACCGCA AATGGTCGTC AGATTGTGCA GGCAGGAGGA 12480

ACTGCCAGTG ATACGGTTAT TCGTGATGGC GGAGGGCAGA GCCTTAACGG ACTGGCGGTG 12540

AACACCACGC TGGATAACAG AGGTGAGCAG TGGGTACACG GGGGAGGGAA AGCAGACGGT 12600

ACAATTATTA ACCAGGATGG TTACCAGACC ATAAAACATG GCGGACTGGC AACCGGAACC 12660

ATCGTCAACA CCGGTGCAGA AGGTGGTCCG GAGTCTGAAA ATGTGTCCAG CGGTCAGATG 12720

GTCGGAGGGA CGGCTGAATC CACCACCATC AACAAAAATG GCCGGCAGGT TATCTGGTCT 12780

TCGGGGATGG CACGGGACAC CCTCATTTGC GCTGGTGGTG ACCAGACGGT ACACGGAGAG 12840

GCACATAACA CCCGACTGGA GGGAGGTAAC CAGTATGTAC ACAACGGTGG CACGGCAACA 12900

GAGACGCTGA TAAACCGTGA TGGCTGGCAG GTGATTAAGG AAGGAGGAAC TGCCGCGCAT 12960

ACCACCATCA ACCAGAAAGG AAAGCTGCAG GTGAATGCCG GCGGTAAAGC GTCTGATGTC 13020

ACCCAGAACA CGGGCGGAGC ACTGGTTACC AGCACTGCTG CAACCGTCAC CGGCACAAAC 13080

CGCCTGGGAG CATTCTCTGT TGTGGAGGGT AAAGCTGATA ATGTCGTACT GGAAAATGGC 13140

GGCCGTCTGG ATGTGCTGAC CGGACACACA GCCACCAGAA CCCGTGTGGA TGATGGCGGA 13200

ACGCTGGATG TCCGCAACGG TGGCACCGCC ACCACCGTAT CCATGGGGGA TGGCGGTATA 13260

CTGCTGGCCG ATTCCGGTGC CGCTGTCAGT GGTACCCGGA GCGACGGAAC GGCATTCCGT 13320

ATCGGGGGCG GTCAGGCGGA TGCCCTGATG CTGGGAAAAG GCAGTTCATT CACGCTGAAC 13380

GCCGGTGATA CGGCCACGGA TACCACGGTA AATGGCGGAC TGTTCACCGC CAGAGGGGGC 13440

ACGCTGGCGG GCACCACCAC ACTGAATAAC GGTGCCACGC TTACCCTTTC CGGGAAAACG 13500

GTGAATAACG ATACCCTGAC CATCCGTGAA GGTGATGCAC TCCTGCAGGG AGGCGCTCTT 13560

ACCGGTAACG GCAGGGTGGA AAAATCAGGA AGTGGCACAC TCACTGTCAG CAACACCACA 13620

CTCACCCAGA AAACCGTCAA CCTGAATGAA GGCACGCTGA CGCTGAACGA CAGTACCGTC 13680

ACCACGGATA TCATCGCTCA TCGCGGCACG GCCCTGAAGC TGACCGGCAG CACCGTGCTG 13740

AACGGTGCCA TTGACCCCAC GAATGTCACC CTCGCCTCCG GTGCCATCTG GAATATCCCC 13800

GATAACGCCC CGGTTCAGTC AGTAGTGGAT GACCTCAGCC ATGCCGGACA GATTCATTTC 13860

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

ACCTCCGCCC GCACAGGGAA GTTCGTACCG GCAACTCTGC AGGTGAAAAA CCTGAACGGA 13920

CAGAATGGCA CCATCAGCCT GCGTGTACGC CCGGATATGG CGCAGAACAA TGCTGACAGA 13980

CTGGTCATTG ACGGTGGCAG GGCAACCGGA AAAACCATCC TGAATCTGGT GAACGCCGGC 14040

AACAGTGCGT CGGGGCTGGC GACCACCGGT AAGGGGATTC AGGTGGTTGA AGCCATTAAC 14100

GGTGCCACCA CGGAGGAAGG GGCCTTTGTC CAGGGGAATA TGCTGCAGGC CGGGGCCTTT 14160

AACTACACCC TCAACCGGGA CAGTGATGAG AGCTGGTATC TGCGCAGTGA AGAACGTTAT 14220

CGTGCTGAAG TCCCCCTGTA TGCCTCCATG CTGACACAGG CAATGGACTA TGACCGGATT 14280

CTGGCAGGCT CCCGCAGCCA TCAGACCGGT GTAAGCGGTG AAAATAACAG CGTCCGTCTC 14340

AGCATTCAGG GCGGTCATCT CGGGCACGAT AACAACGGTG GTATTGCCCG TGGGGCCACG 14400

CCGGAAAGCA GCGGCAGCTA TGGCTTCGTC CGTCTGGAGG GTGACCTGCT CAGAACAGAG 14460

GTTGCCGGTA TGTCTGTGAC CGCGGGGGTA TATGGTGCTG CTGGCCATTC TTCCGTTGAT 14520

GTTAAGGATT ATGACGGTTC CCGCGCCGGC ACGGTCCGGG ATGATGCCGG CAGCCTGGGC 14580

GGATACCTGA ATCTGGTACA CACCTCCTCC GGCCTGTGGG CTGACATTGT GGCACAGGGA 14640

ACCCGCCACA GTATGAAAGC GTCATCGGAC AATAACGACT TCCGCGCACG GGGCCGGGGC 14700

TGGCTGGGCT CACTGGAAAC CGGTCTGCCC TTCAGTATCA CTGACAATCT GATGCTGGAG 14760

CCACGACTGC AGTACACCTG GCAGGGGCTC TCCCTGGATG ACGGTAAGGA CAACGCCGGT 14820

TATGTGAAGT TCGGGCATGG CAGTGCACAA CATGTGCGTG CCGGTTTCCG TCTGGGCAGC 14880

CACAACGATA TGACCTTTGG TGAAGGCACC TCATCCCGTG ACACCCTGCG TGACAGTGCA 14940

AAACACAGTG TGCGTGAACT GCCGGTGAAC GGGTGGGTAC AGCCTTCTGT TATCCGCACC 15000

TTCAGCTCCC GGGGAGACAT GAGCATGGGT ACAGCCGCAG CCGGCAGTAA CATGACGTTC 15060

TCACCGTCCC GGAATGGCAC GTCACTGGAG CTGCAGGCCG GACTGGAAGC CCGTGTCCGG 15120

GAAAATATCA CCCTGGGCGT TCAGGCCGGT TATGCCCACA GCGTCAGCGG CAGCAGCGCT 15180

GAAGGTTATA ACGGCCAAGC CACACTGAAT GTGACCTTCT GATAATTCGG CATTGTCTCT 15240

CTGTGGTCCC GGTCATCATG ACCGGGACCC GGACAGGTGC AAACGCTTCA GTGCCACATT 15300

CACTGGCATT CACAATAACA TGATATTCAT CACGGAGTGA CTATGTTACA GATAGTCGGT 15360

GCGCTGATTC TGCTGATCGC AGGATTTGCC ATTCTTCGCC TTTTGTTCAG AGCATTAACC 15420

AGCACAGCGT CTGCGCTGGC AGGGTTCATA TTGCTGTGTC TGTTCGGCCC GGCTTTACTG 15480

GCTGGCTATA TCACTGAACG CATAACCCGG TTATTCCATA TTCGCTGGCT GGCAGGCGTA 15540

TTTCTGACGA TTGCCGGAAT GGTCATCAGC TTCATGTGGG GACTTGATGG TAAACATATC 15600

GCACTGGAGG CTCATACCTT TGACTCTGTA AAATTTATTC TGACCACCGC TCTCGCCGCT 15660

GGTCTGCTGG CTCTTCCCGT GCAGATAAGA ACCATTCAGC AGAACGGGCT CACACCAGAA 15720

GATATCAGCA AGGAAATTAA CGGGTATTAC TGCTGTTTTT ATACTGCTTT TTTCCTTATG 15780

WSDOCID <WO__9822575A3_IA>

GCGTGTTCTG CATACGCACC ATTGATCGCA TTGCAGTTCG ATATTTCACC CTCACTGATG 15840

TGGTGGGGCG GGTTGTTGTA CTGGCTGGCT GCATTAGTGA CGCTGCTATG GGCGGCCAGC 15900

CAGATCCAGG CGCTGAAAAA ACTGACCAGT GCCATCAGCC AGACACTGGA AGAACAACCG 15960

GTGCTCAACA GTAAATCGTG GCTGACCAGT TTGCAAAACG ATTACAGCCT TCCTGACTCA 16020

CTGACGGAGC GCATCTGGCT CACGGTCATT TCACAACGGA TTTCCCGGGG AGAACTGAGG 16080

GAATTTGAAC TGGCAGACGG AAACTGGCTA CTGGACAATG CCTGGTATGA AAGAAACATG 16140

GCGGGTTTCA ACGAAAAGCT GAGAGAGAGC CTGTCATTTA CCCCTGATGA ACTGAAAACC 16200

CTCTTCCGGA ACCGCCTGAA TTTATCACCG GAAGCGAATG ACGATTTTCT CGATCGTTGC 16260

CTGGACGGCG GTGACTGGTA CCCCTTTTCA GAAGGCCGCC GTTTTGTATC ATTCCACCAC 16320

GTGGATGAGC TTCGTATCTG TGCCTCCTGC GGGCTGACAG AAGTACATCA TGCCCCGGAA 16380

AATCATAAGC CGGATCCGGA ATGGTACTGC TCCTCTCTTT GTCGCGAAAC AGAAACACTG 16440

TGTCAGGACA TTTATGAACG TTCTTACACC GGTTTTATTT CCGATGCAAC GGCGAATGGT 16500

CTGATTCTCA TGAAACTGCC GGAAACCTGG AGTACAAATG AGAAAATGTT TGCTTCCGGA 16560

GGGCAGGGAC ATGGGTTTGC CGCTGAACGG GGAAACCATA TTGTCGACAG AGTCCGTCTG 16620

AAAAACGCAC GGATCCTCGG TGATAATAAT GCCAAAAATG GAGCAGACAG ACTGGTCAGC 16680

GGAACAGAAA TCCAGACGAA ATATTGTTCA ACTGCAGCCC GTAGCGTCGG TGCGGCATTC 16740

GACGGACAGA ACGGACAGTA TCGTTACATG GGAAATCATG GTCCCATGCA ACTGGAAGTC 16800

CCCGTGATCA GTATGCCGGC GCTGTGGAAA CCATGAAGAA TAAGATCCGC GAAGGTAAAG 16860

TACCCGGTGT AACCGATCCC GAAGAAGCGT CCCGGCTGAT TCGTCGGGGA CATCTGACTT 16920

ATACCCAGGC CCGTAATATC ACCCGGTTCG GGACCATCGA ATCGGTCACT TATGATATTG 16980

CCGAGGGGTC GGTTGTCAGT CTGGCGGCCG GAGGGATCAG TTTTGCCCTG ACGGCATCGG 17040

TCTTCTGGCT CAGCACCGGC GATCGCGATG CTGCCCTGCA GACAGCTGCT GTCCAGGCAG 17100

GAAAAACCTT CACCCGCACA CTGGCTGTCT ACGTCACAAC CCAGCAACTT CACCGGCTCA 17160

GTGTTGTTCA GGGTATGCTG AAGCATATTG ATTTTTCGAC GGCCAGCCCG ACTGTCCGGC 17220

AGGCGCTTCA GAAGGGGACC GGTGCAGGAA ATATCAGTGC CCTGAACAAA GTGATGAAGG 17280

GGTCGCTGGT GACATCTCTG GCACTGGTAG CTGTCACAAC CGGCCCTGAC ATGATCAAAA 17340

TGTTGCGGGG ACGGATCTCC GGTGCGCAGT TCATCAGGAA TCTTGCCGTG GCATCTTCCT 17400

GTGTGGCAGG TGGTGCTGTC GGGTCAGTGG CGGGCGGGAT ATTGTTCAGT CCACTGGGAC 17460

CATTTGGTGC ACTGACAGGG CGTGTGGTTG GCGGTGTTCT GGGGGGAATG ATTGCCTCCG 17520

CTGTATCAGG AAAAATTGCC GGAGCGCTGG TTGAAGAAGA TCGCGTCAAA ATTCTGGCAA 17580

TGATTCAGGA GCAGGTGACA TGGCTTGCCG GCAGTTTCCT GCTGACCGGA CATGAGATTG 17640

AAAATCTGAA CGCGAATCTG GCCCGTGTTA TCGATCAGAA TGCTNCTGGA GATCATTTTC 17700

GCCGCCGGTA 17710

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

AATAACCAAT AGATGCTTAA GTTTACGATA TGCCTCAACC CGCGTCTGCT CTAAGCTGAT 60

AAGGCCAGTT TTGTAGAGAT CCGCTGCCAA GGTTGCCTGC GTTTGCACAT CCATGTAACC 120

GGCGGTGATT TCATTCATGG CATCGTTATC TTGACCAGTC AGCTTAGCAC GCTCCTGTTC 180

AAGCTGCTTG GTTAGGGCGT CAACTCGGCT CTGTAATGAG ACTACGGCCG GTGCGGTTTC 240

CTTCATATAG CTGCGCAGTT GTTTTAGCTC CGCCTGTTGA CGCACCAGCT CTCCTTCAAT 300

CTGGCTGACC ACTCCCAAGC GTGCGCTGCT GGTAGATTCA GGGCTGAGAA GTTGGTGGCT 360

ATTCTGAAAT GCTAATACTT TAGCTTTTTC ATCCTGTAAG CGTTGATATG CTCTATTTAC 420

TTCTTTTTCA ACAAAGGCCA ATTGTTCGAG CGCAACCTGA TGACCTAATT TGTTAATAAA 480

ACGCTCCGAT TCTTTGAGCA TTAACTCAAC AACTCGCTGA CCGTATTGGG GATCAAATGT 540

CTGCAACTCA ACGGTAAGTA CTCCTGATAA TTCATCAAGG TGTAACGTCA AATGTTTGCG 600

GTAATAATCA AGAAAATCTT CCCTACTGAC TCCCTTATGC AACCGCGAGA AATAATCTGC 660

ACTATCACTC TGGAAATGTG CTTTAAGTGC AAGTTCTTTG TCCAACTTGG CCAGCATATC 720

CCATGACTTC ATATAATCCT GAACGAGTAA TATATCCTGA TGATTACTAC CACCTATCCC 780

TAACATTGAT AACGCATCAG GCAACATTTT AACTTGATCG GCTTGTTTAA TCATTAATTC 840

AGCCCGGSTC ACATAACGAT CGGAAGCAAT GAAGCCAAAA TAGAGCACTG CGATAGAAAA 900

GCAGATAACT ACCCAAAGAA AACTGCCTAG CTGTAAACTT TTCTTCCACG AGCGGTGTAC 960

AATTTGATAT CCTCTCGAAT CAATCAAAAA TAGTTTTGGA TTATTGCTCA GTTTTCTTAA 1020

CTTTCGCGTA AGGCGAGATA TTGAGGATGA AGAATTCGGA GATGTCATAA TCAGTTGCTG 1080

CTCAAAGTGA CTGGTAAATT TTGATGGCAT CATCAATATT ATCAAAAACT TCTAATTTAC 1140

CATCACGTAA CAAGATGCCC ATATCGCATT GTTGTCGTAG ATTTTTCATA TCATGCGAAA 1200

CCATAATCAA ACTAGCTGTT TCTCGCTTTT TGTTAAATAC ATCAATACAT TTTTGTTTAA 1260

AACGTGCATC ACCTACTGAG GTAATTTCAT CGGTAAGATA TATATCAAAA TCAAAAGCCA 1320

TACTAACAGC AAAAGAAAAT TTTGATTTCA TGCCGCTAGA GTATGTTTTA ATAGGCAGCT 1380

CATAATGTTG TCCAATTTCA GAAAACTCTT TAACCCACTC TTCTACGGGG CTTGTATCGC 1440

GTACACCATG AATGCGGCAA ACAAATCGCG TGTTTTCACG ACCAGTCATA CTACCTTGAA 1500

ATCCCCCAGC TAGTGCTAGA GGCCAAGATA CTCGGCAGAG ACGAGTTACT TTCCCCCTGT 1560

TAGGCGTATC CATCCCTCCT AACAAACGTA ACAAAGTAGA TTTYCCKGCT CCATKGATAC 1620

CTAGAATACC TATATTACGG TCCCTTGGTA GCTCAATATT TACATTCCTC AGGACATAAT 1680

TTCGTCCAAA TTTAGTTGGA TAATATTTTG ATACATTATC AAGAATAATC ATTTTTCTTA 1740

ACGCTAACTA GCAATCAATT GGCGATGCCG TAATCGGTAA CAACTCATAG CAAAAGTGAG 1800

CAA 1803

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGGACCCAAG GTAAAAACNG GTAAAAAAAA CMATTGACCG ATTAAACTTT ATTTCTCTGC 60

CCGCATTAGT CTGGAGAGAG GATGGATGTC ATTTTAATTT NACTAAAGTC AGTAAAGAAG 120

CAAACAGATA TCTTATTTTT GATCTGGAGC AGCGAAATCC CCGTGTTCTC GAACAGTCTG 180

AGTTTGAGGC GTTATATCAG GGGCATATTA TTCTTATTGC TTCCCGTTCT TCTGTTACCG 240

GGAAACTGGC AAAATTTGAC TTTACCTGGT TTATTCCTGC CATTATAAAA TACAGGAAAA 300

TATTTATTGA AACCCTTGTT GTATCTGTTT TTTTACAATT ATTTGCATTA ATAACCCCCC 360

TTTTTTTTCA GGTGGTTATG GACAAAGTAT TAGTACACAG GGGGTTTTCA ACCCTTAATG 420

TTATTACTGT CGCATTATCT GTTGTGGTGG TGTTTGAGAT TATACTCAGC GGTTTAAGAA 480

CTTACATTTT TGCACATAGT ACAAGTCGGA TTGATGTTGA GTTGGGTGCC AAACTCTTCC 540

GGCATTTACT GGCGCTACCG ATCTCTTATT TTGAGAGTCG TCGTGTTGGT GATACTGTTG 600

CCAGGGTAAG AGAATTAGAC CAGATCCGTA ATTTCCTGAC AGGACAGGCA TTAACATCTG 660

TTCTGGACTT ATTATTTTCA TTCATATTTT TTGCGGTAAT GTGGTATTAC AGCCCAAAGC 720

TTACTCTGGT GATCTTATTT TCGCTGCCCT GTTATGCTGC ATGGTCTGTT TTTATTAGCC 780

CCATTTTGCG ACGTCGCCTT GATGATAAGT TTTCACGGAA TGCGGATAAT CAATCTTTCC 840

TGGTGGAATC AGTCACGGCG ATTAACACTA TAAAAGCTAT GGCAGTCTCA CCTCAGATGA 900

CGAACATATG GGACAAACAA TTGGCAGGAT ATGTTGCTGC AGGCTTTAAA GTGACAGTAT 960

TAGCCACCAT TGGTCAACAA GGAATACAGT TAATACAAAA GACTGTTATG ATCATCAACC 1020

TGTGGGTTGG GGTGCACACC TGGTTATTTC CGGGGATTTA AGTATTGGTC AGTTAATTGC 1080

TTTTAATATG CTTGCAGGTC AGATTGTTGC ACCGGTTATT CGCCTTGCAC AAATCTGGCA 1140

GGATTTCCAG CAGGTTGGTA TATCAGTTAC CCGCCTTGGT GATGTGCTTA ACTCTCCAAC 1200

SNSDOCID: <WO__ 9822575A3 IA>

TGAARTTCAT CATGGGAAAC TGGSATTACC GGRAATTAAW GGTGATATCA CTTTTCGTAA 1260

TATCCGGTTT CGCTATAAGC CTG 1283

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TCAACCTGAC CAACCACTAG AATCAACTCA CGTCCGTCGT TAGGGGGCTC ATATTCTTGT 60

GTACTCCCCA CATTGTATTT ACTGACTCGT GATGATTGTA ATTGCGCTAA TAATGACTCT 120

GCGCGTGCTT CTTCTTTCGC ATCTAAAACG TACGTAGTGA GTAACTGCTC AAGCTTACTC 180

GGACGGCGGC TATCAAAATA GATTCCAACG GGGTCAATCG AGAGTGATGA AGGTCGACAT 240

AAATTAGACC CCAATCCGTT GGAGCGGATA AAACCATCTT CAATCCGGAT CACTGATTGC 300

AGTTCAGGAT AACGGTTTCC CCACACCAAC ACCTGTTCAT CATCTTTTAA CTGTGAGGGC 360

ACAGTACGAA CAAAACAAAG TTCATCTGCC AAATACGCAC AAAATGTGCG TATAAAAGCA 420

CGCTTCCACA GAGAAAAACC AACGAGATAA AGACGACGCC AAGGTTTGGG CTCTACCTGC 480

TGCTGAGCCA AAATCGCTAC AACATCTTCT ACCTCACAAC GTTTTCCCAA TATAGGATCT 540

AAATAACGCG GATAACGGAT CAACGCCGCC GCAACTAAGC GGGGCAATGA AATAGATGAA 600

ACGCCTTCGG CTGACATTGC TTCTTCACGG CGTATACAAC GTTTACTGTC ATGCGTTAAC 660

CCCCACCCAG CATAAAATGG CATACCGAAG CAATATACAG GTTTGCCCAA CAGCAACGCT 720

TCCAAAGCCA ACCTGCGATG AAACTGTGTA CACCGCATCC ACCATACGAA TTATTCTATG 780

CGGATGGCAA GTTCACTCAC CACCTCAACA TCAGCCAGTC GAGGATCACG CCCCACTAAA 840

CGTGCTAACA CGCCGCTTTT TTTGCTAAAG CGTGTATCTG GGTGTGTTCG CAACAATAGA 900

CGCGCATTAG GGTGATTACG GCGAGCCTCG ACCACCATAG AAACAAAATC AGCTTCGCAA 960

GCAAGAGCCC CAGAAATTGA CAAGTCTCCC GCTACTTGAT CCACAAGCAA AATACGCGGT 1020

CTTGGATCAT CCAGTAAACG TGCTAAGTTT GAATGAGCCG TGAGGTGAAT AACTCAGGTT 1080

GTATATGTGT CGGTAAATCT AAAGAAGGCC CGTCAGTAGC ACGGGACAGA GCCATTAAAT 1140

GTATGCTCAG TGCTATTGGG TATAGCAGTT ATACTTGGTG ATTCCTAAAC GCAAAATATC 1200

MGAGATCAGA TGCTCCAGCG CGCGCAAAGT AAAGCCGTAT CCAACAGGTT CCAATAATAA 1260

GCTGTTCTAA TTGACTCGTC TGATGTGCAT CATAATATAT CCCCAGAGGG TCAGCAATAA 1320

GAGAAACCGC CTTTCCTCCT TTTGCTGGGT GCCCGATATA GCCAATAAAA CCATCTTCAA 1380

GTTGCCAATA AGATATTCCT AACTCTTGAG CTTTCTGTTT AATCTGCTTA GTATTAGATT 1440

TTTTTCCCCA GCCAACTAAA ACGTCATTTT TAGAAAAAGC CTCGTCTCCT TTCATATAAA 1500

GCAATGGGTG ACCAAGCATA GGCTCAATAT TATTTTYTCT GGCAAGAATC CCTTTCGATC 1560

CCGTATATAA ATACATGTTG TCTCTGTGAA CTGAAGATTC TCTACAATGG TGTATAAAGT 1620

GTGATTTAGA TGAACAGCTC TGCGCTCTCT AATGACTTTG CAATACTATC TTTTGCTGAA 1680

GTGAGAATGT CCGCCTTTAA CTCGGGCCAC CTAATACCAA TTGTAGGATC ATTCCATGCA 1740

ATGCCTCTAT CACTGGCAGG GGCATAATAA TTAGTTGTTT TATACAAAAA TTCGGCCGAT 1800

TCAGTCAGTG TTACAAAACC ATGGGCAAAT CCTTCCGGAA TCCATAATGT CGTTTGTTTT 1860

CCCCTGAAAG ATGAACGCCA ACCCATTGTC CGRAGCTCGG TGAGCTTTTG CGAATATCTA 1920

CCGCAACATC AAACACTTCA CCGGCTACAC AACGCACTAA CTTGCCCTGG GCATGGGGAG 1980

GTAACTGATA GTGCAAGCCA CGCAGTACCC CTTTAGAAGA TTTTGAGTGA TTATCCTGCA 2040

CAAAGGTAAC TGGATATCCT ACAGCCTCTT CAAACAACTT GTGATTAAAA CTCTCAAAGA 2100

AAAAACCACG CTCATCTCCA AATACTTTTG GCTCAAAAAT AAGCACACCA GGAATTGCTG 2160

TCTTGATTAC ATTCATCTAT ATGCCCACAT TTAATTAAAT ATTTTTAGGG GAAGCATATT 2220

CCCTCCCCCT TCTCAATTAC ATCACGCCTT ATCAATCATT TTTAATAAAT ATTGCCCATA 2280

GGCGTTTTTT GCCAACGGAG CAGCAAGYTC ACGAACCTGG TCGGCACTAA TAAACTTCTG 2340

GCGATAAGCA ATCTCTTCCG GACAAGCCAC TTTCAATCCC TGACGCGTCT CGATGGTCTG 2400

AATAAAGTTA CTCGCTTCAA TTAGGCTTTC GTGGGTACCG GTATCAAGCC AGGCATAACC 2460

ACGCCCCATC ATTGCCACCG ATAGATTGCC TTGCTCCAGG TAAATACGGT TCACATCGGT 2520

GATTTCCAAC TCACCACGCG GCGATGGCTT GAGACCCTTG GCAACGTCCA CAACGCTGTT 2580

GTCGTAGAAA TAGAGGCCGG TGACTGCGTA STACTCTTAG GCTCCAGTGG TTTTTCTTCC 2640

AGTGAAATAG CGGTACCTTG ATTATCAAAT TCGACCACTC CATAACGTTC CGGGTCGTGC 2700

ACATGATAGG CAAATACAGT AGCACCGGTC TCTTTGGCCG CGGCTGCCTC CAACTGTTTC 2760

TGTAGGTCAT GACCGTAGAA GATGTTATCC CCCAGCACCA GTGCACACGG GGCTGAACCA 2820

ATGAATTCTT CACCTAGAAT AAAAGCTTGT GCCAACCCGT CTGGGCTTGG CTGAACCTCA 2880

TATTGTAAAT TCAGTCCCCA GTGGCTGCCA TCACCCAGCA ATCGCTGAAA GGANGGAGTA 2940

TCTTGTGGAG TGCTAATGAT CAAAATATCG CGAATTCCAG CCAGCATCAG GGTGCTCAGC 3000

GGCCGCAGTA CTGGATCATC GGCTTGTCAT AGATGGGCAA CAACTGCTTG CTCACCGCCA 3060

TAGTAACCGG ATAGAGACGT GTACCAGATC CACCGGCCAG AATAATACCT TTACGTTTAG 3120

TCATGATGCT TGTTTCTTAT TTTTAAATTA CATAAGAATA AAGTGGCTTG AGCCGCGCCT 3180

TTCTGTTTTA TCCTCACCTG TGGTTTACTT CCCCATGATC TCAGTCAACA TCCGCTCAAC 3240

ACCGACTGAC CAGTCCGGCA AAACCAGATC AAATGTACGC TGGAATTTTT TAGTATCAAG 3300

TCGGGAATTA TGAGGGCGTT TCGCCGGGGT CGGAAAGGCG CCTGTCGGCA CTGCATTAAG 3360

3NSDOCID <WO_ 9822575A3 IA>

CTGTGTGACT GCCAGTTCAA CTCCTGCGTC TCTGGCTTTG TCAAACACCA ACCGGGCGTA 3420

GTCAAACCAA GTGGTAGTAC CGGAGGCAGC CAAATGGTAC AGCCCGGCAA CGTCGGGTTT 3480

GCTCTGTGCA ACTCGGATTG CATGGGCGGT ACAATCGGCC AGCAACTCAG CTCCAGTTGG 3540

AGCGCCAAAC TGATCATTAA TGACCGATAT CTCGCGACGC TCTTTGCCAA GACGCAGCAT 3600

AGTTTTGGCG AAGTTGGCAC CGCGCGCAGC ATAAACCCAA CTGGTACGAA AGATAAGGTG 3660

ACGTGAGCAG AGTGCCGCAC CGTGTTCCCC TGCCAGCTTG GTTTCGCCAT AGACGTTGAG 3720

CGGGGAAATC ACATCGGTTT CCACCCAAGG ACGTTCACCA CTTCCATCGA AAACATAGTC 3780

GGTGGAATAA TGTACTAGCC ACGCACCTAA TGCTTCAGCT TCTTTGGCAA TAACCGCCAC 3840

ACTAGTTGCA TTGAGTAACT CGGCAAATTC CCGCTCACTC TCCGCTTTGT CGACTGCAGT 3900

ATGGGCCGCT GCGTTAACAA TCACATCCGG CTTGACGAGA CGTACCGTTT CAGCCACCCC 3960

TGCAGAATTG CTAAAATCAC CGCAATAGTC GGTGGAGTCA AAATCAACGG CAGTGATGTG 4020

CCCCAGAGGC GCCAATGCAC GCTGCAGCCC CCATCCACTT TCTGGCCACA CCAGACTCGC 4080

CAGCAAAAAA GTGAGTGCTG TCAATAACTC AACCAGCGGA TAACGCTTGC TGATTTTCGC 4140

CTGACAGTCG CGGCAGCGCC CTTTGAGCAT CAACCATGAG AGCAGCGGAA TATTGTCACG 4200

AACGCGGATG GTCTGCTGGC AATGCGGACA GTGCGAACGC GGTAGCGCAA GGCTTATTTT 4260

TGACTGCGCA CTCGGCATTT CACCATGAAA CTCCGCCATT TGTTGGCGCA GCATGATGGG 4320

GTAACGCCAA ATCACCACAT TCAAAAAACT GCCGATGATC AATCCTCCGA CGGTTGCCAG 4380

TATGGGCATC GCCGCGGGGT ATTGCTGAAA AACATCAAAA AGCATGGTTA AAGGTTATTT 4440

GTTGTAACTT GCCGGATGCG GGCCTGCGGG TGTATGCCAT ACGGCTTTCC TTCAGGCCCG 4500

ATGCGCCTTA TTTCATGCCG GATGCGGCGC GAGCGCCTTA TCCGGCATAC AGGCTTACTC 4560

AGCTGACATC TTATGCTCGG TAACCTGATT AATGGTTTCC GGCCCTTGCT GCGGTTTCGG 4620

CAGATTAAGC GCCGCCAGTG TCTCGTAAGC CGACTGGCTC ACACCGCCCT CGAAGTTCAT 4680

CTCGCTCGCT CCCGGCAACT GGTAAGCATT CGCGCCCGGA TTCCATTTCT TAAAGAACTC 4740

CGAAAGATCC GTCTGGGCGA CCCAGGATGC ACACAGCATC AGCTTGTCGG CAGCGTTACC 4800

GTTGGATTCG GCACAGTAAT TTCTTTCGCC AAACTTGGTT TTGCCAACCT CATCGCCGCG 4860

TGCTTTACGG TGCATCAACT GGAACAGGTT CCAGCCTTTC ATCCCTTCAC GATCGCTGTA 4920

GAACTTAGGC AGGTCACCTT CTGGATACCA CTGTTTGATA TCAAAGTTTT TCTCTGCCCA 4980

CTCTTTCAGC TGTGCGTACA TCAGCAGACG GTCACCCGCA CCGCCGCGCG CCCATGCCTG 5040

ACCGTTGCTC TCCTCCAGAT ATTCCGGCGC GACGGTAATG TCGTCAGCGA CACGGTTCAT 5100

CTTGCCGAGA TAGCGATCCT GCATGTACAG CGCCAGCACG TTGTTCGCTA CTTCAGTTGC 5160

GCCAGGAACA GTCAGCGGCG TTTCGGCGGC GTTGTGACCA ACTTCGTGCC AGATCAGCCA 5220

GTCGTTCAGC GGCGTCGTCG GCAGCGTGGT GCTGTTCGTC GAGAAGCTGC TGTTCATTAC 5280

JSDOCID <WO _ 9822575A3 IA>

CGGATAACCA GAGTGCGCAT CACCGATGGA GATCTGCACA TCGTTGGTGA AACGATGCTT 5340

GTGGCCCGTC AAGTTTTTAT AGGTAAACAT CCGGTGCTTA CCGTCTTCAT CATTACGACC 5400

GTAGAAGTCA TTCATCGAGC TGGCAAAGGT ATCCAGATCT TTAGCGAATT CTGCTACGCC 5460

ACCAGTGAAA TTGCTGGCCT CAAGGTTCTT CTTCGGCGTG GTGTAGACGA AAGCGTCTGA 5520

CTCCAGCTCG CCCAACGGCG CAGGGGAGTT CAGAGCGTTT TTCCATGCGC CATCTTTATA 5580

GAACGGCGCT TTCACCACAC CAGTAAAGGT GAATTCGGCT GACTCATTCT GTGGGCTGTT 5640

GCCCTTGATA TAAATCAGAC CACCGTAAGG AACCGTAAAC TTCACCTCAC CATTGGCTTT 5700

CAGCTCATAG GTTTTCGTCA CTTTTGGCGG ACGGTTCAGA GCGACTTCAT GCTTCTCACG 5760

TCCGGTAAGG TCGTCGGCCA GCGCCACGGT GACAGTCACA GGAACTGATG CAGAAGACTC 5820

AATGGTGACC TCTTTCTGAG CCGGAGCCCA CAGGCCAGTA GACTGCATGT TACCCGCAAA 5880

CCATTTGGTC GGATTCGAGT ACAGGCTGAT GGTTTCAGTA ACCTTCTCAC CTTCTGCCGA 5940

TACCGCTCCC GGATACTTCT CGACATCAAC TTTGATGTTC AGATCCCACC AGGAACGACC 6000

CAGCATCAGG CGCGTCAGCG GTTTTTCCAT ATAGTTGAGC GGATAGCTCG GGTTCATCAT 6060

GCCCGCTTTA TTAACGCTCT TCTCGCCGTA GATCATGTTG TTATCGACCA GCGATTTTTT 6120

CAGCTCATCA GAAACACTGC GTGCCGCCAG TATAGGCATC GTTGGCGTAG CAGTTCAGGA 6180

ACTCGGTGAA CGTTTTAAAG CCCAGCTCGT CATCCTTGTC GTTTTCATAG CGATATTCAA 6240

TTTTATTCCA CAGCCAGACC GACATGTTCT GGTACAGACG TTCCAGATCG ACGCTGCTCA 6300

GACGCTCACC TTTGCGACCA TTGGTCCGGA AGTAGAGCTC ATGCTGATAC AGACGCTGAA 6360

TGTTGGTGCC TAAATCCGCA GCCTGCACCA TCGCTTTTGC CGTGTCGGCG TTAAGGCTTA 6420

GTTGCGTATA CTGTGGAACA TACATGCCAC CAGTAACCGG AACCCCCGTG CCAGGACGAT 6480

ATTCCAGACA GTTGACCTCG TAGTGGTAAG TTGGGTCCTT ACACTCCTTT AATCCAGGAA 6540

ACTTCTCAAA GATTTTTGCC TTCGCAGCCT TCAGAGAATC CTCTGTTTTA TGATCGGCCT 6600

CATCAATAAA GGCATAACGC GTTTCCTGTT TGCCATCTAC ATCTTCCAGC CAGCTGGCAA 6660

CTTCCAGCTT CGGTTTGTCA TCAGGTTTGT TTTCTACCTG ATATTTCCAC TTAACTTCCC 6720

CTGTCTTACT ATCGATGGTG TACGGCAGCG CACCATCTAC GGCAGGATAA CGTTCATAGA 6780

CCCAAATGCC CGTTGCGCGC TGCTGACGAA CGCGGTTCGG ATACCCTTGC GGATCC 6836

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

3NSDOCID <WO 9822575A3_IA>

GGAAAAACNC GCCGTATATT AGCCCGCGCG GAAAAAGCCC CGTNACGGGC AAACGCAGCA 60

AGGTTTTATC CCAGCGCAGG CGCATGGCAG GATTTTTGAG TAGCCGTTGC CCCAGCACCA 120

GAAGCCCCAG CAATCCCGCC AGCCAGTAAA CGCCGCTGGT CTGTAACGTG TCGCTCATGG 180

CGATGAGCGT GCGGGTGGAG GCGGGCAGCG CGTGTCCGAG ATGATCAAAC TGTTCGATGA 240

TTTTTGGCAC CACTGCCGTC AGCAAAATAG TGACCACGCC CGTTGCCACC ACCAGCAGTA 300

CCAGCGGGTA GAGCATGGCC TGCAGCAGGC GTGAATTTCC AGNACCTGCC GCTGTTACGG 360

TGTAACCCGC CAGGCGATTG AGCACCACGT CGAGATGTCC GGATTTTTCT CCGGCAGCAA 420

CCATCGAACA AAACAGGGAA TCAAAGACGC GGGGATGTTC GCGCAGGCTG TCCGACAGGK 480

TGTAACYTTC CTGAATCCGC TGCGCAGCGC CATTCCGAGG CTTTTTACAT GCAGTTTTTC 540

ACTTTGCTCA CTGACCGCCT GTAAGCAGGT TTCCAGCGGC ATTGCTGCCT GTACCAGCGT 600

TGCCAGTTGG CGCGTGAACA GCGCAAGATC TGCCGCCGCC ACGCGACGAT GTGCGTGCCG 660

CCGACGCTGC AACATCCCCC CTGTCGAAGT ATTCATCCGG GCTTCAATAT GCACGGGGAT 720

AAGCTCTTTA CCGCGCAACA ACTGGCGGGC ATGACGCGCG GAATCCGCCT CAATCATACC 780

TTTGGTTTTG CGACCATTAC GCTCCAGCGC CTGATAGTAA AACAGTGCCA TTACGCCTCC 840

ATGGTTACCC GCAGAACTTC ATCGAGAGAG GTTTCTCCGG CGAGCACTTT CTCAATGCCG 900

TTGCTGCGGA TACCCGCAGA GTGTTGTCGG ACATAACGTT CCAGCTCCAG CTCCCCGGCC 960

TGACGGTGGA TCAAATCACG CAATGTGGCA TCCACCACGA TCAGCTCATG GATGGCAGTC 1020

CGTCCGCGAA AACCTTTGTG ATTACAGGCG GGACAGCCCT GTGGATGGTA CAGAGTGACG 1080

GTACGGGCGT CGGTAATTCC CAGCAGGCGT TTTTCTTCGT CGGTGGCAGG CGCGGCCTGA 1140

CGGCAGTCGG AGCACAGCGT GCGGACCAGT CGCTGCGCCA TCACGCCCGT CAGACTGGAA 1200

GAGAGCAGGA AAGGCTCCAC GCCCATATCC TGCAAACGTG TGATCGCCCC CACCGCTGTG 1260

TTGGTATGCA GCGTGGAAAG TACCAGGTGT CCGGTCAGTG AAGCCTGAAC AGCGATTTCT 1320

GCGGTTTCGG TA 1332

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CCCAACGTTT ATCGTATTTC ATTAAAGTCC CTTGCCCGAT GCTATCTCGA GTTACATGAC 60

GAAATCGCTG ATTTGGATGT CATGATTGCG GCAATTGTCG ATGARCTGGC GCCTGAACTG 120

ATTAAACGTA ATGCTATTGG ATACGAAAGC STTCGCAGTT GCTGATCACG GCAGGAGACA 180

NSDOCID: <WO 9822575A3 IA>

ATCCCCAACG ATTAAGATCA GAATCAGGTT TTGCGGCACT GTGTGGTGTC AGCCCTGTTC 240

CCGTATCTTC AGGAAAAACG AATCGTTATC GACTTAACCG GGGTGGAGAT CGTGCTGCAA 300

ATAGTGCACT TCACATCATT GCCATCGGAC GTTTGCGAAC TGACGATAAA ACGAAGGAAT 360

ATGTCGCCAG ACGAGTAGCG GAAGGGCATA CAAAAATGGA AGCAATACGC TGCCTGAAGC 420

GCTATATCTC ACGCGAAGTT TATACATTAC TGCGTAATCA AAACAGGCAG CTCAACAGCA 480

TCCCGATAAC GGCTTGACTC TTAGAAGGGC GTCCAGGGCA GCCACTATAC AAGCAGGCAG 540

TTCCGGCAGT TACTGTGGCG TTACCAGATC AAACAGAGTC TGAGTCGACG AGGAAATTGC 600

TGGGATAACA GCCCGATGGA GCGCTTCTTC AGGAGTCTGA AAAACGAGTG GATACCGGTG 660

ACGGGTTACA TGAACTTCAG CGATGCTGCC CATGAAATAA CGGACTATAT CGTTGGGTAT 720

TACAACGCGC TCAGGCCGCA CGAATATAAC GGTGGGTTGC CACCAAATGA ATCGGAAAAC 780

CGATACTGGA AAAACTCTAA AGCGGTGGCC AGTTTTTGTT GACCACTACA TTTAGTGCGA 840

CACGGGAAGC GCGATATGAA CGATACGATA CATCAATGGT TTATTGCGGT GATAACCTGA 900

AGGGTGAGAT TGAGGCTATT TATAATAGTC TTGAGAGGCG TCAGGTTTAG AGCAGGAATG 960

CTGAGTAGCC ATCTTATCGA TTGTTTTCGA GCGTAAGATG GCTGAATGGA ATGGCTATTA 1020

TTGCACAGTC CTTAATTATA ACATTCATAC CGACATGATT ATCTTCTGTC CGGAAGAATC 1080

AGAGGCTGCG GTTTCAGACT GTCTGCCGGT ACATTCCTCT CTCCGTTAAA AACCATAACG 1140

GGTTCATTAT CTTCGTCTGT CAGCAGATTG AATGGCGGTA TATTTTCAGT ACGAATGCCG 1200

GTCAGCCACT GAAAAATACC TGCGAAATGA CGGGCACTGA TTTTTCTGCT GACGGACTGA 1260

TGAGACGTGA TGTCACTGGC GGTAATAATC AGGGGAACGC TGTAGCCTCC CTGCACATGA 1320

CCATCATGAT GAACAGGATT AGCACTGTCG CTGACCGACA GACCATGGTC AGAAAAGTAA 1380

AGCATGGCAA AATGACGGGA ATGCCGGCGA AGGATACCAT CAAGCTGCCC GAGAAAGTTA 1440

TCCCAGTTTA CTGATGCTGG CGAGGTAACA GGCAATTTTT CGGGGATACT GCCCCAGGTA 1500

ATGATTCGGC CAGGAGTTAA GCCGGTCACA CGGGTTCGGA TGAGACCCCA TCATGTGCAG 1560

GAATATCACT TCGGAGAGGA TTTATCCGCC AGTGCACGTT CTGTTTCCTG TAACAACAAC 1620

ATGTCATCCG TTTTACGGGA AGCAAAGCTG CCTTTCTTGA GGAAAACGGT ATGCTCCGCA 1680

TCAGAAGCAA TAACAGAGAT GCGTGTATCA TGCTCCCCCA GCTTTCCCTG ATTGGATATC 1740

CACCATGTGC TGTATCCTGC TTTTGCTGCC AGCGCCACCA CGTTGTTGCC GGAGTCAGGG 1800

TTCTGCTCAT AGTCATAAAT CAGTGTCCGG CTCAGGGAAG GTACGGTACT GGCTGCTGCC 1860

GATGTATAGC CGTCAATAAA TAAACCGGGA GCAGTATTCA GCCACGGTGT GGTTGGCACG 1920

GGATAGCCAT ATACCGACAT ATAATCCCTG CGCACACTCT CACCAGTGAC GATAACAATC 1980

GTGTCATACA ACGGTACACC CGGCAGGATT TTCCAGTTGT CAGCCCCGTG CTGATTCAGT 2040

TGTTTATAAC GCTGCATTTC ACGCAATGTG TCAGTTGTCC CCACAACAGT TCCTTTAACC 2100

ATCCGCAACG GCCAGCTGTT TACTGAGCAT AATACGAACA GCAGCAGTGC CAGCCAGTTA 2160

CGGTGACCGC GGTGGTGTGT TCGCCAGAAA ATCACCATGA ATACCAGAAT CGCGGCACTG 2220

ACCAGAAAAT GATAAACAGG AATCATCCCG GTAAACTCCG CTGCCTCATC AGTTGTGGTC 2280

TGCAGCAACG CAACAATAAA ACTGTTGTTG ATTTTACCGT ACGTCATACC GGCAGGCGCA 2340

TACAGTGCAC AACAGAACAG AAATAACAGC GCTGTAATGG ATGTGAGGGT ATTTCTGTGT 2400

GCAAGAAGCA GAAGAAAGAA CAGCAGCAAC ACATTCCCGG TGGTATTCTT CTCAGTGTAT 2460

CCGCATGCAA TTGTGGTTAT GACAGAAACA ACAAAAAAGA ATAAAAACAA TATAATCCTG 2520

AGAGTGTTGC CCGGACAAAA CAGTTTTCTG ATATTCATCG GAGTATATCG ACAACATTAT 2580

TATGAAGAGA ACAGGATAAT AAAAATCAGA AGTTATCTGT GAAACAGATA ACAGACANCC 2640

CTGCAGTATA ATATTACTGC AGGGTGTTCC TTTTTAATTA CAGAAATACG TAATTATCTT 2700

AATTGCAGAA ATATGCGCAA TTATCGTTCA GAAGCAGTGT CGTCAGAAGT TATAAGTCAC 2760

ACCAAGCAGG ATGTCATGAC TTTTAACATC AACCTCTGAT TTATATTTAT CCCCTTCTGT 2820

ATCCTTGTAA TACAGGGAGG ATTTACCAGC ATCCAGATAG CGATAGCTGA GGTCAAGAGC 2880

GATATCCGGG GTTACGTCAT AGCGAACACC GGCCCCAATG CTCCATGCGA AGTTGTCAGC 2940

AGAGCCTGAG CGTGATATAG AATAACGCAC TCGCTCACCG TAGCCATAAT CCCAACTACC 3000

GCTACCTGTT GATTCCTGAT GAATTCTGGC GTAACCAATT CCGGCAGACA CCCATGGCGT 3060

AAATGCACTG TCGTTTCTGA AATCATAGTA CGCATTCAGC ATCAGGCTGT TGACTGACAC 3120

CTCATTCTTC AGGTCACTAT GTCCCGCGTG GTCCTTATAG AGGTTGTATG TTGTGTCAGC 3180

TTTTCCACGG GCGTAAAACT CCAGTTCTGT ACGCACAGGA ATACTGAACT GCGGATGCAA 3240

GTCATAACCA AACGCTATAC CTCCACTGAA TACCGTGTTA TGGCCATCCC CCCCCTATAC 3300

TTTGATGTTT CCTCTTTATT TTCGGACAGG AAACTCTGGT CAGAAAGAGA TACTGCTGAA 3360

GTACCTGCTT TACCGGTCAG ATAAAAACCG CTTTTACCTT CCTCAGCACC CGCATTTGCT 3420

GCAANCATAC AGGCAGCGGT AACTGCTGAA ACAGCAAAAA CTTTTTTCAT TTCAATTAAC 3480

TCCATTATTT CACTATTTTT GTAAATAGCA CTCCTAATAT TTTAAAACCA GTCAAAAGAT 3540

AGTATCAAGC AAATTATTCA TGTCTAATGA ACAGATAAAA TCGACTATGT GTCGGCAAGA 3600

CTCTGCTCCA CCGATATTCC TCTTATTTCC GCCTCGATGA AATACCCCCG TTACCTTATT 3660

TGTACCCCTT ATAATGGGAT GTTGGCCAGC CAGACCCGGC ATGATTAGTT CTCCCTGTCG 3720

ACTATGCTCC GGGAGGGATG TCACCGGGTC TGGTGAGGCG CGGATAACCG CTAATAGGGG 3780

AAGGTCAGGT ATTTTACACC GGGACCGTCA GGGCAAGATA ACGAAAGCCA GCTCCCCGCA 3840

TGAACTGACG CCAGATAGTT TCTGTCCATT GCTGCTTTTC TCATCTTACG TCTTAACCCT 3900

GCCTTGAATA CCTTATCTCT CGTCAAAATA TTAATAGCGA TATGCCGTAT CCCTGAAAAT 3960

AATCCCGCTG CGTTTCCTCT TCTTACTTGC AGTCGTCTTC ATTCATTACC ACGTCCAGAC 4020

NSDOCID <WO___9822575A3 IA>

GCCATGCAGC TTATTCTCCA CGTGCCAGTG ATTTCGGATC GCTGTGACGA ACTTCTCTGC 4080

GGTTAAATCA GCAGAACTGA TATAATATCT GACCATTATT TCTGACTCTT GCTTTTGTTC 4140

TGCTATTATT GACCGAAAGG AGACTGCCAG GCATATTTTT TCAGCCCTTT CCATTCAAAC 4200

GTGAATTCAA TCAGCTCATC AGGGACNTCG CCAAACCATA TGAAGACGGG ATCCTNCTCT 4260

GCCGTGACTC TTGTCACTAA TTGCGTAACA GTCATGCTCN GGGATAATTA AATCTTTCAG 4320

CGGAAATAAA AAGATTATCA GATATGGGGA TGACACCACA GCACCGCTGA GGCCAGTATG 4380

GATAAACCAT GTACCTTATT AACCAAA 4407

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TTTTTTGCAA GAGAATTTCC CTGAACCTGA AGCTCATCAT CGCCATCTCC GCCGTTCAGG 60

TAATTATTAC CTGCTCCCCC AATTAACTTA TCGTTGCCAT CACCGCCATA GAGCTGGTCA 120

TCTCCGTTTC CACCACTCAG TGTGTCATTA CCTTTATCAC CATATAAGCG GTCATTCCCG 180

TCATTTCCTT CTATATGGTC ATCACCATCC GCGCCATGGA AGATATCAGC AAATTTACTG 240

CCAAAAAACT TGTCGGCACG CGTGGTCCCA ATAAGTTCTT CCACGGAATA TAAGTTATCA 300

GTCTCTGTTA AATTTTTACC ATTGATATGA GTGAATTCAT AACTCCGATA TTGCGTTTTT 360

TCAGTTCTTT TTCCAACTGA AACCTCCTGC TCCTTCACAA CTTCCTGTAA AACCTTAACA 420

TCACCACCAA GTACACGTGT TACCGTGTAA TTACCCGCTT CGGTTGCTTT TGTGCCATCA 480

ATGGTCAGAT AACCGGTGTC TGTTTTATCA TAATAAACAA CATCATGTCC TTTACCTGCG 540

TAGATATTGG CTGAGCCGGC AGATAAAAAG ACCTTATCAT CCCCGTCTCC CAGGTGTGAC 600

TCAATACGAA TTTCCCGATA CTGGTTATTA CCGACTGATG CATGCTGAAT CAGGTTAGAG 660

TAATCATATA CAGACCCCTT GTCCTGNAAC CCCCTTCACC GTCCATTTAT CAACACCCTT 720

GACTAATAAC TCGGTAATAT ATTCATATTT TCCGGACTGC CTCCTTTCAC GAATTTCCTC 780

ACCGGGAGTT TAACAATGGG CGTAACNAAT TTGCAATAAC GTGG 824

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GNGGCCGCAG TACTGGATCA TCACCGAAGT TTCGCGCGGA AAAGCGTTAG AGAAAGATCT 60

AATGCTTCAT GATGGTGATG GACTTTTCCT GATGGTGAAA TCCAGCGGGA AATGCTCTGG 120

CGTTTCCGTT ATCAACATTC GACAACAAAG CAGCGGACAA TGATGGGACT CGGTGTCTTT 180

TCCACACTTT CACTTGCTGA TACCCGAGGG CTAAGAGTGG ATTATATTTC CTTATTAGCC 240

AACAGAATCG ACCCGCAAAT TCAAGCTAAA GCCGTAGACG AAGAGCAATA TTTGAAAAGG 300

TGGGCACCTA CGTTACCAAT ACTGGCTTAA TGGCTACATA CGGCGGTCAG GGTCAGTTTA 360

CGCTTACAAA ATATAAAACA ATTTGATACA AAATATTCCT CTTATTCTAA ATAAAAGTAT 420

CTTGAAAACC TTCCAACTGG AAGGTAGATT GAATTTATGC TAAACATAAA GAGGAATTGC 480

TTATGAATTA CGTTATCCGC ACTACCACCG TCGTCTTTAG TCTCATGCTG GGCAGGTTAC 540

GCAACTGCTG 550

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CACTAAAGGC CCTGGATGTT TTCGCTCAT TAGTAGACAT CTCGCTGATA ACGGCGCTCT 60

ACGCGCACTC ACTTAAAAAT TCATCCGCCG CTTCGGTGTC CATGCCACCA AATTCGGCAA 120

TCACTTCCAG AAGTGCCTGC TCAACGTCTT TCGCCATGCG ATTAGCGTCG CCGCAGACAT 180

AAATGTGGGC ACCATCATTG ATCCAGCGCC ACAGCTCCGC GCCCTGTTCG CGCAGTTTGT 240

CTTGTACGTA AACTTTTTCT TTTTGATCGC GCGACCAGGC AAGATCGATA CGTGTCAGCA 300

CGCCATCTTT GACGTAGCGC TGCCAMTCCA MCTGGTACAG GAAGTCTTCC GTAAAGTGCG 360

GATTACCAAA GAACAGCCAG TT 382

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TAAATCAGCA GAACTGATAT AATATCTGAC CATTATTTCT GACTCTTGCT TTTGTTCTGC 60

TATTATTGAC CGAAAGGAGA CTGCCAGGCA TATTTTTTCA GCCCTTTCCA TTCAAACGTG 120

NSDOCID: <WO__9822575A3_IA>

AATTCAATCA GCTCATCAGG AACATCGCAA ACAATATGAA GACGGATTTC TTCTCTGCCG 180

TGACTCTTGT CACTAATTGC GTAACAGTCA TGCTCTGGAT TATTTAATTC TTTCAGCGAA 240

AATAAAAGAT TATCAGATAT GGGATGACAC ACAGCACCGC TGAGCAAGTA TGTATAACCA 300

TGTACTTATA ACAAAAGGAG ACGTAAGAAG GGGAACGGGT ATCAGAGGGC CAATCAAAGC 360

AGGTATAATG AACGCCAGTA TAATTGTCCG CAACCCAGAA ATATATTATT GAACTGGTTA 420

TCTCCTGCGA ATGCATATAC TGCAACGGCC GTTAAAATAG CATTATATCC ATAAAGCCCG 480

GCAGAGATTT TATCAGGAGA AAGCTCAGGA ATACAGAATG ATACCACCAC ACTCAGAAAC 540

GAAGCGACAA CCGTAATCAT CAGTAGTTTC CGGCTCCCTG CAAGTAGTCC CAGCATAACA 600

AGAATACCGC CGACAGCATC AGGAAACATA AAAATCTCCA TAAAGCTACC AGACAATGCC 660

ACCGGATAGT TTTTCAGCAA AACAGAACCT GCACTTCGCC CGAAGGTACT GACATATCAT 720

GAGGCATTAT TCCGGAATGT AATAACCACG TAGCGATAAT AAAGGGGGCG GTCAATACGG 780

GTAACCCTCT GAGCACTGAC GACAACAGGG GAGTAAACAA AACAATACCA AGAGTTCCGA 840

CGATAAGTAC AGCAATTCCG GAGACTGACA CAGGGACAAG CATGCCACAG GCTATGCCAT 900

ACAGAACAGC ATTATATCCC CATATACCTT CATTAATCTC CTCATCAGGA TACCGCAAAC 960

ACCAGGCAAA GAACGGAGAA AGTGCTGCAC TGATGGCTGA GAAATACAGT ATTTCGGGGT 1020

GCCCCATATT AAAAGAGGCT ATTCCAGTCG CCAAAAAAAA GAACAAGCCA GAAACAACAT 1080

TGTTCTGTAA TAATACCTGT GAATACCCCT TACTAAAGGC GGTTATCACC TGTTTTACTC 1140

TCATGTAAAA TGTCACACAC ACCTCATACA TAAACCATTC TCCGCTTCTG CGGGACAGTA 1200

CCGCCCCTGA CTCCACCTCA CAGCGGATTG TGTATTTTTA AACAATCACA GTCTTCTCAT 1260

ATACTTTCCA TTCTGAAGCT TATCTCTTCC TCCGTGATAA GCTTCCGTCG CGGGATGTGT 1320

TATACGCCCT GTAAGACAGT TATAAAGGAC ATCAATGCCA TAGTTAATGA YTACCGAATT 1380

CCGGTGGATA GTCAGTACTG GTTTGCCACA AAACAGTGCA GTCACACATG ACAGGAGAAG 1440

ATATGAGCCG GATACCGCTG CTCTGAGACT TAACGCTCAT GTAAACTTTC TGTTACAGAT 1500

TCTTCCAGGG ACTAAGAAGA TAACTGANTT ACGTTCGCAT TCCAGTSTTT ATTTCTGCAG 1560

TGACAGCCAT ACCCGAGCTT AATGGAATGT GCTTATTCCC GGTTGACAAA TCATTCTCTT 1620

CAACAGAAAC AATGACATTA AAAACGAGTC CCAGTTTCTG GTCTTCTATT GCATCTAAAT 1680

TTATATTTTT TACCTTACCC ACCAGATAAC CATATCGGGT GTAAGGAAAA GCCTCCACTT 1740

TAATGATGGC ATTCTGCCCG ACGTTAATAA AACCAATATC TTTATTTTGT ACCAGAGCAG 1800

TAACCTCCAG CGTGTCATCT TCCGGAACGA TGACCATCAG TGTTTCCGCT GTTGTAACAA 1860

CCCCACCTTC AGTATGAACC TTCAGTTGCT GAACTTTTCC CGAAACAGGG GCCCTGATTA 1920

CTGAAGCCTG TTGACGCTCT TCATTTTTCT CTAACTCCAG AGTTAATAAC TCAATGCTGT 1980

CTGTTGTTTG TCTTAGCTTG TCTAAAATTT CATTTTTAAA AAGCTGCGTG ACAAGCTGAT 2040

NSDOCID: <WO 9822575A3 IA>

ATTCTTCTTT TGCAGACAAT ATCTCACTCT CAATTTGCTC CAGTTGCGAT TTATAAACCC 2100

GTAATTCATT TGCTGCCTCA ACATATTTAT TCTCCTGCTC AAGTACAGCA TGTTTTGCAA 2160

TTGCCTGTTT ATGCAACAGG CTCCTGAAAT CATCCAGACG GCTTTTTTCA ACCCTCGATA 2220

CATTTTCATA ACGGTTTATA CGGGCAAGTA TTGTTAAWCG CTCTGCTCTT TTCTTATCCA 2280

GATTCAGTTC TTTTTGATAC TTCTGATTTT GCCATGTGGA AAACTGTTCT TTTATCAAAG 2340

AAGTTAAACG CAGTACTTCC TCTTCAGATA CATTCTGAAA ATAAGGCTCA TCAGGAAGTT 2400

TCAGTTCAGG AAGTTTATTT AATTCAATTG ACCGGCTCAG AATTTGATAC CGAATTTGTT 2460

CCAGCCTGGC CTGTAACAGT GATGACTGCG TTTTTAACGT ATCAGCTTCA GCTCCCAGCG 2520

CTGTAAGCTT TAATAACACA TCCCCTTTCC GGACTGACTC TCCTTCTTTT ACGAYAATTT 2580

CTTTAACTAT CGAGTTTTCA ATAGGTTTAA TTTCTTTNTA CGCCCACTGA GTGTTAATTT 2640

CCCATTTGCA GTGGCAACAA TTTCCACCTG GCCTAAAACA GATAAAATGA AAGCAATAAC 2700

CAGAAACCCC ATAATAAAAT AAGCAACCAG ACGCGGCCGT CTGGATACCG GCGTTTCAAT 2760

TAATTCCAGA TGAGCGGGTA AGAATTCATT TTCGTCCTTT TCACGTACCG GAGTATCTAA 2820

CTGCTTCCGG ATTTTCCATG TTTCACTCCA GACAAGTTTA TAGCGCAACA GGAACTCGCT 2880

GAACCCCATT AACCATGTTT TCATATTCTT CTGTTCTTTC TGTTAGTCTG ACTGTAACTG 2940

ATATAAGTAA CTGTATAAAC TTTCCGGTTC AGAAAGCAGC TCCTTATGTT TACCCTGTTC 3000

AACAATTTTC CCTTTTTCCA TGACAATAAT GCGGTCTGCA TTTTTTACTG TAGACAGACG 3060

ATGAGCAATG ATTATAACCG TTCTGCCCTT ACATATTTTG TGCATATTGC GCATGATGAC 3120

ATGCTCCGAC TCATAATCCA GAGCACTGGT TGCTTCATCA AAGATGAGTA TTTTAGGGTT 3180

GTTCACCAGC GCCCTTGCAA TTGCGATGCG TTGACGTTGA CCTCCGGATA ATCCTGCCCC 3240

CTGTTCCCCG ACAATGGTGT TATACCCCTC ACGCAATTCA GAAATAAAAT CATGAGCACC 3300

TGSTAATTTC GCTGCATAAA TAACTTTTTC GACGGACATG CCAGGATTAG CCAGTGAAAT 3360

ATTATCAATA ATACTGCGAT TAAGCAGCAC ATTGTCCTGC AACACAACCC CCACCTGACG 3420

ACGTAACCAG TTAGGATCGG CCAACGCAAG ATCATGTCCA TCAATTAAGA CCTGGCCATT 3480

TTCAGGAATA TAAAAACGTT GAATTAATTT AGTTAATGTG CTTTTTCCTG AACCAGAACG 3540

TCCGACAATA CCAATAACCT CCCCCTGCTT AATACT 3576

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ISDOCID <WO__9822575A3_IA>

TCAGCCCGGT GAGCGGGTTT GACAATTCCG CACTCACCAT TGGGCTAAGG GTTATCAGGT 60

GGGGTTAAGG AAATGGCAAA ACCTACCCCC GTCCAAACTC CAGTCGCTGC ACATTCACCA 120

TCCCTGGCTT CTCACCTGCG CTGACATCAA TTTGTGTCAC CCGCAGCGCA TATTTTTCAT 180

CCAGTGCTTT TAACCAGTTC AGCAGGTCAT TAAACACCAC AGGTTCTATC CAGACCTGGA 240

TATTCTCCCC GCGCTCGGCA ATCCGTTTGA TGACCACCGA GTGCGCGGAA GCTGTCACTG 300

ATGACCCGCG ATACCTGTGC TGGCGTTGTC GTGCCGGATT TTCGCGCCGC AATAATATCC 360

GGCGCGGCGC TCTTCAGTCG CGCGTTCATC GCCACCAGCT GCTGCAACAT CGTCTCCTGT 420

TGCTCAATCC GTTCGCTCAA CGGCTGCCAG ATGAGAACGT AATATCCGGC GCTAAACAGG 480

AACACTACCG CTGCCAGTAA CATGCCTTTT TCACGCGGCG AACGCCCCGC CAGGTGTTGT 540

GTCAGCCAGT GTTCGCCACG GCTTAACTGG CGTTCACGCC ATTGCTGAAA ATAGTGAATA 600

AATTTATCGC GTAACATGTT ATTTCCTCCG CAACGTTACG CCGCCGGAAA CCGCATCACC 660

CTCTTTCTGT AACGCGTCCT GTTGCACAAC ATAATCTGCC GCCAGTGCGC TACGAGTTTA 720

TCGAAGCTGG CAAAGTTCGC AGCCCGTAGC TGGAGGTGAA GCGTCTGGCG TTTTTGATCA 780

AAGGTGAAAC ACGCATTTCG ATGTCGGTAA GTGACGCTGA TTTCAGGGTA CTGGCGATCG 840

CTGACAATTC TGCGAGCAGC CGGGTATCGT CGGTCTGTGG GCGATATTTT TTCAGCGCCA 900

TCGTCACCTG AGAGCGTAAA TTCACAATCC GCTTCTGCTC CGGGAATAGC GTTAAGAACT 960

GTTTCTCCGC CTGGGTGCGG CTTTGCGCCA CCTGTTCGCT GACGCTCCAT AACGTCACGC 1020

CCCGTTCCAC TACCAGCGCA ACCAGAATCA ACAATATCGG CAGAATCATC ACCCGCCAGC 1080

GCGCCCACTG TTTTCGGTAG CTGACACGAG GCTGCCACGG CCCTGTTAGC AGGTTCCCTT 1140

CCGGTTCGCC ATAAGTGGTA ATGGCGGGCA GAGCGTAACG GTCAGCGTTC GGCGTCTGCA 1200

CCAGCCCATG CAGACAGTTC TTCCGGTGCA ATGCCGACCA CGGTTAGTGA AAGCGGTAAA 1260

TCCTGCTCAT TGAGCTGTGC TCGGAACATG ACCGGAGCCA GCGCCCGCCC GGCGCTCCAT 1320

CCCCGGCATT CATCGATGCG GMAGATAACC CGTTGCGCAT CGCCAGCCAT AAACCCACAA 1380

GGAATGGACA TCCAGTCCGG CGCGACGATA GCGCGGGTGA TGCCGTTTGC CTGCAACCAC 1440

TGCGCAATGT TGCGCATATG CTGCTGGTGA ATCACAGCTA CGGTTGCCAG TTGCTGGTCG 1500

ATTTTCAACG GGGCGAAATG CAGTTCATCG ATATCCTGGT TCAGCTCTTC TTCCAGCAAG 1560

GCGGGCAGAA TCGTCGGTAT CTGCTTGCGG GGCACATCAG GCAGTTCAAC CTGCCAGACG 1620

CTGATCCATT CGCCGGGAAT GTAGAGTCGA ATCGCATCAG TTTGCAGCCA TTGCTGGAGA 1680

CATTCATCAG CAACGTCAGG CCAGATGCCG CACTCCACGT CGGCGGTACG ACGCTGCCAA 1740

CGGATGGGAG CGGAAMGNCA AAGCGGGAAA AAAATCTCAA GCATGGAACT CACTCACTTT 1800

CTCCTGTCTG ATGCCAGAGA ACAGAAAAGT GTTGTGGGCC CATGCGGACA ATTAACGAAT 1860

TCATCGTCAG TTCAATCTCA TTCACGGTGA TATCTGAACG CAGCCAGAAG TAATTGCTGT 1920

CCACGCTCAG GACGGTTTTT AGCTGTTTTT TAGTACGCTC ATCGACGTCA GCAAGTAACG 1980

GCTGTGCAAG AAACTGATCG ACATCTTCCC AGCCCTTCGC ATGACGTTGT TGTAATAACG 2040

CTCGCGCCTG AACAGGGCTT AACCACGGGT CAAACAGCGC CTCAAGAATC ACACTTTGCG 2100

TGACGTCTAA GGTATTGATG TTGATTTGCT GGCGGGTCAT CGGCAGCGCA CAGACCAGCG 2160

GTTTCAGTTT TTGATAAAGC CCGGCGTCCA TTCCCTGCAC CACGCGCATC TCGCTGATAT 2220

CAGCCAGCGG TTGATTAGCG GCGTAAAACG GCACCGAACG GGCGAGATAC TCGCTGTCTT 2280

CACGGCCCAG ACGCGTCTGC ACGCTGCGGT CTTCGTCAAT AAACTCCCAC AGGCTTTCGG 2340

CTATCAGTTC GGCCCGATAA GCAGGCACAT CCAGGCGCGT GATCAGGGCA ATCAGTTGTT 2400

GTACCGCGAG CGGACGCGAC GCCGTCGTCG GCTGAGCGAG GGCATTCAGG TTAAAGCAAG 2460

CCTGTGCGTC ACGCAGAGTG ACGGCGATTT GCCCTGCGGC AGTGGGAAAA AACGCGGGCC 2520

GGAAGCCCNA CGTGCGCCAG ATGCACGCGC TTTTCATTTT TCAGGCTCAG ACTGAGTGCG 2580

CTCAACGCCA GGCTTTCCGC ACTGGCGCTG TACCACAGCG CCTGCTGGTA CTCCTGCTGG 2640

TGCGCGTTCG CCCAAGTTGT TTCTGCATCC GCCCGGAAAG CGTGATGGTC ACCAGCATCA 2700

TAACCGCCAG CAATACCAGC ACCACGACCA GTGCCATTCC GCGTTTTGGT GGTGAGGTGA 2760

TCATGATAAT TGCGGCCCGC GTAACAACCA GATGCGTTCA ATTTCGCCCC ATTGTGGCGA 2820

ATGCAGGGTT ATGCGTACTG CCACGGGGAT CGCCTGCACT GATGACCAGC TCTCCTGCCA 2880

GCGCGTGCCG TCGTAGAACT GCAAACGGAG CGAATCCGCC GGGATTAATT TTTGCGTTGT 2940

TGGCTTCACG CTGCCTGCCG CATCGGTCAG TGGCCAGGCT AACCGTTCGA GATAACCACC 3000

ATGAATGCGG TAACCGACGG TGAGCAGATT ACTGCGCGGC AGACGCATCA ACGGATTAAC 3060

CACGCCGCCA CGTACAAAAC GCATCCCTTC ACTCTCAGAC GCCAGCACGC CAGCGCCCGC 3120

CAGTAACGCT RGTTCACGCT GGCCCTGATC GCCTCTTACC GGACGCGGCA TCATTTGTGT 3180

CAGATCGTGG GTCAGAAAAC TCATCGTTTG CTGCATGAGG TTTAGTTTTT GATCGTGTCC 3240

GGCGACGGCG CTATTCACGC GTGTAACCCG TTTGTCACCT GCTGCGCCAT CATTGCCAGT 3300

GAGGCAAAAA TGGCTATTGC CACCAGCATT TCCAGTAACG TGAAACCAGC GCGAGTCCTT 3360

CTCACTGTTG GTCTCCCACG GCGCTAAACC ANGCGCGTCG TGACTGAATC ACTGACGAAA 3420

AGTCNTCATG AAGACTGACT TCAATATCCA CNGCATGGAG CAGCGCATTA NCGGTATTCA 3480

GTGGTGTTGG TTCGCCAGAA CCAAGCGGCT TTCCTGCCAT AATCGCTCTC GGCCCTGGGT 3540

G 3541

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

WSDOCID <WO_ 9822575A3 IA>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTACTGGACA TCTTTGATGA ACAAGCTCCT CAGTGTAAAT TGTACGTCTC TGATCGTAAT 60

CTTCCTGAGG GCGTTGAACA TCTATCCGCT GAATTTATAC CCTATACTCC TGAGTCGGCA 120

GATTTTCTGA TTCAACGTTT TTTCTCTGAA ACTATCCATA TTGAAAGTGC AATTGTTGTT 180

ACAGCACTTA AAATTGCCAA TCAGATTGCT CTATCTCAAA ATGAGACCAA GAATGTGTAT 240

CTGCTTGGAT TTGATTTTAC GATAAAGGGG GGGTTCACTA GCAAGATCCC CTGCGCAGCC 300

TTGCATGCCG AACCAGAATA TCAAGAGCGA ATTATCAGTA GTCAAGAACA GCTATTGCAG 360

ATGCTCCTTG CAGAAAAAAC ACGCCTGAAT ATCAATATCA ATCATGTTGG TAATAAGCCT 420

TACAGCGTAT ATTCTGTTGA TGCATTTAAT CAAGTGTTCG CTGCCCGCCA TCGTGGAGTC 480

GTGCTGCCCA CACATGCCCA GATTTCCACT ACATCATCAC AAAATGGGGT GAAGGTGATC 540

GCAGAGATTA CTACTAATCA CTTTGGTGAT ATGGACCGAT TGAAGTCAAT GATTGTAGCG 600

GCCAAGCAGG CAGGGGCTGA CTATATCAAA CTGCAGAAGC GTGATGTTGA AAGTTTCTAT 660

AGCAGGGAGA AGCTGGAGTC ACCGTACAAC TCTCCTTTTG GCACCACCTT TAGGGACTAT 720

CGGCATGGCA TTGAACTCAA TGAAGAGCAA TTTTCCTTTG TCGACTCTTT CTGTAAAGAG 780

ATTGGTATCG GCTGGTTTGC TTCTATTTTA GATATGCCCT CGTATGAGTT CATTCGGCAA 840

TTTGAACCAG ATATGATCAA GCTACCATCA ACTATATCTG AACATAAAGA TTATTTGGCT 900

GCTGTTGCTT CTGATTTTAC TAAAGATGTA GTAATTTCAA CTGGTTATAC TGATGAGGCC 960

TATGAGCGTT TTAYCCTKGA TAACTTTACC AAGGTTAGAA ATATTTATCT GCTGCAATGC 1020

ACCTCGGCTT ATCCCACACC GAATGAAGAT ACCCAGCTAG GTGTGATAAG ACATTATTAT 1080

AATTTGGCGA AAAAGGATCC ACGTATTATT CCTGGTTTTT CCAGCCATGA TATTGGTAGC 1140

CTTTGTTCCA TGATGNTGTC GCAGCCGGTG CAAAAATGAT TGAAAAGCAT GTTAAATTTG 1200

GCAATGTGGC TTGGTCTCAC TTTGATGAAG TTGC 1234

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ATGGGACCTT TCTTCAATGA TGTTGCCGAG TGGTTAGAGT CATTAGGTCG TAACGCTGTG 60

AATGTTGTAT TCAATGGAGG AGATCGTTTT TACTGCCGTC ATCGACACTA TCTGGCTTAT 120

TACCAAACGC CGAAAGAATT TCCTGGTTGG TTACGAGATA TCCACCGGCA ATTTGACTTT 180

GATACCATTC TCTGTTTTGG TGACTGCCGT CCATTGCACA AAGAAGCAAA ACGTTGGGCG 240

AAGTCTAAAG GGATCCGCTT TCTGGCATTT GAAGAAGGAT ATTTACGTCC GCAATTTATT 300

ACTGTTGAAG AGGACGGTGT AAACGCGTAT TCATCGCTGC CGCGCGATCC TGACTTTTAT 360

CGTAAATTAC CAGATATGCC TGCACCACAT GTTGAGAACT TAAAACCCTC GACGATGAAA 420

CGTATTGGTC ATGCAATGTG GTATTACCTG ATGGGATGGC ATTACCGACA TGAATTCACT 480

CGCTACCGTC ATCACAAATC ATTTTCTCCT TGGTATGAGG CTCGTTGCTG GGGGCGTGCG 540

TACTGGCGTA ACTATTTTAC AAAATAATGC AACGTAATGT ATTGGCTCGG TTAGTGAATG 600

ATCTGGACCA ACGTTACTAT CTTGTTATTT TACAAGTTTA TAATGATAGC CAAATTCGTA 660

ATCACAGTAA TTATAATGAT GTGCGTGATT ATATTAACGA AGTTGTATAT TCATTTTCGC 720

ATAAGGCACC GAAAGAGAGT TATTTGGTGA TCAAACACCA TCCGATGGAT CGCGGTCACA 780

GACTCTATCG ACCATTAATT AAGCGGTTGA GTAAGGAATA TGGCTTAGGC GAGCGAGTCA 840

TATACGTACA CGATCTCCCA ATGCCGGAAT TATTACGCCA TGCAAAAGCG GTTGTGACAA 900

TTAACAGTAC AGTGGGGATC TCTGCACTGA TTCATAACAA ACCACTCAAA GTGATGGGTA 960

ATGCTCTGTA CGACATCAAG GGGTTGACGT ATCAAGGGCA TTTGCACCAA TTCTGGCAGG 1020

CCGATTTTAA ACCAGATATG AAACTGTTTA AGAAGTTTCG TGAATATTTA TTGATGAAGA 1080

CGCAAATTAA TGCTGTTTAT TATGGTGTAA AATCAAAAAG CAATAGAAGG TCCGCATTCC 1140

TAAACGGTAG CAGATGATGG TTTTCATGGG CGTTTCAGGT TACTCAATCA GCCAACAACC 1200

GCAGCGAAAA CCCTGCTTTC TCGACCAGTT CAGGCCGGTT TTACCTCCAA TGCTTTCCGT 1260

CAGAACTGAG ATTTCAGCCA GTTGCCGGAT AAGTGTGTCG ATTTGCAGCA GTATACTTTT 1320

TCGTACAGCC AGAATGTGGC AGACTGAGGT GGAATAGATA ACGTCCGTAT GCCCGCTCAC 1380

CACCTCCGGG CGGGAGTGTG TGGTATCTGA CATCATCATT TTTCCTTTCT GTTTATAAAT 1440

GAAAACGCCA GCCGTGTTCA GGCTGACGTC AGGGAAGTGA AATCGGGTGA GTGATCTTCA 1500

CTGGTTCTGG TGCAAAAGTT ACTGTTGGCG CAGGGTACGG ATACCCTCCC TGGCCTGTTC 1560

GATACAGGGC AACAGTGCTG CCGAATCTGT TTTATCCTCA TCGTTGTCGA AGATAATTCC 1620

CGATTCGCAG TCGATATTGT CCTGCAGCCA CGTAATCAGA ATATCCAGCG CTGTTTCCGT 1680

GGTTAATGAT TTCATGTTGT GAATTTCCGG ATTACCAGTC GAAAGTGGGT AAACCTGGCA 1740

GACATCTGGC ACTGGCATCC AGATGAATGA GACTGACACC ATAACGCCGG ATGAGTGTGA 1800

CGACCAGACG ACGGAACGTA ACAGATAACC GGTACCGGTA AAATGAATCC ATTCTGATTC 1860

ACCAAAGTCA CTGGTCTGGT GTAACAGCGA GTACAGCCAG GCGTTGTCCT TTTCCGTGAT 1920

ATGTGCGGTA CTGCAGCGTA TGCCGGAAAG AGTCGTAAAC GGTTGTGGAG TGCAGGTTGA 1980

CTGTTGGTCA GATTCATCCA CCACGCGGAG TGAATAACCG TTTTCAGCGA CCTTGTTAAT 2040

CAGTTCAGCG AGATTAATAC CATCGACGTC AACGACAATG CGCCCCATAT TCAGTGCCTG 2100

NSDOCID <WO 9822575A3 IA>

TACGTTAACG CTGTCGGCTT CCGGCGTCAG GGAAAGTTTC ATTGTTTCAC CTCCGGGTGC 2160

TTACCCAGGA TAATATTATT TACCGCTCTG TAATTGTCGC GGGTCATCAG GCCGGTCGCC 2220

CTGCGAGCCC GGAGGATATC GATGCTGTTT ATTAACTGAG AGCGGGTACA GGCGCTGAAT 2280

CCCGGCTGGT CGGTACGCAC CAGCGCGTAT TTTTCCACGA GAAAGTTCAC CGCATCACAC 2340

AGTGAAATGC CTGCCTCAAT ATGCTGCTCG ATCACACGTT CATCGGCAAA CGGTGTGTCA 2400

TTCAGTGTGA GGCCGTAGTG CTGGTCCAGC AGTCGGGACA GAAGTATCTG CCAGATTTCA 2460

ACAGGAGACG GGCGAGAACT GGCCGCCTGC CCGGGTAATA CAGGTAATGT TTTCATACTG 2520

AAGATTTTCC TGATATGCAG ATATAAAAAT GGGAAAGTGG CGTGGTGAAA ACACCAGGCC 2580

GTAGCAGAAG GCTATTCTGG AGAGTTAATT TTTCATTTCG GGCGTCGGAT AAACAGCCAG 2640

ATAAACGTAA CCACAACTGC TGAGGGTATC GGCTTTGCAG GTCAGCCCTT TTGCATACAG 2700

CGTGACGGTA TGCTGATGGC GGGGATTCAG TTCACCGCTG GTGAGCATGA GTTCCAGTTG 2760

TTTCATCAGC AGCGGAAAGG CCTGGTCCAG GTGGTACGCA TCTGCATTGC TGTATAGGCC 2820

TCTGATACCG GCGCGGTCGG CAAGGTAATG CAACCGGTTA CCCTCCTGCA CCAGACGTGC 2880

CCCGAAACAG GGCGTCACGG TGCAGGGCAG CCCCCACCAG GGGCGGTCGT GATTGTCGTC 2940

GGGAAGTGTT GTCCCGGGGA GTGTGTCTGA CACGATAAAA TCCCTACAGA AAATCGGCTA 3000

AGAATGCTCC GGTATTGGCG ATAATTCTGC TCATCAGAAT TCCCACTCAG TTCAGGGTGA 3060

CGCTCATCAG CCGGACATAC GGGCCAAAAC TGTCCTTACG GCGTTCAGCA AACACGGCCA 3120

GCACACCGGG AATATCCTGT ACTTCACGAC CGGTATACGC CTCAGCACTG CCGTGCCAGC 3180

GGTACTTACC GGTGCAGAAC GGAAATAGAC GGGATGCAGG ATGCTGTTGG TGAATACGCA 3240

TGGCTTCACC ACGGGTGATG ATTTTCATAA TGGGATACCT CTGAAGACAG AAGATAAAAG 3300

TGAAAACAGG TGTGATGTGG TTGTGACGGT GACGGGTTAA AGCAGACCGT GTTCCGCAAA 3360

GGAGAAAACC TGACTGCCAC CAACTATCAG ATGGTCCGGT ACCCGGATAT CCACCAGGGC 3420

CAGTGCCTGT ACCAGACGTT CCGTGATAAG GCGGTCTGCC TTACTGGGGG TGACTTCACC 3480

GGACGGGTGA TTGTGTGCCA GTACCACGGC GGCGGCATTG TGGTACAGGG CGCGTTTAAT 3540

CACTTCCCGG GGATGGACTT CCGTGCGGTT GATGGTGCCG GTGAAGAGGG TTTCACCGGC 3600

AATCAGCTGA TTCTGGTTGT TCAGATACAG TACCCGGAAC TCTTCACGCT CCAGTCCCGC 3660

CATCTTCAGA ATCAGCCATT CCCGTGCCGC ACGGGTGGAG GTGAAGGCCA CGCCGGGTTC 3720

ATGAAGATGG CGGTCCAGGG TTTTCAGGGC CCGCAGAATG AGACTGCGCT CGCCGGGCGT 3780

CATCTCTCCG GGCAGAAAGG AAAGTTGTTG CATTGTGCTT CTCTCCATTC AGTCGATGAT 3840

GCGCATAATG GCGCTGCATT CCGGATGCTG CAGGGCGTAA TCCCGCAACC GGTAATAATG 3900

GATCGTCATG GCATAACACT CCGTACGACA GGCATGATGA CTGTACGTCA TCAGACAGGC 3960

GGCAATGCCG GCGGCTTCCG GGCTCATTTC AGCGCGGTTA CCGTTCATGG CATTGAACAG 4020

BNSDOCID: <WO 9822575A3 IA>

TACCCAGTTT TCGTCATCAT CGTCATCCGG TTCGGGTGCC ATAAATGCCC CGCCGTTGTT 4080

CAGGGTGTAC AGATTCCAGA TACCACCGCA GTAGTCTTCG CACAGACGGT CCATCCAGCC 4140

GAAGACACGG GGCTCCAGGG TCACCCACTG TGGAATGAGG CCAAAGTGCT GCGGCCAGAA 4200

GCTGATGCGC TGTTCATCAG GGACTATGGT GGCAACCAGC TGAGGCTGGT CATTCCCTGA 4260

TGCAGCGGTT ACGGAAACAG AAGGAGTGGT GGAATTATGC AAGACGGTTG TCATGAGATT 4320

ATTCCTTATA AAAAGTAAAT GAATGGAAGA AACCCCGGGG GAAGGGACAG ACGTGAGTCA 4380

GAACTGCGCT TTCAGGGAAA CGGCATCAGC GCATACTCTC CAGCAGCGTT TCAGCCATCA 4440

CCCACAATGC GCGGTTGAGC TTAATGTCGG TGTCGATGCT GTGAATGGCA CGGGTATGGA 4500

TACGTTTTCC TCTGGCACTG CGACCGGAAA TTCCGCCTTT CAGCATATTC TCCTGAATGG 4560

TCTGATAAGC ACTCCACAGG TCCTTACCGT AATCCTCCCG GCGTCGTGGT GTCAGAATGT 4620

CGGCGGTGGT GACGGGCTGA TGTTCGTCAC CATAACGGTA AGTCAGTGCC GCCTGTGCCA 4680

GCGCCTGGCG TGCCGGTGGC GGCAGAATCA GCGACTGCAT GGCATCACGC TTTTCCTCAA 4740

TCCGGTCAAA AACCCCCACC ACCTCGTAAG CCCCTTCAAT AACTTTCTCC ACCACATTTC 4800

CCCGGTGCGG AACACGCACT TCCCCCAGAG ACTGACCACA GACGCATCCG TTCTGGCAGA 4860

CGAACCTGAA GTAACCCGGC AGCATCTGGT AGCTGGAGGT ACCGTCATGA GAGTTGAGCA 4920

GAATAATTTC AGGGACATGT TCTCCGTTTA TCTCTCCGGC CCGCCGCAGA CGCAGCATGT 4980

GTTTGGTGTA TTCCCGGCGG TCCGGGTCAC GTACGCGGGT CTGGCAGGCG AAGAATGGCT 5040

GAAAGCCTTC CCGCTGCAGG CTTTCCAGTA CGGTGATGGT GGGGATGTAC GTATAGCGTT 5100

CACTGCGGGA GGTATGCCGG TCTTCACCGA AAATACCCGG TACATGGTGC ATCAGTTCTT 5160

CGTGTGTCAG CGGACGGTCA CGGCGTATCT GGTTCGCATA ACCAAAACGA CTGGCTAGTC 5220

GCATAATTTG CTCCTTATCG GTGGTTAAGA TTTACTGGTG TAATAAATGA AAAAGCCACG 5280

TCTCCCGGAG AAGACGCGGC CTGACAGATG AAATGAATGA CGTTTATTGT CTGAGAAGCC 5340

CTTAACTGGC GAGCTGAGTA TTAAGCTGTG TTCCGGCATC ACCAGCGCAA CTGACCTTCA 5400

GCATTACGGA TAACCAGCCG GGAATATGTT CCCTGGTCAT CTTCAGTAAA CACATTGCGG 5460

TAAGCTGTTA TGACAGCAAC CGCCTGCCCG TATGAGAAAG ATCCTTCAGC CAGGACATAC 5520

TCTGTGTGTA ACCCGGCATA TCTGGTTTCT CCTGATAAAT AGCCTCTGCC ATACGTTGTG 5580

GCAGAGGCTG AAGCATGAAA CTGACTTCAG GGATCAGTTA ACATTTTTTC CGGAAACGGT 5640

AATCAGCAGT GGATGGTAGT CCTGGGGATC GAAAACCGAT AACGGCAGAC TGACACGATG 5700

GCCGTTACTT TCTTCAGTTG CTTTAATGAT TTCGGTTGTG GCGACATTTT CCACGCACTC 5760

CGTTTCCAGA AATGCGTCTG TGGTTCGCGT GGCATTACTG TCACCAAAGG CTTCCGTTTC 5820

CATTTTTCTG GTCACCAGCG TCTGACCATA TTTGTCTTTG AGTTGCAGAG TGATGGTGAG 5880

GGGGCCAAAT CCTTCATCGT TTCCGCCATT ATCCAGCCGG AACTGGTAAG CACAAATATT 5940

TCCCGGGAGC CATATCGTAT CTGTATTGCG TATACTGATG TAACGTTGAT CCTGTGCCCG 6000

GAGTGGGGCA GACCACGTTA ACCCCAGAAT GAAGGCGGTA ATCATGCAGG TTTTGAACAG 6060

GTGAATCATG GTATTTACCT CTCTGAGTCA TGACGATTAC ACTGACAAAT CAGGTGATAA 6120

AACGTAAAAG GCGCAGAATA GCCGTTATGC CGGTAACTCC GGGGGTAATG TTTCTTCCAG 6180

TCGGTTAACC ATATTGCCGA GATGGGATGC ATCATATTCC ATGACGGGGC GTTGCCTGAT 6240

GATACTGACC ACCAGTGGTT TGATTAACAT GTTGGTCGCG GCCCGTTGTT GTATACCGGC 6300

GGCGAAAATG ATC 6313

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGTTGGCCGC TTGCGCAGAT AAAAGCGCGG ATATTCAGAC GCCAGCACCG GCTGCAAATA 60

CGTCTATTTC AGCAACACAA CAACCAGCTA TCCAGCAACC GAATGTCTCC GGTACCGTCT 120

GGATCCGTCA GAAAGTCGCA CTGCCGCCTG ATGCTGTGCT GACCGTGACA CTTTCTGACG 180

CGTCGTTAGC CGATGCACCG TCAAAAGTGT GGCGCAGAAA GCGGTGCGTA CTGAAGGTAA 240

ACAGTCACCA TTCAGCTTTG TTCTGTCATT TAACCCGGCA GATGTTCAGC CGAACGCGCG 300

TATTCTGTTG AGTGCGGCGA TTACCGTGAA TGACAAACTG GTATTTATCA CCGATACCGT 360

TCAGCCGGTG ATCAACCAGG GCGGAACTAA AGCCGACCTG ACATTGGTGC CGGTACAGCA 420

AACCGCCGTG CC 432

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GGGCTGATTA CGATTTTATC AATCTGTCTA TAGAACATGA ACTGAATGAA GGAATAGCTG 60

GCAGAGAGAG GTTATGCCGG ACTGGCGGAT AACCGGAACC GGTTGGCAGA GGTGGTTACC 120

CGTAAATTGC AGGACAGCTT TTATATGAAC TTTCCTGGGA TGCGCTGAAC ACGGCATACA 180

GTGAACACCC AGAGTGGTTT TCCGGGCTTG TCTCCGGGGA TGAGAATTAA AAAGTGGATT 240

ATGCTGCTAT AGCGCGGCGT GATTTCCTGC AGGGATTTCC ATTTATAAGA ATACGCCGCT 300

3NSDOCID: <WO 9822575A3 IA>

TCGGGGAATC TCCGGTTCTC CTGAGAGTTA CGATTGTTTT TTTACTCAAA TCCACAACAC 360

CTGAACTGGA ACTTGTGTTG CATCCCTGAT TGTTACTCTG CAGGAAACAT CTTTTTTACC 420

ATCAAAGGAT GACTGTTTTC CTTTCTCCCC TCCGTAAAAC ACAACTTCGA TCACATTTCT 480

GACATTTTTT CCAGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTAA 540

ATTTCAGCAC TGACATTCCG CTTACGTTAA TTTACACTGA ATACCCCACG AGGAGAATAT 600

GCAGCACCGG CAGGATAACT TACTGGCGAG CAGAACGTCG TTGCCTGGTA TGGTTTCCGG 660

TCAGTGCGCA TTTAAGCTCC GCACTTTCTC TCCGGTGGCA CGCTATTTTT CCCTCCTCCC 720

CTGCCTTTGT ATTCTTTCGT TTTCGTCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG 780

TGCAATTCAG CAGCAACAGC AACAGTTGCT GGATGAAAAC CAGCGCCAGC GTGATGCGCT 840

GAAGCGCAGT GCGCCGCTGA CTGTCATACC GTCTCCGGAA ATGTCTGCCG GTACTGAAGG 900

TCCCTGCTTT ACGGTGTCAC GCATTGTTGT CCGTGGGGCC ACCCGACTGA CGTCTGCAGA 960

AACCGACAGA CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCACGG GGCTGACCGC 1020

GGTCACGGAT GCCGTGACGG ACAGCTATAT ACGCCGGGGA TATATCACCA GCCGGGCCTT 1080

TCTGACAGAG CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT 1140

GCAGCAAATC CGGGCGGAAG GCGCTGACCT TCCTGCCCGC ACCCTGAAGA TGGTTTTCCC 1200

GGGAATGGAG GGGAAGGTTC TGAACCTGCG GGATATTGAG CAGGGGATGG AGCAGATTAA 1260

TCGTCTGCGT ACGGAGCCGG TACAGATTGA AATATCGCCC GGTGACCGTG AGGGATGGTC 1320

GGTGGTGACA CTGACGGCAT TGCCGGAATG GCCTGTCACA GGGAGTGTGG GCATCGACAA 1380

CAGCGGGCAG AAGAATACCG GTACGGGGCA GTTAAATGGT GTCCTTTCCT TTAATAATCC 1440

TCTGGGGCTG GCTGACAACT GGTTTGTCAG CGGGGGACGG AGCAGTGACT TTTCGGTGTC 1500

ACATGATGCG AGGAATTTTG CCGCCGGTGT CAGTCTGCCG TATGGCTATA CCCTGGTGGA 1560

TTACACGTAT TCATGGAGTG ACTATCTCAG CACCATTGAT AACCGGGGCT GGCGGTGGCG 1620

TTCCACGGGA GACCTGCAGA CTCACCGGCT GGGACTGTCG CATGTCCTGT TCCGTAACGG 1680

GGACATGAAG ACAGCACTGA CCGGAGCTGC AGCACCGCAT TATTCACAAT TATCTGGATG 1740

ATGTTCTGCT TCAGGGCAGC AGCCGTAAAC TCACTTCATT TTCTGTCGGG CTGAATCACA 1800

CACACAAGTT TCTGGGGGGT GTCGGAACAC TGAATCCGGT ATTCACACGG GGGATGCCCT 1860

GGTTCGGCGC AGAAAGCGAC CACGGGAAAA GGGGAGACCT GCCCGTAAAT CAGTTCCGGA 1920

AATGGTCGGT GAGTGCCAGT TTTCAGCGCC CCGTCACGGA CAGGGTGTGG TGGCTGACCA 1980

GCGCTTATGC CCAGTGGTCA CCGGACCGTC TTCATGGTGT GGAACAACTG AGCCTCGGGG 2040

GCGAGAGTTC AGTGCGTGGC TTTAAGGAGC AGTATATCTC CGGTAATAAC GGTGGTTATC 2100

TGCGAAATGA GCTGTCCTGG TCTCTGTTCT CCCTGCCATA TGTGGGAACT GTCCGTGCAG 2160

TGACTGCACT GGACGGTGGC TGGCTGCACT CTGACAGAGA TGACCCGTAC TCGTCCGGCA 2220

CGCTGTGGGG TGCTGCTGCC GGGCTCAGCA CCACCAGTGG CCATGTTTCC GGTTCGTTCA 2280

CTGCCGGACT GCCTCTTGTT TACCCGGACT GGCTTGCCCC TGACCATCTC ACGGTTTACT 2340

GGCGCGTTGC CGTCGCGTTT TAAGGGATTA TTACCATGCA TCAGCCTCCC GTTCGCTTCA 2400

CTTACCGCCT GCTGAGTTAC CTTATCAGTA CGATTATCGC CGGGCAGCCG TTGTTACCGG 2460

CTGTGGGGGC CGTCATCACC CCACAAAACG GGGCCGGAAT GGATAAAGCG GCAAATGGTG 2520

TGCCGGTCGT GAACATTGCC ACGCCGAACG GGGCCGGGAT TTCGCATAAC CGGTTTACGG 2580

ATTACAACGT CGGGAAGGAA GGGCTGATTC TCAATAATGC CACCGGTAAG CTTAATCCGA 2640

CGCAGCTTGG TGGACTGATA CAGAATAACC CGAACCTGAA AGCGGGCGGG GAAGCGAAGG 2700

GTATCATCAA CGAAGTGACC GGCGGTAACC GTTCACTGCT GCAGGGCTAT ACGGAAGTGG 2760

CCGGCAAAGC GGCGAATGTG ATGGTTGCCA ACCCGTATGG TATCACCTGT GACGGCTGTG 2820

GTTTTATCAA CACGCCGCAC GCGACGCTCA CCACAGGCAG ACCTGTGATG AATGCCGACG 2880

GCAGCCTGCA GGCGCTGGAG GTGACTGAAG GCAGTATCAC CATCAATGGC GCGGGCCTGG 2940

ACGGCACCCG GAGCGATGCC GTATCCATTA TTGCCCGTGC AACGGAAGTG AATGCCGCGC 3000

TTCATGCGAA GGATTTAACT GTCACTGCAG GCGCTAACCG GATAACTGCA GATGGTCGCG 3060

TCAGTGCCCT GAAGGGCGAA GGTGATGTGC CGAAAGTTGC CGTTGATACC GGCGCGCTCG 3120

GTGGAATGTA CGCCAGGCGT ATTCATCTGA CCTCCACTGA AAGTGGTGTC GGGGTTAATC 3180

TTGGTAACCT TTATGCCCGC GATGGCGATA TCACCCTGGA TGCCAGCGGC AGACTGACTG 3240

TCAACAACAG TCTCGCCACG GGGGCCGTCA CTGCAAAAGG TCAGGGCGTC ACCTTAACCG 3300

GCGACCATAA AGCGGGAGGT AACCTGAGCG TCACAGCCGG AGCGATATCG TTCTCAGCAA 3360

TGGAACGCTT AACAGCGACA AGGACCTCAG CCTNGACCGC CGGCGGCAGA AATTCACTCA 3420

ACAGAATGAA AAACTGACTG CCGGCCGGGA TGTAACGCTT GCCGCGAAAA AACATCACAC 3480

AGGGTTACCG GCCA 3494

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GNCCCAAGCT TAGGTTCGCG GCCGCAGTAC TGGATCTATT GCCAGCTTCA CCGCCAGACT 60

GTCAGTCAGT ACATCACCGT ATTTCTGCTG GCAGGTTGCC GGGCGGCTGC ACAGTCACTG 120

ATCAGTTGCT TCTGCTGTGC CGTACTCAAC TCTTCGTACT TTTTGATAAT ACCGCCGCAG 180

TCACCGCCTT TCGCCTGACA GGACTTCATT TCAGCAGAGC AGGCATCTAT CTGCTTATTG 240

CTCAGGTAGT TATTCTCAAC AACAACCACA GGGGATTAGA AGCCTTTTAG CCTGAAATAT 300

TTTGCGAGAG CACATCCAAT ACCAATAAAT GAGCCAATCA CACATCCGAT AAACAAAACA 360

TGCCGAATCT CTTTCAAACT AATATTTAAA TTACCTGTTA TCAACCACTC CACCAAAGAA 420

AAAAACACAT CAATACATAG GAATGACACC ACTATAGAAA GAAATGCGAT TATAAAAATA 480

ATAAACAATT CTGATAAGTG CTGAGAATTG CCGCTCATTT TTTCACCTCC GGAATGTAAG 540

ACTCAATCTT TTTACCTTCA TACTCAGAAG CAAAAGAAGC CGACACATCC CCAGCTATAC 600

CAGGAATCCT ACTGGGTGTC ATTTCTTTTG ATAGCCCCAA TTCTCCTTTA ATATCGGTAT 660

ATTTTTGAAG TGTTGGATTA AATTTCGGGT CCCAGCCGTC TTTTAACCAG TTAGCACCAC 720

TATTAATGCC CCATGAAAGG CCTTTACCAA TGCCATATCC AATAGCAGAA CCAGCACCAT 780

TGATCAACGC ACCAGATGTT GGGGCTTTTC CTTCGAGCCA GTTTCCTAAT GCTCCTCCAG 840

TTGCATTCCA GCCAACTGTG CCTACAACTC CATTCCCTGC ACTAATCACA TTAACCCAAC 900

CACCGATAAT CGCTGTTGTA GGATCTATAG TTCCATCCGT CAGATAGCTA ACACCTGCAT 960

TAGCTCCTGC CCCTAATCCC CACATGGCCT GAGCACCGCC AGTAAGAGAG CTACACTACC 1020

AGTGGCCAAC GCTCCGGCAT ACGCTTTATT GACTGCTTCT CCTCGCTTAC AGGCTTCACC 1080

GCCTGGGGCA TCGTTACAGG AAAGTACATC TGCGCCATGC GTCTGAGCAG CTTTGCTCTG 1140

CTCGGACTCT GTGCCACCAA CCAGGTTATT CTCAGCAATG TTCTTCCCGA CACCAGCCCC 1200

AGCAGCCGCG CCAGCCACAT CGCCACTGGC AATGCCGCCA GCCATACCCG CTGACAGCGT 1260

TGCCAGCGTG CTTACGGTTT GCTTCTGATC TTCTGTCAGT TTCGACGGAT CTACGTCCGG 1320

ATAGAGGCTT TTCGCAATGG CTGACGAGAT CACTTCACCA GTACCCGCAC CAATTGCGCC 1380

TGCTGCCGCA CTGTTGCCCT GAAGGGCTGC TGTCACACCA CCGAGAATGG CATGGGCAAT 1440

GGCTTTTGCC GCTGTATTGT CATCAATACC CGCGTGATGA CCGATGATGT TCGCCAGCTC 1500

CGGCGCCGAA GCTCCGGCCA GAGCACCTGC TAAATTACCC CCCGCCAGCC CCTGAAGTGC 1560

AGCCGTTGCA GCCTGGATAC CGCGCTGCAT ATCGCTGCCG GTACCATACT TTTCCTGTTC 1620

CTTTTTGTAT TCCGGCGTAT CACGCAGTTT TGCCAGATAT GCCTGCCGCT GTTCTTCCGT 1680

CGCATCCGCC GGAACAGGCC CATATTTATC CTGCGCAGCT TCAACGCATT CAGTTCCCCC 1740

TGCGTCCGCG CAATATCCGC CACCTGACTG CCTATGTCAC TGATAAGCCC CACTGTCTGC 1800

AGACGCCTCT GCTCCTTCTC CTTGTCAAAT ATCGGGCTGA TACTGTCATT AGCGTGCGCA 1860

GGGTCACGGC TCAGGTTCGC CAGATTCTGC TTCTGATTGC CCCTGTCCCG GATGGTGATA 1920

GTGCCTTCTG CCACTGCGGC CTGAGTCGTT CCTTCCGCAT GTCCGCTGTG ACCTCCGGCG 1980

GATATCATGC CACCCGGCAT GTTACCCTGA AATTTATCCC CGAAGCTGCC ACCACCGCTC 2040

AGACTGATTC CACTGTGACT GACTTTATAA TCCGCTTCGT TGTGAAGGTC ACTGAACCCC 2100

AGCGTTCCGG TATCCAGGTG GTTTTTATCC GGTGTGGCAG TGGAGGCAAT CACCGCACCA 2160

JSDOCID <WO _ 9822575A3 IA>

TCCAGTTGGG TATGTTTACC CACTGTGATG TCGAAGCCGC CGTCACCGGC AAACATTCCG 2220

GTTTGTTCAG CAACGGAGTC AAAGCGGCTC TTCATCTTAT CCCGGGAGGC AGCGATGTAA 2280

CCTGAGCCGG TCATGGAGCC AAAGGTAAAA CTGCCGCCGG CASCCACGCT GGTCTGTTTA 2340

CTGTCGTACT TACTGGTGTC CTGCTGGCTG CTTATCAGCA GGTCGTGGCC CACATCGGCG 2400

ATAATCCTGT TGCCGTTGAC CTGAGCACCG TTCAGTACCG TATCCCGACC ACTGTTGATG 2460

GTGACGGTTT TACCGCTGTC TGTTGTGGTT TCAGTCCACT CAGTACCGTT ACCTTTCTCG 2520

CTGCCTTTTG CCGCATTAAC GCTGGCAAAG ACACTGATAC CGGCACCTTT ACCTGCACCG 2580

ATACTGACAC CCACGCCACC GCCACTGCTG CTGTTCCTGC CCGTTGTTTT TTGTGTGTTT 2640

GCCGCGCCAC TCAACAGAAC ATCATTCGCA GCATCCAGGT TTGTGTTACC ACCGGCCTTA 2700

AGCTGGCTTC CGGCAATCAC AATATCTCCG CGGTTATCGC CCCTGTTTTT ACCGGTTGCG 2760

ACAACAGACA GATTATTCCC GGCATTCAGC GTACTGCCGG ATACTGTGTC ACTTTCAGAA 2820

TGTTGTTGTG ATTTCGATTT CTGGGTGGTG AGCGACAGGC TGACTCCCGT CGCATTCGGG 2880

TCACCGGTTG CGGAGGCCAT TGCCGCAGCC TGTCCGGCCT GCACACCAGA CAGCGCTGTC 2940

TTTGTAGCCT GCAGGGTTTT CAGACGGCTG TCACTGCTCT CCTTCGTCTC CTGTGCACTG 3000

GTGACCGCAT TATTGATGGC ACTGCCCACT GTGCCGGAAA GGGCAACCGT CAGCCCGCTT 3060

TTCTTCTGCT CAAATTTTTC GTCCACAGTA CGACGGTCAT GCCCCGGGTC AACCACCACA 3120

CTGTCACCGG TAATGCTGAT ATCCCGGTTC GCAATCACAT CCGAACCGCT GATATGAGCC 3180

TGTTTGCCCG CGGTAATACT GACATTACCG GCAGTGGAGC CGATGGTACT GGCACTCTGA 3240

CTCTGCGTTG TCCCGGCCTC GCGGCGGTCG TGCGTTGTCT TACTGCTGCC AATGGTGAAG 3300

CCAATACCGC CGGTACCCAT CAGACCGGAT TTCTTCGTTT CCTTAAAGCG CCAGGACGTA 3360

TCTGTACTGG TGGCAGCAAG AACATCAACA TGGTTACCCG CCGCCAGTGA CACATCCCGG 3420

TCAGCCACCA CATCCGAACC CTCTACCGTC AGGTTATCAC CGGCGTTAAC GGTCACGCGG 3480

TTCCCCGACA GCAGGGAACC TGYTTCACGG GAGGCACTGT CCTCACTGAT GGTGTGGGTG 3540

GTTTTCTTAC TGAGAAAACC TCCGCTTTTT TTCTTCGTTT CCAGATAGTG ATAGTCACTT 3600

TCTGTCGCCG TGGTCAGGGC AACATCACGA CCGGCATTCA CGCTGATATT GCCGGTTGCG 3660

GTAACGGATG ACGCAACAGC GGTGATATCC CGTCCTGCGG TGACGGTGGT GTCACCACCK 3720

CTGGCGATTT CCGTTCCCTG CTGACGGACT GTCTCGTTAA TCTCTTTCTT TTTCTTCGAC 3780

GTATAGCTGT CGCCTGCGCC GGCAGACTCT GCCACCAGGT TCACATCACG TCCGCCCCGG 3840

ATGACCACGT TATTTTCCGC AGCCATACCG GCAGCCTGAC TGGCAATATC ACGACCGGCA 3900

ACAAGGAGGA GGTTATCGCC CGCCGTCACC GTGGACACAG CTGCGTGGCT TTCATGACTT 3960

TCTGACCTGC CGTTGCGACT GTTTTTGCTT TCCCTGACTG CATTCAGACT CAGGTCGTTA 4020

CCTGCAGAAA GCAGGGCGCT GTGCCCGGCA GAAACAGAGG ATGCTGTGAC ATCCAGATTA 4080

TGGCCTGCAG CCATCGCCAG GTTACCGCCG GCGCTGATGC TGCTGCCCTG TGAGGTGGTG 4140

GATGATGAAC TGTTGTCATC AGTGTGCCAG AAACCGGACT GACTTTTGCT CCCGCTTATC 4200

AGGTTTACGG CAATGTTGAT GTCATTACCC GCAGACATTC CAAGGTCTCC ACCGGACGAG 4260

ACCGTTGCCC CGGTAATATC AATGTTTTTC CCTGCATCCA GTGAAAGTGA ATCAGTGCCT 4320

TTAATGGTCG CAACCGGACC GGTGTCCGTA CCGCTGAGAT GCACACCACC ATATCGGCTG 4380

TCACTGCCCG CATTCCATTG CTGACGCCGG GTGATATTGC TGATGTTGCC ACTCACGCTT 4440

TCCAGTTGTA CGGTTTTACC GCTGATGACT GAGCTGATAT TGCTGATATC CCCGATGGCG 4500

CTCAGGTCCA GGCTACCGCC CGCGCTTATC AGCCCTGCAT TCAGGTTGTC GATATAGCCG 4560

GTACTGTCGA GCGAAAGGTC GTTCTGTGCG TTGATGCTGC CGCCGCTGTT GGTGATATTG 4620

CCGTCCGCAA GCTGCACGTT GTTCCCGCTG ATAACGCTGC CGTTATGCAG GGTGATATCT 4680

TCCGGCGACA GATACAGTTT CGGGACCATG ACTGTCTGTC CGTTGATGGT GACTGACTCC 4740

CACCACAGCA TGCTGCCGTC AAGCTGAGCA ATCTGTTCAG CTGTCAGCGC CACACCAAAC 4800

TCTAATCCCA GTCCTTTCTG TTGTCTGGCC GCGTTATCCA TCAGATACCG CATCTGTTCC 4860

GTGTCTGAAC CCAGTCCGTT GAGATAACGT GAACCCGTCC GGCTCAGCAC CGCGTTACTG 4920

ACATACCGGG TATCAAAGAC CGCATCCCCC AGGAAACGAT AATCTTTTTC CGGTTTCAGC 4980

CCGAGGCGGT CAAGAAAATA CGATGAGCCC AGAAACTGTT TTTCATCGGT ATACGACGGA 5040

GCCGTTTCAC GTGGCGCCTG ACCCGGTTTC GCTCCAAGAA GCTCATACAG TCCGGCAAAC 5100

AAATGGCTGT CCACCTGTCC GAGACCATCC AGTTTCGGGT TCACCGTAAT CAGATACGGA 5160

CTGTCCGGGT CCGTGGACGG AACCAGGTAT CCATTGTTGC CGGAAGGCAG TGGCCAGTCA 5220

TCACTGATAC CGGTCTGACC GGTCAGTGGC GAACCTCCGG CAATATTTTT CAGGGCACCT 5280

GCCAGTTCAT CGTGCCATTG CGGAGAGCCA ACCACCACCG GCTCATACTG CTGCAGCGCT 5340

GTCTGTGTCA GACTGTCTCC GCCGGTCTGC TGACTTAACG TATTCAGTAC AGGTGCAGAG 5400

ACCACCGGAC TGACACTACC TGCATGTGCA GTGGTTGTTC CGTTATTGAT ACTGCTGGTA 5460

AAACGGGTCT TAACATCCCC GCCCGCCTGA ATAACGGAAT AATACGTCTT ACCGGGCGTG 5520

TAATCTTTTT CCCGGCCATC CAGTGAAAAT CTGATGGTAT TGTTTTCAAA TTCCGGTGAC 5580

AGCAGGGGCA GTTTATCCAG AGAGCCTGTT GCATAGCTAC CGTAAAACGT TTTCGGGTCG 5640

TAGCGGTATA CCAGATATTC ATTCTCTGTC CCCGTCTGCC AGCTCTGATT GCTTAACTCT 5700

CTGCCCGAGA GTGCGATATC CCCATTCGCC AGGATAAATG ACGCCCGGTT TTCCAGTCGT 5760

TCAGCCTCAG CAGAAAGATT ACGCCCTGAC GCAATGCGGC CTGCCGGATT ATCAGCACCG 5820

GTTACTGTTG TGATGTTCTG GCTGCTGAGA AAGCGCTGTG TGGCACTGTC AGCAAACGGA 5880

GCGTAATAAT AAAGCGTATC CATTGTGATA TTGCATGCCC CGTGCCCGTT GCAGGGCGTA 5940

CCGTGCTGAT TTTCAACTTC ACGGGTGAAA TAGCCATAGC TGCCGTCAGG AAGAAGGGAA 6000

NSDOCID <WO___9822575A3 IA>

AGGGGAATAT CAACCAGAGC ATTTCCCATT CCCTGAATGG ATGAGGGGTT AGTCCGGGTT 6060

GTTGTTGTGG CAGAAAATCC CTCCCGCTGG TTCAGAAGAT GCCCGGTTCT TACAACAATA 6120

TCGCCCTGAT GCGTCTCAAT ATTCCCGGAA GTATTGATAA TCTCTGTGTT TGCACCGCCG 6180

GAAGCATCCT TCTGTACCCA CAGACTGTTG CCGGCCAGGA TATCACCATG CTGGTTATGC 6240

AGACGGTCTG TAAACAGCTT CAGGTTATTC CCCGCATAAA TCAGCGCACT GTTCAGCAGG 6300

GTACCGGCCA CATTCATTGT CAGACTGCCT GCCGTGCCGG TAAAACCACT GATGGTGATA 6360

TCACTCCGGC TGTTCAGACT CACATCGCCA CCGGCCTGAA GTGAACCCGG TGCGTTAAGG 6420

AAAAGACGCT GTGCGCTGAA AACACTGTTG CCTTTACCGG CAGTCAGCGT TCCATTGTTG 6480

GTGAATGCCT CTCCGGCACC GAGCACCATG GCATCACCCT GCATGACACC GCCGTTGGTG 6540

ATGGCATTTT GCGACGTGAC GGAAAGGGTT TTCCCTGCGG CCAGGGTACC GTAATTCGTG 6600

AGGGCAGCAA TCAGTTTCAG TGTGACATCA CCGGTGGCCA CCACCTGCCC CTGACCACTG 6660

AAGTCCTGAG CGTCAAGCAG CAGGTTGCCT GCACTGTACA GCCGCCCTGT ACCATTTTGC 6720

AGCAGTGAAC TGCCCTTGAC GCCAAGCCCG GAGGTTCCCA GCAGGGTACC GCTGTTGCTG 6780

AATGTGTGGT AATTCACCAG CAGGTCCGCA CCCTGAAGCG TACCGGTATT ATTCAGCGTG 6840

GTTCCTTTAA CGTCGGCACT GCCGGTGGCA AGTACGCGTC CGCCGTTGAC AGTATTCACC 6900

ACATCCAGCA GCAGGGTGGC AGCCTGTACC AGTCCGCTGC CGGTGTTCGC CAGCACCTGC 6960

GCCGTCAGCG TGAGGTTACT GCCGGAGAGG ATTTTGCCGT CGTTCTGCAG ACGGTCAGTG 7020

GCGTTCAGGG AAACCCCGCC ACCACCCTGT ATCGTGCCCT GGTTACTCAG GGTCGCAGTA 7080

CTGACATTCA GTGCATTCCG GCTCATCAGA ACACCACCGG AACGGTTGTT CACGCCACCG 7140

GAGGCGGCCA GCGTCAGCGT TTCGCCCTGC AGATGCCCGC CGTTTGTGAG TTGTCCTGCC 7200

GTGATGGTGG TGGCATTTCC CTGTAATTGC CCGTCGTTTG TGACACTGTC TGCCTTCAGC 7260

GTCAGCACAC CTGCACTGAG CAGTTTTCCG CTCGCGTGAT TGTGCAGCGT CTGATTCACC 7320

GTGAGCGTGA GAGCATCCAC ACCGGTGATG TCACCCGCAC TGGTCAGTGA GTTCGCCTTC 7380

AGGGTCAGAT TTTTTGCAAT CCATTGTCCG CTGTTGCTTA AATTCAGTGC ACTGAGCGCC 7440

ATTTCACCGT TCGAGGTGAC TTTGCTGCCT GCTGTGCTGA CGAGCTCACC CGTCAGACGT 7500

GCAGTCAGGC TGTCAGCCGC CTGGATCGCC CCGCTGTTTG CCAGACTGTC TGCGGTGATC 7560

AGCACCCGTT TGCCCTGCCA GTGTCCGGAA CTGGTAATAC TGCCTGCGGT GATTGTCAGA 7620

TCGCCGCTGG TCAGCAATGA ACCTCCGTTA TTCATCAGCG CAGGTTGAGG GGATGCCATA 7680

CGGGCGGCAA GCGTCAGCGC GGCTATCCCG GTGAGCGTGC CACTGTTGGT GACACTGTTC 7740

TGGCGAATCG TGACATGGTT ACCCTGGACA GTGCCGCTGT TATCCAGTGA GTTTCCATCA 7800

AGGGAGAGCG TGCCGGCCGA AAGCAGACTG CCCCGGTTGT CCATGGTGGC TGCTTTCAGC 7860

GTGGTGTCAC CCTGGCTCAT GATATCGCCG GTACTGGTCA ACTGACCGGT TGCCGAAGCA 7920

GTAAGGTTAC CGGTTGCCAG CACGGAACCA CTGTTCGCCC AGTTGTCCCG CYTGCACGGT 7980

GAGATTCTGT CCCTGCGTGG TCCTGCGGTA TGCAGTGTTT TACCCCGGAG GGTGAGGTCG 8040

CCCGCCGTCA GCCAGCGCCC GTTACTACCC TGTGAGAGGG TGTCGCCAGC AAGCGCCAGT 8100

GCACCGGCGC CCTGCAACAG GCCGTCACCA TCCAGCGTGG TCGCCCTGAC GCTCAGCGTG 8160

TCAGCGATGA TTTTTCCCGG ATTGCTGAGG GAGACAGCAT TTAACATTAA ACCATTATCA 8220

CCGGTGATAA GCCCGCTGTT GCGGATGTCC GGTATATCCA GCGTCAGGTC TGCAGCACTG 8280

TACAGCGTGC CGTTCTGCTG ATTATCAAGC CTCTGTGTGT TAACGGTAAG TGAGGCCTCC 8340

CCCTGCAACA GACCGCTGTT GGTCAGGGTC TGTGACTGTG TATTCAGGGC GGAACCAACA 8400

AGTACGCCGC TGCTGGTCAG TTCCGGCGCA CTGAGGCTGA GCGACGGGGC ACTGCTTTTC 8460

CCGCTGTGGG TGAGCTTTTC ACTGGCGTTC ACCACCATGG TCTGTTGTGC TGCCTGCGTA 8520

CCTGCAAGAC GTGCATCTCT GGCGTTGATG CTGAGATTTT TACCGCTCTG AAGCTGTGCG 8580

CCCGCTGCGG TACTCAGTTT GTCTGCCTGA ACCCGGAGGG TGTCACCGGC ACTGTTTTCC 8640

CCGTCCAGCG CCACTGTTGT CACATTCAGC GTCATCGCAG CATCGCTGTG GGTGACCGAT 8700

TTTTTACCGG AGCTCAGCGC CTGCGCACTG ACCGTCAGCC CTTTGCCGCC GGACAGCACA 8760

CCGTTCTGTG TCACATCCTG CGCCTTCAGC ACCAGTACAT CATCGCTCAC CAGCGAACCT 8820

GTACTGGTCA GTTTCCCACT GGCCGTGATA TCCACTTTGC CCTTCGCGCC AGTGCGGCCG 8880

CTCTGGGTAA AGTCGCGGGT ATTCACGGTC AGGGGACCGC CACTGAGCAG GGAGCCACTG 8940

TTGCTGAGCG TTGTACTGCC GAGCGTCAGG GAAGCCCCCT GAACAGCACC ACTGTTATTC 9000

AGCGTGCCGG CATCGAGTCC CGCATGACCT TTCGCCAGCA ATATTCCGTC CTGTGTCAGC 9060

GTGGTGGCGC TGGCCGTGAG ATTCTGCCCG GCGGTTATCT GTCCCTGTGT TGTCAGCGTG 9120

TCACTGGCGA CAGTCACGAT ATCGCGGGCC GCGTTAATCT GGCTGGCGGT ATCCTGTGTG 9180

ATGTTTTTCG CGGCAAGCGT TACATCCCGG CCGGCAGTCA GTTTTTCATT CTGTTGAGTG 9240

ATTCTGCCGC CGGCGGTCAG GCTGAGGTCC TTGTCGCTGT TAAGCGTTCC ATTGCTGAGA 9300

ACGATAATCG CTCCGGGCT 9319

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ATGAGGCGAT TAAAGCAACA TTGGGCAGTG ATAATGCCCC CACCCAGCCA CCTAACGCAG 60

CGAAGAGTAA TACATCGCCC ATGCCTAATG CTTCTTTACG CAGAACTATT CCGGCTATCC 120

NSDOCID <WO___9822575A3 IA>

AGCGSAGGGA GTAAAAAGTG ATAAATCCCA CCAGTACGCC GGTAACTGCG TCTTGTAGCG 180

TTAACGGACT CTGTTGCGCC CATGCTGCAA TCAGCCCGGT CCACAATACG CCCTGAGTAA 240

AAACATCGGG CAGCCATTGG TTGTCGAGGT CAATGACGCT CGCGGCAATC AGCCAGGCGG 300

ATAATATCAT CACCGCCAGC CCCCATCCAC TTTCTGGCCA CACCAGACTC GCCAGCAAAA 360

AAGTGAGTGC TGTCAATAAC TCAACCAGCG GATAACGTTG CTGATTTTCG CCTGACAGTC 420

GCGGCAGCCC TTTGAGCATC AACCATGAGA GCAGCGGAAT ATTGTCACGA ACGCGGATGG 480

TCTGCTGGCA ATGCGGGACA GTTGCGAACC GGGTTAGCCA AGGGCTTTAT TTTTTGGACT 540

GCGGCACTCG G 551

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CATTTACCAA ACCCCGTTCG AATATCTTAT CTATTGCCCA TCTCATATTA AATATAACCG 60

ATAATTTGGT GGATACTAAT AGTAATTACC TTGTTATTGA AAATATAATT ATTGTTATTT 120

TTAGCCTCAT TAATTAAATT GAAAAATCCT CTCTAATTTT TGTCAGATTA GGGCTGTAGA 180

AAGGATCGAG TTCAAGATGT TTACCCCATT TGCTTTTCAT AAAGTCCACT TCCCTGGCAA 240

ATCTGGCTAG TTTCTCCGGT GAATCTTCGG CTCCTCGACT AATCGATTCA TAGTGGTAAA 300

GCTCGGCATA AGGTGTCCAG AGATTACGAT ACCCCGCTTC GNGTACTTTC AGACAGAAGT 360

CCACATCATT AAAAGCAACA TGCAGATTCT CTTCATCCAA CCCGGCAACT TCCTCATAAA 420

TATCTTTGCG AATAAGCAGG CAAGCCGCCG TGACGGCCGA GAGAGTTTGT GTCAACAACA 480

AACGGCTGAA ATAGCCCGGA TGGTGGCGAG GATAATGTTT ATGGGAGTGT CCAGCTACAC 540

CACCAATACC GAGAATCACT CCGCCATGTT GTAAAAGTAT CATTACTGTN ATAGG 595

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TGGCAGTTGA ACAGATTTTC ACATCAGCAA CAGATTAGCG AACGGGACTT GGCATTAGCC 60

GAGCGTTTTA GTGAANGTTT AGCTCTAACA CGTCTATTAG AAGAGCGCAC GCAGNATTAT 120

NSDOCID: <WO 9822575A3_IA>

CACTGAACTA GAGATTGAAA AACAATTGCT TACCACCAAG TTGTCTGGCG TAGAGCAGCA 180

GTTAAGGGCT GAGCAAGAGT CGCTTCAGCA GGCCCAGTCT GCATTGCTCT CAGCAGCAAA 240

AGAAAAGCAA CATCAACTTG ATGAGTTGGA ATCGGTGCTC AATGAGCGGT ACAGTGAGAT 300

TGCAACCTTA ACCCGTTGGC TGGAAGAACG TGATCAGGCA CTCCTTAGTG CAGCAAGTGA 360

ACAACAACAG ACCAATGANA CCATATAGAG CTCAGCCAG 399

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1013 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

ATACTCTGCT TGTTGAGCAG CCATTACGTC GCTTTGTGAC GCAATATTAG ACTCGTGCAC 60

TGCTATTAGT TGAGTCAGTT CATCACATTG TTTAGAAGCC GCAGCCAAAG CAAGAGTTTG 120

CTCATCTATG CTTTGCTGCA ATGTTTGTTG CACAAGTTGC CCTTCTTCCA GCTGTTGCTG 180

TAGATTTGCA CTTACCTTTT TCAGTGCATC ATATTCCAAG CCTAACGTAT CGTGCTGTGC 240

TTCCAGTAAT CCATAAGCAT GCTGCAACTG GTTTTTAGTT TGCTGCTCAC CGTCAAGCTG 300

TTGCTGCAAT GCATTAGCCT GCTGTTGCAA CAAGTTCACC ATATTGTCTC GCTCGGCCAG 360

TGTACGAACC TGTGTATCCT GGATATGTAG CGCTTGTTCC AACTGAAGCT GTAATTCGGT 420

AATTTGCCGC GAATGTTCGC TCAATGCTCT GTTGCTCTTG CTGAGCGCGA GAGTAAGGTG 480

AGATGCACGC TGTGTTTCTT CACTCAATTG TAACGTCAGG GTATTGACCT GTTGCTCCAG 540

TTGATGGCGA GCTTGCTCCT GGCTCGTGAT GCGACTCTGT TGCTGCTCTA GTTGATGCAG 600

AGCTGTATGC AACTCATCGT TGGCTTGTAT TCGCTCCTGC GACCATACAC TCAAGTTTGT 660

TTGGGCCTCA TTGAGCTGTT CTTGCAATAA TGCCACCTCA GATGTCAGCG AATTGATATG 720

TTGCTGGGCA AAAGATAGCT CATCAGATTG CACTTGAGCA TGTGCAAGCT GCTTTTCCAT 780

TTCTAATATG CTGTTATGTT GTGCAGTAAT GCGCTCGGCA AGACGCCCCC TTTCCAATGC 840

CTGCTGTTCT ACCAATAGCT GCCGTTCAGC CTGAATGTCA TCTTGTTGTG TAGACAACTG 900

ACGTTTTAAC TGGGAATTCT CCCAACTCTC GCTACAAGAT TTNCCCAAAC GACAAAAGAT 960

GTCTTGGACT TGTNTGGGTT ACACGAGCAT TTTCTGAGGA TTTTATACCA ATN 1013

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

NSDOCID <WO 9822575A3 IA>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GATATCCACA TCGAGACGTT TGAAAAGAGT CTGGTGATCC GTTTTCGTGT TGACGGCACA 60

TTACATGAAA TGCTGCGTCC GGGGCGCAAA CTGGCCTCGC TGCTGGTGTC GCGTATCAAG 120

GTGATGGCGC GGCTGGACAT TGCCGAAAAG CGCGTGCCGC AGSATGGACG TATTGCGCTG 180

TTGCTGGGCG GCCGGGCGAT TGACGTGCGT GTATCAACCA TGCCTTCCGC CTGGGGGGAA 240

CGGGTGGTGC TGCGACTGCT GGACAAAAAC CAGGCTCGCC TGACGCTGGA GCGTCTGGGT 300

TTAAGTCTCG AACTGACTGC GCAGTTGCGC CACTGTTACA CAAACCGCAC GGCATTTTTC 360

TGGTGACGGG GCCGACCGGT TCCGGCAAAA GCACCACGCT GTACGCTGGA TTGCAGGAGC 420

TGAACAACCA CTCGCGTAAC ATTCTCACGG TTGAAGACCC TATCGAATAC ATGATTGAAG 480

GGATCGGTCA GACGCAGGTT AACACCCGCG TCGGCATGAC ATTCGCCCGT GGCCTGCGCG 540

CAATTTTGCG TCAGGACCCG GATGTGGTGA TGGTCSGTGA AATCCGCGAT ACCGAAACCG 600

CAGAAATCGC TGTTCAGGCT TCAACTGGAC CGGACACCTG GGNACTTTCN ACGCTGGNAT 660

ACCAAAAAAA AGGGGTGGGG GGATTATAC 689

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CTCAGCAGAA CCGAGATCTT CCATCAGCTG GCGGGCCTCG GAAGANTCCC GCTGCCAGAC 60

CGCATTCAGC CGCTGTTCAA ATTCGGCCTC GTCGATTTGC CTCAGCGTAA AGGGCGCGTT 120

CAGCCCCCGT TGCAGCTCCT GCAAAACAGA GAGCGACAAC GGATGCACAT GGAGGATCTC 180

CAGCGACGCT TCGCACCATG CCACCAGGCT AAACCGACGG CTGAAACTAT AGGGCAGACG 240

CACGGTGTTA GCGGTGGTTT CCTGTGCTAC AGGCACCATT AACGCGTTCT CCCGGCATTA 300

AGGAACGCAC GAACTTCTGG CGGTAAGGCC TGATTTTGCG CAGGCAATAT CGCTGCGCAG 360

TGTGCGGCAT CAGGCTTAAG CCCTGCTCAT CGCGGTAGAT TTGCTCGGCG CGCATGTAGT 420

TATATTTGCG CTGCGACACA CCGTCTGCCG CCATACCGTC ACGCAGAATG GTCGGGCGGA 480

TAAACACCAT CAGGTTACGT TTTTCTTTTT TATCCGCCGT CGATTTAAAC AGGTTACCAA 540

TCAACGGGAT ATCGCCCAGC AGCGGCACTT CTCGCCACGC TTTCTCCCGC CTGGTCGTCC 600

ATCAGACCGC CAAGCACAAT TAGCTCACCA TCGTTAGCCA ACACGGTGGT TTTCAGTTTG 660

CGCTCACCAA ACACCACGTC GAGGCTGGTC TGTCCTTCCA CCTTCGACAC TTCCTGCTCA 720

ATCACCATCT GTACCGCGTT TCCTTCGTTA ATCTGCGGCG TGACTTTCAG CATGATGCCG 780

ACTTTTTTCC TCTCTACCGT GTTGAAAGGA TTGCTGTTAT TGGAGCCAAC GGTAGATCCA 840

GTTAATACCG GAACGTCCTG GCCCACCATG AAGAAGGCTT CCTGGTTGTC CAGCGTGGTG 900

ATGCTCGGCG TGGAGAGCAC GTTCGAGCTG GAGTCGTTTT TGACCGCCTG TACCAGCGCC 960

ATCCAGTCGC CTTTCAMCAC GCCAACCGCC GTACCGCTAA AGCCAGAAAG AAGCTGAGCA 1020

AGCGTGGAGA GATCGCCGTT AGTATCCGGA TTTATGGTGG TAGCGCCGTT TTCACTGATC 1080

ACCGTGGAGC CTTTCTGCGG TTTTGCYTGA GAAATCGTGC GCCCAGCGTA CCAATAGGGA 1140

TCTGCGTACC GTTAGCAAAC TGCATTAATC CGGCATCTTT CGACGCCCAC TGCACGCCGA 1200

AATTGATAAT TCACCTTCGG CAACTTCCAC GATCAACGCC TCGACATGTA CCTGAGCACG 1260

GCGAATATCC AGTTGTTCAA T 1281

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CAATATTAGC GCACGGCACC AAAGGTGATG AATGAGCAGG CTGRAATATT ATTTTCCCGC 60

GGTGCAGAAA TCCTTGTTCT TGGTTGTACA GAAATTCCGG TTATTCTGGC GCAACGTTAA 120

AGAGCAGCCT TCCCGCTATA TTGACTCACG GCGTCACTCG TTCGTGCCGG AATAAAATGG 180

TACGAAAATC GTGTCGGTAA ACATTATCTT TTAACCCAAT AATCATTTAA ATCGCAGCCA 240

GAAAGTTATT CGCTTTTAAC TGAATTATAT TTATAACGGA GAACATTATG GTTTGGCTGG 300

AAATTATCGT AGTACTTGGT GCAATAKTTT TTGGTATTCG CCAGGGGGGA ATCGGTATTG 360

GTTTATGTGG CGGGCTTGGG CTTGCCATTC TGACTCTGGG ACTTGGTCTG CCTATGGGGG 420

G 421

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GTTAACAATG GCGTAACAAA TTTCAATAAC GTAGAAGATT TGCTGTCAGA AAGGTCAATA 60

TTTCCTTTCA ATGGGTCAAA GACTTGCTTC TGGAATTCAT CCGGTTTTTT CTCCAGACGT 120

ISDOCID <WO__9822575A3 IA>

TTTCCTTCTT CATAATAGTC AATATAACTT TTACCACTGA GTGTTTTGKC YCCATTTCTG 180

GTGACACCAG CTAACTCACC TATCAGCGTA TCCCMATGTT GCTGGGTAAT GAGGACTGAT 240

CTTTCAACAG AATACTCTTT ATTATACTGA GATAATATTT TAAAGTTATC TTCTAAAAAT 300

GCAGCATGGC GGGCATCATA TCCCATTTTC AAAGTAATTT TTGCCGTGTT TTTTCTCCCA 360

TTCAGCAATA ACATCGGCCA TTTTACTGGC GACATGTTCA AACATTGCCT GTTTTGAAGC 420

CTCAAGGATG CCTGAAATTA TCCCCGTAAC AGCCCCTACC AGCGCGCTTA CCGGTGCACC 480

AACCAGAGAT GTCGTTGCAG CAGCACTAAT ACCTGAAGAT ACTGAAGCCA GAACAGTGCT 540

TATCGTTGTT AACGATGCAT CAATAGCTCC TGTTTCTTTG TGGAAAGCAG CAAGTAAACT 600

GTCACCATCG TATCCAAGTT TTTTGAATCG TTGTGAATAC TCCTCTATTT TATTGGCACG 660

TTTAAACTTA TCGGCAATGG ACAGGAATGA GAGGGGACTA ATTGCCAGTG TCACAACAGA 720

AGCAATTAAA CCGGCAGCAG CAGCAGATGT AGATAACCCC TGTGCTGCAC GCTGTGCGAY 780

NAATATATTG AGAAATACCT TTTCCAACAT TACCCAGTAC TTTCGTTGTT AATTCAACAC 840

CTGCTGCAGC TTTAGTTCCG GTATCTGCAT CTGCATTGCT CAGAATGAAA CTTGCTGAAA 900

TCGCAGATAA AATACCCGAT ACAGTATCTA ACCCTGCACC GATATTATCA AGGTTAGGTA 960

AATTCTGTAA CTTATTACCA ACACCGTTCN GGNCTGTTGG TATTGGGATA ATACACTT 1018

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGCAATGTTC AAATCGATAT TGTGCAGCAC CTGGGTTGGG CCAAAGTGCT TGGAGACGTT 60

TTTAAATTCA ATCACAGGAT TTTCATCCTT CTTTCCAGAC GACGCAGAAT AAAGCTCAGC 120

ACCAGGGTAA TAATCAGATA GAACACCGCC ACGGCGCTCC AGATCTCAAG GGCGCGGAAG 180

TTACCGGCAA TAATTTCTTG CCCCTGACGG GTCAGTTCCG CCACGCCGAT CACAATAAAC 240

AGCGAGGTGT CTTTAATGCT GATGATCCAC TGGTTACCCA GCGGCGGCAG CATACGACGC 300

GTGCCAGCGG TAAAATGACG TAGCGAATGG TTTCCCMACG TGAAAGACCG AGCGCCAGTC 360

CTGCTTCACG AAAACCTTTG TGGATAGACA GCACCGCACC 400

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

INSDOCID <WO_ _9822575A3 IA>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CGTGTTCCCC TGGCCNGCTT GGTTTCGCCA TAGACGTTGA GCGGGGAAAT CACATCGGTT 60

TCCACCCAAG GACGTTCACC ACTTCCATCG AAAACATAGT CGGTGGAATA ATGTACTAGC 120

CACGCACCTA ATGCTTCAGC TTCTTTGGCA ATAACCGCCA CACTAGTTGC ATTGAGTAAC 180

TCGGCAAATT CCCGCTCACT CTCCGCTTTG TCGACTGCAG TATGGGCCGC TGCGTTAACA 240

ATCACATCCG GCTTGACGAG ACGTACCGTT TCAGCCACCC CTGCAGAATT GCTAAAATCA 300

CCGCAATAGT CGGTGGAGTC AAAATCAACG GCAGTGATGT GCCCCAGAGG CGCCAATGCA 360

CGCTGCAGCT CCCATCCTAC CTGACCATTT TTGCCAAACA ACAGAATATG CATCAGGTAC 420

GCTCCCTATA GTTTTGTTCA ATCCAGGATT GGTAGGCACC ACTCTTGACG TTGTTAATCC 480

ATTGTTGATT ATCCAGATAC CACTGCACGG TCTTGCGAAT ACCAGACTCA AAAGTCTCCT 540

CTGGCTGCCA ATCCAACGCA GCGCTCATCT TGCAAGCATC AATCGCATAT CGGCGATCGT 600

GTCCGGGGCG ATCCGCCACA TAAGTAATTT GATCGCGATA AGAGCCAGCT TTCGGTACCA 660

TCTCGTCAAG CAGATCACAA ATAGTATGTA CTACATCCAG GTTCTGCTTC TCGTTGTGAC 720

CGCCTATGTT ATAAGTCTCC CCGACCAAGC CAGTGGTCAC TACCTTGTAG AGTGCTCGTG 780

CATGATCTTC CACATACAAC CAGTCACGAA TTTGGTCACC TTTACCATAA ACCGGCAGCG 840

GCTTGCCATC CAGCGCATTG AGGATCACTA GCGGGATCAG CTTCTCGGGA AAGTGGTAAG 900

GGCCATAGTT GTTGGAGCAG TTAGTGACAA TGGTTGGCAG GCCGTACGTA CGGTACCAAG 960

CACGCACCAG ATGATCGCTG GAAGCCTTGG AGGCAGAATA GGGACTGCTA GGAGCGTAGG 1020

AGGTAGTTTC GGTAAAGAGC GGCAATGCCT CACCGGAGGC TACTTCATCC GGATGGGGCA 1080

GATCGCCATA TACTTCATCG GTAGAAATAT GGTGGAAGCG AAAGGCCGCC TTGCTCAACT 1140

CGCCCAGACT GCTCCAATAG GCGCGAGCCG CTTCCAGCAA TGTATAGGTG CCTACGATAT 1200

TGGTTTCGAT AAAGTCGGCT GGCCCTGTGA TAGAACGATC AACATGGCTT TCAGCAGCCA 1260

GATGCATCAC GGCATCTGGC TGGTGCAGAG CAAACACCCG ATCCAACTCA GCACGATTAC 1320

AGATATCAAC TTGTTCAAAC GAATAACGCT CACTTGACGA TACACTGGCC AAAGATTCCA 1380

AATTGCCAGC ATAGGTGAGT TTATCCAGAT TGATAACGGA GTCTCCAGTA TCACTAATGA 1440

TATGACGCAC CACGGCAGAG CCGANAAAAC CAGCACCGCC AGTAACGAGA ATCTTCATAT 1500

ATTTCGCTCT CTTATTTTAC AATTAATAGC TATTAAAAAT AAACTTGTTG ACTCCGATAT 1560

ATTAGAAATA TCGGGATACC GAACTAAATA TTTTTATATG CTTTTGCCAA GCAGACTCTA 1620

TATCCACCCT GTATCACTAT GCTTTCTGGC ATACAATATC CCATCATTGA CACAATGATA 1680

AACATATAAA TAAAGAAAAT TTTAAATCAT ATAACCAAAT TACTTTCATT TATTATCAAT 1740

AAGTATTTTG ATAAGAATAC CTATACCACA GGGAGCCCCC TGAAACATAA TATTAGCGAA 1800

NSDOCID: <WO_ 9822575A3_IA>

GAATGATAAC TGATAGTTAC CATCTTAGAG ATAAAAACTT ATTTGTGTGG CGGGATG 1857

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGCTCTTTCG TGTAAAATAA AATACAGCAT ATCCTATATA GCTTACAATC ATTAAATGAA 60

GTCGCCAATA TTTATATGTT TTATCAATAT CAGCTTGACT CATTGTTATT TCTTTGTCAG 120

GAGACTCTGA AAATATGGAC ATATATAACC TCTTTTATTA TGAAATATTT TCAATAATAA 180

TAATCCGTTA GTAATCCTAT CATAGGGTAA TGTCTCATCA TGTTAAAATG ATCACATTTA 240

TAATCATGTC AAAAAGAACA ACAGAAAAAA TCATATAAAA TCAATTAAAT ATAATTGCCA 300

CATATTGTTG TTATTWAAAC ATTGGTGGTG AATTTAAAGC GAGAACAGTT TGTAACAGTG 360

ACTCCTTGCA GACTAAGTTA GAGTCTCCTT CTAAAATTAG ACGGWKTTCT ATTGATGGAT 420

AATAGTAAGC GCACCGTGAA KGACGTGGGG TAAAAATTAG TTTACAGATT GAGTGACATT 480

CCAGGGCAAC AACTCTTTCA CGCGGTTGGC AGGCCAGGTG TTGATTACAC TGATCACGTG 540

GCGTACATTA CCGGACTCGA TTCCGTTAAG TTTGCAGCTA CCGATCAGGC TGTACATCAC 600

TGCCGCACTC TCGCCTCCAC CATCAGAGCC GAAGAACATG TAGTTACGCC GCCCCAGTGC 660

AATACCCGGA GGCGTTTTCA CACAGGTTAT TGTCGATCTC CACCCAGCCA TTGCGGCAGT 720

ATTCGTTCAG AGCGTCCCAT TGCTTCAGCA GATAGGTGAA CGCTTTCGCT GTATCCGAGT 780

GGCGCGACAG TGCTCATCTG CCCCTGGAGC CACTCATACA ACGACTGCAT TAGCGGTACC 840

GTTCTGGCTT TTCTGACCGC CAGTCGCTCT TCTGCCGGAC TGCCGCGGAT CTCAGCCTCG 900

ATAGCGTACA GTTCACCGAT ACGCTGCAGG GCTTCCGTGG TGATGTCAGG TGGCGCTCTT 960

GCATGCACAT CGTGGATTTT TCTCCGGGCA TGGGCCATAC AAGCCGCTTC GGTTACCTGA 1020

CCGCTTTCGT AAAGAGCATT GTAACCCGCA TATGCATCGG CCTGCAGGAT ACCTCTGTAG 1080

TCCGCCAGAT GTTGCTGTGG GTGGATGCCT TTGCGGTCGG GAGAGTAT 1128

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTTTGCTTAC GAACCGTGAA ATATGACGGT CCCATATAAC TGCCTGATAC TTGTATATCA 60

TATACTTGTG CATGCATGTC ATCATTAAAA AGTACTTTGT CACCGTCTTT AAGTTGAAGA 120

CGTGTAAAAT CTTTATACGG CAAGTAGACG GAAAACGGGC GCTTTCCCTG TCGCCAATCA 180

CACCGACATG ACTGACTTTT GCGAGAGGAA GTGCATAATT CACCAATTCA GAGCCTAATG 240

CATTGCGCTG GGTAAGCTCA AATCGGAATG GGTTTCGAAC CTTTCCCGCA ACATTGATCA 300

TTGGACCTTG TTGCTCAACT GAAAATCACA TCTTGATCTT TTAATGCCAG CTTCGGGAGT 360

TTCCCATACC GTATGAAATC ATAAAGATCA ATTTGCKGTG NTTACTGCTA TTTTGTGCGT 420

GAACACCTTA ATTTTTGCG 439

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TATTCGTAAT TAGTTATAAA CAGATGATGT AAACACCAGT TGACTAGAGT CAATCTTATA 60

CTGGCAACAT CTATGATTAA TTTGTGTGGT TATAATTTTA AATATCTTAT ATTTATGGGC 120

TATTATTGAT ATCTGTCAGA GTATCAATAA TAGAAGGTAA TTGTTTTACA TACTATCAAC 180

TTTTGGATAA CGTTTTAAAA TGCACCTTGC ACATCGTATT TTATTATTTT CACTAATCTT 240

TTTTATAACG GCCTGCGCAC ATGATCCAAA ACAAGTTGAA GCCTCTCGTC CATTGGTAAC 300

AGCGATTAAT TCTTCTTATT CTCTTATTCC TGAAGATTTG CAGGCACCAT TAAATAACCA 360

AGATCAAGGC ACGACATTCA ACAAAAATGG CGTAATTTAT ACTATTGAGG AAAGGTATAT 420

ATCGGCTTTA GGTTCTCAAT GCATAAAGTT AAGTTATGCG ATGAATAAAA ATTATTCAAA 480

GCGAAGTGTT GTATGTAAAG AGAATAACAA GTGGTATCAA GTACCTCAGT TGGAACAAAC 540

ATCAGTTAGC ACTTTGCTTA TTGAAGAATA AAGTTGAAGG TAGACGGTTA GAAAATAATG 600

AAAATTTCGC AACTTAGCAC TCTTCTCTTT CTTATTTCTG CATCAGCATT CGCCGCAATA 660

GAGCAAAATC AATCTAATGG TTCACATTTA GATTATGATC TTGCTGCCTC GACAGGAGAG 720

TCTCGGAAAA TGCTAGCAGA CATCACTGGA CAGCCTAATA CAACCTCCAC AACAGGAAGC 780

TTCACACAAC AGAATCGTAA TGGGATGTTG CTTCCAGGAG AGTCAGATGT ACGAAAATTA 840

CTGCCGCAAT CTGAAGCAGG CTTACCTCCT CCGTATGGTG CTAATTTATT TGCCGGAGGC 900

TATGAA 906

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

NSDOCID <WO_ 9822575A3 IA>

(A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGGCCTGAT ATATGCCGTT ATTACAAAAA GAGGATCAAC CACACTGCCT TTTGGACCGT 60

GTTTAAGTCT GGGCGGTATA GCAACACTTT ATCTACAGGC ATTGTTTTAA TGATAACCAC 120

GTCATTATCA AAGTGACATT TTAACTCTTA TTAATAACCT TAGAGATTAT TTACCATGTC 180

GATAAAACAA ATGCCAGGGA GGGTATTAAT ATCGCTATTG TTGAGCGTTA CAGGATTATT 240

AAGTGGCTGT GCCAGCCATA ATGAAAATGC CAGTTTACTG GCGAAAAAAC AGGCGCAAAA 300

TATCAGCCAA AACCTGCCGA TTAAATCTGC GGGATATACC TTAGTGCTGG CGCAAAGTAG 360

TGGCACGACG GTAAAAATGA CCATTATCAG CGAATCGGGT ACTCAGACCA CGCAGACACC 420

TGACGCCTTT TTAACCAGCT ATCAACGACA AATGTGCGCT GACCCAACGG TGAAATTAAT 480

GATCACCGAG GGAATTAATT ACAGCATAAC GATTAATGAT ACACGTACAG GTAACCAGTA 540

TCAGCGGAAA CTGGATCGTA CCACCTGTGG AATAGTCAAA GCATAACGTC GGGTAGATAT 600

AAATTGGCGC GGGTTGTTTT TCGTGACGCA CGAATTTATC TCATTCAATG GCTGACAAAA 660

ATTCGTCACA CTCTTAACCA GAGACAATCT CTTAATACAG ACAAAGAGCA TCTGCGCAAA 720

ATTGCACGCG GGATGTTCTG GCTGATGCTG CTTATTATTT CTGCAAAAGT GGCGCATTCA 780

CTCTGGCGCT ATTTCTCCTT TTCTGCGGAA TATACGGCGG TTTCCCCATC GGCGAATAAA 840

CCGCTCCGTG CGRATGCAAA AGCGTTCGAT AAAAATGACG TGCAATTAAT CAGCCAGCAA 900

AACTGGTTTG GCAAATATCA GCCCGTCGCC ACGCCGGTAA AACAACCCGA ACCTGCACCT 960

GTGGCCGAAA CGCGTCTTRR TGTGGTGTTG CGTGGGATCG CCTTTGGTGC CAGACCCGGC 1020

GCGGTTATTG AAGAAGGTGG TAAACAGCAG GTCTATTTGC AGGGTGAACG CTTGGCTCGC 1080

ACAACGCAGT GATTGAGGAA ATCAACCGCG ACCATGTGAT NTGCGCTATC AGGGAAAAAT 1140

AGAGCGCCTG AGCCTGGCTG AAGAGGAGCG TTCCACCGTT GCCGCGACCA ACAAAAAAGC 1200

TGTCAGTGAC GAAGCAAAGC AAGCTGTTGC TGAACCTGCT GTCAGTGCGC CAGTTGAGAT 1260

CCCNGCTGCC GTGCGTCAGG CACTGGCGAA AGATCCGCAG AAAATTTTTA ACTATATCCA 1320

GCTTACGCCT GTGCGTAAGG AAGGGATTGT CGGTTATGCA GTGAAACCGG GGGCAGATCG 1380

TTCTCTGTTC GATGC 1395

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

INSDOCID <WO_ 9822575A3 IA>

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CACTTGAATA AAACTGACAC CGTTTACCTC CATAATAGTG AGCATAGCCG CCATTGCGGC 60

CTGATCGGCG AACCGGAAAT CGCAACCTGC GAACGACAAC CGAACCGGCA AGCGTGCGGG 120

AAGGACGGAT ACCGGACTCT TTCGCCACTT CAGCAATCAC CGGCAGCGTG GAAAAAACAA 180

TAAACCCAGT ACCGGCCATA ATGGTCATAG ACCAGGTGAT AATCGGCGCG ATTATGTTGA 240

TATATTTCGG GTTACGCCGC ATAAAATTAC CAGCGACGGT ACCAGATAAT CCATTCCCCT 300

GCGGCCTGTA AGGCTGAGGC CGCCACAACA ACGGTCATAA TAATCAGGAT CACGTCGACT 360

GGCGGCGACC CCATAGGCAG 380

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTTTACGGTT TAATAGGGGA ANGCCGACTG GATGNAAAAA TGGAATCTGG AGCCCAGAAT 60

AAATCTGAAT TTAATGTGGA CTGGATATGC TCCAATAACC CCGGCAGGGA GTCATCTGTG 120

CGAAGATATT TGCGTTATGC TGTAATATAA TAATTCAATG TATTTCAGGA ACAGTAATAT 180

ACTACAGTTT CTACTTTCTT GTATTTAATA AATTGTTCCG CATCGCTAAA AGCAGGTCTT 240

TCAGAAGCCA CAAGAATTCT GTGGTCCCAG TATTTTTAGT TATCCTATTT TTATATCTAA 300

CTTGTAATAC TTACAGCATT TTCATTCATC CTAATGGAAG GCTGTAATAA TCTTTGAGCT 360

TAGAAACATC AAAATTATGC ATCTCATTAA TTTTGTCAGT CACACGACCT CTGGTAAAAA 420

TAAAACCCCC AGAAATATGC CATTTCTAGG GGGGGCGTAA GAATCAATAT ATTTTAGTGT 480

TGTTACATTT AGCTCTTAGC TCTTAGCTCT TAGCTCTTAG CTCTTAGCTC TTAGCGTTTG 540

TAGTTTCATC GCAATGAGTA AAAGGACAAC AAGAATAAGT GATAACGTTA AGAGAAGAGC 600

ATAGAAACCA TTCCAGTGGT ATATTTCTAT TATTTTAGAC AATGGATAGC CAGCCGCGGA 660

CGCACCAAGA TATGCGAATA AACTAACAAA ACCAGTAGAA GCACCAGATG CATATTTATG 720

TGAGTTTTCA GCAGCTGCCA TTGCGATCAG AAATTGTGGC CCAAAGATAA AGAAGCCAGT 780

GATGAAAAAT AATAACGAAA AAACATATTT ACTATCAATA GAAACCAACC ATAGACATGC 840

AGAAGCAATG ATTATACCAA TTGTATAAAT AACATTCATT TGAGAGCGAT TGCCCTTAAA 900

CAGAATATCT GATCCCCATC CAGCTACGAT AGCACCAAAA AAGCCTCCAA CCTCAAACAT 960

NSDOCID: <WO_ 9822575A3 IA>

CATTACTGTT GCATTTGCTG TTAGCAAGTC ATATT 995

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TAAAAGCGAC TCCATGTGAA ATTTCTGTTT GTCGTTTTTT CCCCGTTGTA GCGGCTCTGC 60

TCCTGGCTTC CCTGATAGTC AGCCCGCAGG CGCCAGGGCC CCAGATTCCC CCCCACAGTC 120

CCGTTATAAC TGAACTGATG AGAGTCTCCT CCCTGATAAT TACGGGAAAC CGTCCCGTTG 180

AGGTTATAAT CCAGCATCAG TCCGGGAATG CCGTCGTCCC AGCGTGAGGG AGGCAGCCAG 240

GTGGCATCAG AATACTCAAG CCAGGCCTGC GGCATATTGA TGCGTAATAC GCCCGCTCCG 300

GTATCAGGAC GAATATCCAC TCCCGGCAAC CCATGAAAAT CCGCACACTG ACCATCATGC 360

CAGTAAACAA CTTTATCCAG AGATTCTGCT GTTAACCCCA TCAGTCTGAC CATATCTGAT 420

GTCAGACAGC TGCGGCAATT TTTTTTCTGC CTTATCTCCT GACAACGCAG GTTCAACAAA 480

TGAMATCTGT AACGATGCGG GAGAAATACT TTGCCCGTTA ACAATCACAT CCAGAAGATA 540

TTGCCCCGGC AGAACATAGC CGGCTTCTGA AAAACGGGTG AAGTCAATAT TTTTCTTGTC 600

CGCTGCGTCA AGTACATCTG TATTAAACTC AACGGCACTG GCTGCGTTAC AAAACAGAGA 660

CAACAATATC ACACAGGTAA TATTGTTGAC TGCAAAAGGT ATTCTGTCTT TCATTCCACG 720

CATCACCAGA TTCACAAAAA AGATAAATAA CCGGACATCT CACCGGAGTG ACTCACTCAT 780

AATCGACCCG GAATCCCAGC ACAGCAAAAT AATTTCC 817

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 709 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTTTTGTCAG AGCGTTCACT CTCTGGCTGG ATGATTTCGG CTCGGGAAAT GCAGGCTTAA 60

TGTGGGGACT GTCGGGGATG TTTGAACGGG TAAAAATAAG TCATGAGTTT TTTCATTATG 120

TCCTGAAAAA CGGGTGTGCA ATGCCACTTC TCCGTGCTGT GGCAGACACT GTTGCCTGTC 180

ACAACAGAGG CGTGATACTC GAAGGTGTTG AAAATGAAGC GTTGTTCCGT ATTGCCAGAG 240

ACATGAATGT CCAGGGCTGT CAGGGATGGC TCTACAGGCG TGTGGGGGTT GATGAATTAT 300

NSDOCID <WO__9822575A3_IA>

CCGCGCTTAT TCAGCAGTAT GAATAATCCT TTTTCACAGA CTGGTCAGCT GTCAACATTT 360

ATGTTTTTTT ATCTGCGGGA ATTTATCCGT CTGCCTGTCG GGACTACTCT GTCATACAGA 420

AATCAGGCCA GAATAAATTG TTGTGGAAAG GTGAGATTTA CCGGATGACT GATGTGCTCT 480

TGTGCACAGG TATACAGGCA GTGTGTTTCC AGTATATGGA AAATGATTAA ATGAATAACA 540

CAGACTTATT AGAAAAAATC ATCAGGCATC AACAAAACAA AGATCCTGCA TATCCTTTCC 600

GGGAACATCT TTTGATGCAA CTCTGTATCC GTGTAAACAA AAAAATACAG AACAGTACAT 660

CTGAGTTTTT TGGTGCATAT GGTATAAATC ACTCAGTATA TATGGTTCT 709

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TCATCAAGGG ACGGGGCATA TCTGGATGCG ACAGGGCAAA CCAACCACTG AGAATCCAAC 60

CTGCCAAAGC CTGACCAGGA AGTCCGACGT TAAAGAAACC AGCTCGACTG GCAACGGCAA 120

AACCAAGACC AATCAAGACC AGAGGACCCA TAGCACGGAA GATTTCTCCA ATCCCACGCA 180

GACTGCCAAA GGCTGTATAG AACAATTCTT CGTAGCCCCA AATAGCATCA TAACCGAAGA 240

TCCACATGAC AATGGCTCCG AGTAAAATTC CTAGGAATAC AGAAATCAAG GGAACCGAAA 300

TTTGTTGTAA TTTTTTAGAC ATCACTCTTC TCCTTTCCCA AGTTYCCACC AGCCATCAAG 360

ACACCAAGTT CTTGTTTATT GGTTGTTTCT GGTGATACAA TACCTTGAAT CTTACCATCG 420

TGGATAACGG CAATACGGTC TGAGACGTTT AAAATCTCAT CCAATTCAAA GCTGACNACA 480

AGGAC 485

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

AGCAGAATAG GCAACATCAC CACGCCGACA AACAGCGAGA AGAGAATGAC GCCAGCCGCC 60

AGGAACACCA GCTCATAGCG CGCCGGGAAG ACGTTACCAT CCGGCAAGAG CAGCGGGATA 120

GAGAGCACAC CGGCCAGAGT GATCGCCCCA CGCACCCCGG CGAAAGACGC GATCAGGATT 180

TCTCGTGTGG TCCACGAACC AAACTCCATC GGCTTCTTCT TCAGGAAGCG GTTGCTGAAC 240

NSDOCID: <WO 9822575A3_IA>

TTTTTCATCG TCCACAGCCA GCCGAAACGG ACCAGCATCA GCGCCGCATA TATCAGAATA 300

ATATTGGTAA ACAGCATCCA GATTTCGACG TTAGGGTCGA TTTCTTGCTG GCCATCAGCG 360

GACGTCTTCC AGRATTACCC GGCAGCTGCA GACCTTAACA GCAGGGAACA CCATGGCCGT 420

TTTAAGGACA ATTTCNAGCA TCGGCCCANG TGCTGTTTT 459

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTAATAGCAC TAATACTGTC CTGCTCTATT CCGCTGACAT TTTCAGTCAG CTGCTGTATG 60

GGATGGGTTA CCCAAAACCA GACCAGCATA CCTGACAAGA GACCGCATAT CACTACCAGA 120

AACAGCGACC AGTACAGTGC ATTCCATAGT GCCTTTGTCC AGGCTGTATC AGTAAGAGCA 180

TTAAGTTCCT CTCCCTGTAA AATAATATAC AGATATCCTT TCGGTTCATC ACTCTGGTAA 240

AGCGGTGCGG TACTGAAAAC TTTTTGCTTA TTTACACTTC GGGGATCATC ACCATATACG 300

GGCCAGACAC TGCCGGAGAG AAATTTTTTC AACGGTGCAA TATTGATATA CCGGCGTTTG 360

AGATGACCCG GAGGGCGGCC TCCACAAGCA GTCGCCCTTC CGGTGAAACC ATATACAGCT 420

CCACACTGGG ATTAAGCGTC ATCAGACGCT CAAACAGACT CGTTAATGTC CGGTGTTACC 480

AGACAAAACA AGCATCGCAA GACGCCACAA ACGGTGCGCT TACTTAAATA AGCCGGTTAC 540

AGGTGAAAAA TCACGTCCTG ATATTCAAAT GTTTTTTCAG GTCATATTTT AGCAGGACAC 600

TACCAGCACC TAACAGCAGC ACATCTTTTA TAACAAAACT GTCAACTTTC CCCAGTTGTG 660

GTAACAGGCT GAGCGTGGTT ATTCCTGTAA CAATAACGAT AATATCTCCC AGTACACCAG 720

CAGCAGGCCT GAAGAAACCG ATAATCAATG CCAGAAATGT GATAGTTTCC ACTATGCCGA 780

GGAAATAGCT CCCTCCATGA ATACCAAATA TAATATACAG GATATTCAGC CAGGTGGGAT 840

ATATCAGGGG CTTGAGAGCC ATAACTTCAA AATCAAACCA TTTATAAGTC CCAAAAAGCA 900

TAAATATT 908

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1057 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

NSDOCID <WO 9822575A3 IA>

CGGGCTAACC CAATATGCTT TATTAACCCG GGATAATTAC CCTGTTGCAT ATTGTAGTTG 60

GGCTAATTTA AGTTTAGAAA ATGAAATNAA ATATCTTAAT GATGTTACTT CATTAGTCGC 120

AGAAGACTGG ACTTCTGGTG ATCGTAAATG GTTCATTGAC TGGATTGCTC CTTTCGGGGA 180

TAACGGTGCC CTGTACAAAT ATATGCGAAA AAAATTCCCT GATGAACTAT TCAGAGCCAT 240

CAGGGTGGAT CCCAAAACTC ATGTTGGTAA AGTATCAGAA TTTCACGGAG GTAAAATTGA 300

TAAACAGTTA GCGAATAAAA TTTTTAAACA ATATCACCAC GAGTTAATAA CTGAAGTAAA 360

AAACAAGTCA GATTTCAATT TTTCATTAAC AGGTTAAGAG GTAATTAAAT GCCAACAATA 420

ACCGCTGCAC AAATTAAAAG CACACTGCAG TCTGCAAAGC AATCCGCTGC AAATAAATTG 480

CACTCAGCAG GACAAAGCAC GAAAGATGCA TTAAAAAAAG CAGCAGAGCA AACCCGCAAT 540

GCGGAAAACA GACTCATTTT ACTTATCCCT AAAGATTATA AAGGGCAGGG TTCAAGCCTT 600

AATGACCTTG TCAGGACGGC AGATGAACTG GGAATTGAAG TCCAGTATGA TGAAAAGAAT 660

GGCACGGCAA TTACTAAACA GGTATTCGGC ACAGCAGAGA AACTCATTGG CCTCACCGAA 720

CGGGGAGTGA CTATCTTTGC ACCACAATTA GACAAATTAC TGCAAAAGTA TCAAAAAGCG 780

GGTAATAAAT TAGGCGGCAG TGCTGAAAAT ATAGGTGATA ACTTAGGAAA GGCAGGCAGT 840

GTACTGTCAA CGTTTCAAAA TTTTCTGGGT ACTGCACTTT CCTCAATGAA AATAGACGAA 900

CTGATAAAGA AACAAAAATC TGGTGGCAAT GTCAGTTCTT CTGAACTGGG CAAAAGCGAG 960

TATTGAGCTA ATCAACCAAC TCGTGGGACA CAGCTGGCCA GCCTTTAATA ATAATGTTNA 1020

ACTCATTTTC TCAACAACTC AATAAGCTGG GGAAGTG 1057

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TACCGGGCCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT TCCTGCAGCC 60

CGGGGGATCC ACTAGTTCTA GAGCGGCCGC CACCGCGGTG GAGCTCCAGC TTTTGTTCCC 120

TTTAGTGAGG GTTAATTTCG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 180

ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT 240

GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 300

AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 360

GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC 420

GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG 480

JSDOCID <WO 9822575A3 IA>

GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA 540

AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCT GACGAGCATC ACAAAAATCG 600

ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC 660

TGGAAGCTCC CTCGTGCGCT CTCCTGTTTC CGACCCTGCC GCTTTACCGG ATANCTGTNC 720

GGCTTTCTCC CTTCGGGAAG CGTGGCGCTT TC 752

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTTGGGTAAT NGACCTCATA TCCCTCCGCC AAAAAAGGAT CTACATGCGA TTTTGCGAAG 60

CCAGCGTTGA TTGTAGGCGA GAGAATGGTT CTGTTGTTTT GGTACATTTC AGTTGTCATG 120

GATTTCACAA ATGTAGCATG ACCTTTCACC TGTCCAAGAG ACTGCAACAC CATCTGTCCA 180

AAACAATAAA TAGGAATCAA ACAGGCTACC AACATCAACA AGTATCCCAA TAAGGCTCGT 240

AGTTTAGTCC TTGACATGAC GCCCCTCCAA TTGCTTTTCT AGTCCTTTGA CAATCCGTCG 300

ATTACGATAC ACGCGATACA GCAAGAGAAG GATGACCGCC ATCGCTCCTA GTAATAACCA 360

CAACCAGAAT TGCCCACGCT CTCTCACCGC TCGATTCCGC TCTGCAATTG GTGCCGTATA 420

CGGAATCCGC TTCCCACGTA CCAACAGACG ATGACTGTTA ATCCTATACG GTGTACNAGT 480

CAACCA 486

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTACGCNTTC AACCAGGTCT TCTGGTTTAC CAACGCCCAT CAGGTAACGC GGTTTGTCTG 60

CCGGAATTTG CGGGCATACA TGCTCCAGAA TGCGGTGCAT ATCTGCTTTC GGCTCACCCA 120

CAGCCAGACC GCCGACAGCG TACCATCAAA ACCGATATCT ACCAGACCTT TAACAGAAAT 180

ATCACGTAAA TCTTCGTAAA CGCTGCCCTG GATGATACCA AACAGCGCAT TTTTGTTTCC 240

GAGACTGTCA AAACGCTCAC GGCTACGTCG CCCAACGCAG AGACATCTCC ATGGAGCGTT 300

TTGCGTAATC CCA 313

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CGGAAATCCC AGTAATTCCA TCCTCANATA TTCCACTCAN CCTCACTGTA ACAAAGTTTC 60

TTCGAATAAT AAAAATCATG CTTTCTGTTA TCAACGGAAA GGTATTTTTA TTCTCTGTGT 120

TTGCTTTATT TGTGAAATTT AGTGAATTTG CTTTTTGTTG GCTTTATNTG ATGTGTGTCA 180

CATTTTGTGT GTTATTTTTC TGTGAAAAGA AAGTCCGTAA AAATGCATTT AGACGATCTT 240

TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA GTGCATTCTT TTTGTTGGTG 300

TTTTATTCTA GTTTGATTTT GTTTTGTGGG TTAAAAGATC GTTTAAATCA ATATTTACAA 360

CATAAAAMMC TAAATTTAAC TTATTGCGTG AAGAGTATTT CCGGGCCGGA AGCATATATC 420

CAGGGGCCCG ACAGAAGGGG GAAACATGGC GCATCATGAA GTCATCAGTC GGTCAGGAAA 480

TGCGTTTTTG CTGAATATAC GCGAGAGCGT ACTGTTGCCC GGCTCTATGT CTGAAATGCA 540

TTTTTTTTTA CTGATAGGTA TTTCTTCTAT TCACAGTGAC AGGGTCATTC TGGCTATGAA 600

GGACTATCTG GTAGGTGGGC ATCCCGTAAG GAGGTCTGCG AGAAATACCA GATGAATAAT 660

GGGTATTTCA GTACAACACT GGGGAGACTT ATACGGCTGA ATGCTCTTGC AGCAAGGCTT 720

GCACCTTATT ATACAGATGA GTCGTCGGCA TTTGACTAAA TTATGGCATT CCGGAGTTTC 780

TGGAAGATAA AAAAAGAAGC CCTTATCAGA AAGCAGACAG GTTATATCAG TATTCTGTCG 840

ATAAATAACC TGCCCTGAAA ATACGAGAAT ATTATTTGTA TTGATCTGGT TATTAAAGGT 900

AATCGGGTCA TTTTAAATTG CCAGATATCT CTGGTGTGTT CAGTAATGAA AAAGAGGTTG 960

TTATTTATGA TTAAGTCGGT TATTGCCGGT GCGGTRCTAT GGCAGTGGTG TCTTTTGGTG 1020

TAAATGCTGC TCCAACTATT CCACAGGGGC AGGGTAAAGT AACTTTTAAC GGAACTGTTG 1080

TTGATGCTCC ATGCAGCATT TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC 1140

TTTCAAAAAG CTTCCTTGAG GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT 1200

TGGTTAATTG TGATATTACT GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA 1260

AGCTGGCTTT TACTGGCCCG ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG 1320

GTACGGGCAC AGCTATCGTA GTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG 1380

AAGTGATGCT AATACCCTGA AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTTAA 1440

GAAGTCGTCA GCCGTTGGTG CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT 1500

CAACCTGACT TATCAGTAAT ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATTCCGCTG 1560

TTTATTTCTC AGGGTATTTA TCATGAGACT GCGATTCTCT GTTCCACTTT TCT 1613

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

NTAGTCCATG GCCCCATGGA GCGAANTCCA AAGTGTGGAT ATTGTCGTTT TAATTCATCC 60

CAAAAGCTGA AATACGCCAA AACCCACGTT CCCTAACATT GGTATCATGC ATAATGACCA 120

CAGCCNTTCA GAAAGCTTTG GCAACCAGCT TTCAAAATCA TGGGTACCGC TTCAAACGTA 180

TGCAAACCAT CAATATGAAG CAGATCAATG CTACCTTGTG AAAAATGCTC TAACGCTTGG 240

TCAAATGTAC TGCGAATGAG AGTAGAAAAA CCTGAATAGT GCTGTTGATT ATATTCTGAT 300

ACTTGCCTGT AAACTTCTTC GCCATACAGC CCCGCATGTT CATCTCCCCC CCAGGTATCA 360

ACGGCAAAGC AGCATGTTTC TAAATCTAGT TTAGAGACTG CTTGGCAAAA TGAGAAATAA 420

GAACTTCCAT AATGAGTTCC CAGCTCAACA ATATTTCTTG GCCGCAGTGT GTCAACTAAC 480

CAGAAAGCAA AAGGAATGTG TTCTAGCCAA GCAGATTGTG CAAGGTATGT AGGACACCAN 540

AAAAGAGATG GTTTGAAAAT GAAATTCAAT TCCCTGCCAA TATCAGTGAT GGGATATAAC 600

TCACGATTCT CTACTAACTG ACTAATTTTT TGACTATCCA TTGAGGAAAA CTCACATGTA 660

TTTATAGAAT TAAATCAAGA AACCTGAAAA TACCTATAGT GCGGTAACTT ATTAACTAAC 720

ATTTAAATAT TAACAATACA CTTGGAAATA TTAGTTAAAA ATAAATCATT ATGATTTCTC 780

ATCAATCCTG GTGCTCACGC AAAGTTGCCA GCCCCATAAT AATAAGACCA TAGAACAAGC 840

AAAGTAATAC ACCCACAGTC GCAAGATTAT AGAATCGCCG TGGATATTCG GCATCTTCCG 900

CTAAAGTTGG TTGGGTAATA ACCAATAGAT 930

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ACGATATCCC CCCTCTGCTT TTGAGAGGCA ATCTGCTTTA ATACATGATT CATCACAACA 60

CCTCTTGCTG CGCTTTGATC TTAATTTTAT ATTTTTGGGT AGGGAAAAGT AATTGCCCCT 120

GATACGGCTC ACCATTTACC AACGTTTCAC AGCTATGTTC CAGAGCTAAA TTAAGACCTG 180

3NSDOCID <WO 9822575A3 IA>

GTAGAATATC CCAGCAATTC ACCCCTTTGA CATTTTCAAA GCTGTCATAA GCACCGGNNA 240

AGGGGGGGCC AACATGTTAT ACATGGAGCA GCCAATGATA CGATATTCAA AGCCCTCTTC 300

CAGTTGCATC AGATCCTGCT TGGTAASGGA GGAAGAGAGG CCACGAATAC GAGAGCGATG 360

ATGTGTAATC GGCATACCTG TGATATGAAG ATCATTCAAT TCAGGTAAGA AGATGCAGGA 420

CTCTTGATGT TTCCCCTCGG TGTAAATGCT GATACCAATG CCCCACTCTT TGAGCCCAGA 480

GACAAAGTTT TCTGTGCCAT CAATTGGATC TAGAACAATG TAAGAACCTT TGGGATTCCA 540

CTCAATATCT CCTAAAGGGG CTAATTCCTC TGAAATTAGC ACATGCCCTG GTAGATGCTT 600

TCTACAGAGT TCGAAAACTA TATCTTGAAC TTTTAGATCC AGTACTGCGG CCGCGATCC 659

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCGGATATA CATCAGGAGA AATTGGAGCA GCAATTGGAT GCGCCATTAA TGCCTGGTTA 60

GGGATCCCCG CATGTGGGCA CGCAAATGGC TCAGAATATG ATCGACCTTC ACCAGATAAA 120

CCAAATCTGA GCGAACCATT TATCCCAAGA CCCACGTATG ACGCTTCACT TCATTCCTGG 180

CATGGCGGAT ACTGAGTAAA TCATCCTGAA TCATTATGTT CAACATCATC AATTCTCCGG 240

ACTTGTTGTC AGATGTCCGG AGAATATTAA CCTTTTCTTC AGAAACAGAW TGATCAAGAA 300

TCACACTCCT TCTTTAAGAG GATTTTATCC AGAAAACTGA CTTTCTTCTA TCAAAATMAC 360

AGTATCCTGT TTTATCAGGA ATAATCTTTA CCTCCGGTAT CATTCCCATA ATCAGATATC 420

AGAAAAATGT GCCAGTAATT TTTTACTGAT GACTTCAAAC ATTTCACATT CATCACACGT 480

CAGATTACTC CAAAGTTCTT TCAGATATGT GTTCTGCGCC AGAGTGAGTC TCTGAATAAA 540

AAACATACCT TCAGAC 556

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TACCTGTTTG TGGAATTTGA CCCAGAAGTG ATTCATACCA CGACTATCAA CGCGACCCGN 60

GTGTNCAGCC ACTTCGTGCG CTTTGGCGTN CGCAGCGATA GTCCCATCGG CGGTTATTCA 120

TCAGCTATCG GTATATAAAC CGAAAGACAT TGTCGATTCC GGCAACCCCT TATCCGGGTG 180

ATAAGGTGAT TATTACCGAA GCGCGTTCGA AGGCTTTCAG GCCATTTTCA CCGAACCCGA 240

TGGTGAGGCT CGCTCCATGC TATTGCTTAA TCTTATTAAT AAAGAGATTA AGCACAGTGT 300

GAAGAATACC GAGTTCCGCA AACTCTAAAA CGCAATCCCA AACAGTGTTT TGACATTAGC 360

ATCCGTGGTG GCAGCCAGCC ATGCGGCATC TTCTCCACGC CAGTGCGCAA TACGTTGCAA 420

AATATGGGGC AGATGGGCTG GCTCGTTGCG CCGGGATGAN GGCTTTGGCG TGAGATCGCG 480

AGGGAGCAGA TACGGNGCAT CAG 503

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTTAACATCA AAATTACCTG CAGCTGAAAT GATTTTGCTG ATTTCATTAA TTAATGGATT 60

AAGATTACCC TGACTTCCAT AGGCTAATGC ATCATTCCCA TACACATAAC TTGCCTTATT 120

ATTACTCTGT TGATACTNAA GTGCCTTTTT AAGGGAATCT GGTGTGATTA CCCTGCCGTC 180

TTTATCAAAA ATCTGCTCTA TCTGGTGATT AGAGATATCA CCTGACTCTT TTTCAAACCA 240

GTTTTTAAAT GTAATACCAT TTTTGTGGCC AATGGAAAGA ACATTACCTT CAGCTTTATA 300

CATGATGAGG TCATTACCTT CTCGCCTGAA GGCCACATCC CGGAAATCAA TATCAGCCAA 360

ACTGAGTTTA TCGTCTTTCC CCCCATCATC GTCAATAATA TGATGGCCAT ATCCTGAAAG 420

ATAACGATAA ATA 433

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCGCTCTGTT CCCGTTCCTG TTCATCACCA TCGCCTGTGG TGCGGTATCT GGCTTCCACG 60

CGCTGATCTC TTCCGGTACG ACGCCAAAAC TGCTGGCTAA TGAAACCGAC GCGCGTTTCA 120

TCGGCTACGG CGCAATGCTG ATGGAGTCCT TCGTGGCGAT TATGGCGCTG GTTGCTGCGT 180

CCATCATCGA ACCGGGTCTT TACTTCGCGA TGAACACCCC GCCTGCTGGC CTTGGCATCA 240

CCATGCCTAA CCTGCATGAA ATGGGGTGGC GAGAACGCGN CGGATTCATC ATGGCGCANT 300

GA 302

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTAATAAG CCAAATACTA CATCACGTAA TACTTGCAAA GAAGTGCGTG GAGTTTGACT 60

AATAATGGGT TTGTCCATTA ATACTTACCC AAATAATCGG CTCATTATAG CAACGAGCCT 120

CCGATTAAAA TTTAAAATAC TCAATCATTT AATAGCAACG TTAGCAGCTA CAGCGATTTG 180

ATAAATAATT TGTGTGATAT CTTTAAATGA TTGCATGGTT TTGCTATCAA CCTGAGGTAG 240

AACCAATATC TGATCCCCCG GTTGTACTTT ACCTTGCCCT TTAAATTCTA CAAGACCATT 300

TGCATGTACA ATAGCAATTC GCTTGTCGTT AGCTCGCTCA GTAAAACCTC CGGCCCATGC 360

AACATAATCA TCCAAATTAG CATCGGCATT ATATACTACT GCTTGTGGCA TCAACACTTC 420

ACCCCCCACT TGAATAAGAT CAGTCTTATT TGGAATAACT ATTTGATCGC CTTGTTCTAA 480

TTGGATAWTG GCAATAACAC CTTTATCTGC AACTACTACT TTACCAAGCG GTKGAACTTT 540

ACGAGCCTTT YCAACAAACT GCATCACTAA CTCTGCTTCT TTAGCACGTA TATTCGCCTC 600

ACCATCAGAT CGCGCGGGTG TGGTAAANTT CATACGTTCC AAGCGGTTTA GAGATT 656

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATATGTTATC TGGATCCAGA TAAAGAGCGT TCTTGACCCG CTATATCCAG ACAGGTCAGT 60

TACACCCTGT CCGGAAAAAC TGATCGGAAT AACAACAGTA TATTTTCTAA TACACTGGCA 120

AATGGTGCCG GCGGTGTGGG GATTCAGCTT CTGGATAGCG CTGGTAATGC GGTTGCTGCT 180

GGACAGAAGA AATATCTGGG ACAGGTAGGA CCATCAACAT CTCTCAATAT TGGATTAAGG 240

GCATCTTATG CACTGACCAA TGGACAGACT CCACCTACTC CCGGACGAGT TCAGGCGTTA 300

GTTGATGTTA CCTTCGAGTA TAATTAGGAA TGTCGGGGAT GGGCTATCCC CGATATTATT 360

GCAGGATTAG TCTGTGATAC AGATATACAG CCCATATGAA CAACTGTTTG CATATATAAA 420

AATGATGATA ATTTTA 436

ISDOCID <WO__9822575A3 IA>

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AATAATTAAA TTTGGAGGGA TCAGTTTTCT GATAATGTTC TGTTATTAAA ACATTATCCC 60

ATGGGGCGTA GTTATATCAA TTAGCAGGAT CTTATGAGTT AACTAACATC AGTTTTGAAT 120

TTTTAATGGG GGTAATTTAT CTTTTACTAA AAATATTTTA ACTATTAATA TAGCATCATG 180

GTTGTTACGG TTTGTTTTAA TTCTATTTTA TAATGTGCTA TATATTGTAT TTTTGTGCTT 240

AGATAAATAT GTTTTTTCAT TACTTTAGTG ATGTTAATAT TTTGCGTGTA GTAAAAATCA 300

TTGTTATAAC AAATGTCACT GTTGCTATAC TTTGCTGAAC TGTTTATCGG TCATTTTGAT 360

TCAATCACTG GTTCTATATT TTTTAATAAC CGTTCTGTAG CGATTAATAT ATTGCTCTCC 420

AGAGGATACA CTATATGAAA TATATTAAAA GTCATTAATT TTNATTCAAT GTTGTTTAGA 480

GTTATGTTCA GTGTTTGGNA ATAGGATGTG TTTCTAAACC GTCTTGGGTT CTATAATAAA 540

TTCTATTCTT ANAGGTTTT 559

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CATGTCCCTT CCTGAATACT GGGGAGAAGA GCACGTATGG TGGGACGGCA GGGCTGCTTT 60

TCATGGTGAG GTTGTCAGAC CTGCCTGTAC TCTGGCGATG GAAGACGCCT GGCAGATTAT 120

TGATATGGGG GAAACCCCGG TACGGATTTA CAGAATGGTT TCTCCGGACC TGAAAGAAAA 180

TTCAGCCTCC GGCTCAGGAA TTGTGAATTT AACAGTCAGG GTGGGAACCT TTTCTCTGAT 240

TCCCGGATAA GGGTGACTTT CGATGGCGTC CGGGGTGAAA CGCCGGATAA GTTTAATTTA 300

TCCGGTCAGG CAAAAGGCAT TAATCTGCAG ATAGCTGATG TCAGGGGAAA TATTGCCCGG 360

GCAGGAAAAG TAATGCCTGC AATACCATTG ACGGGTAATG AAGAAGCGCT GGATTACACC 420

CTCAGAATTG TGAGAACGGA AAAAAACTTG AAGCCGGAAA TTATTTTGCT GTCTGGGATT 480

A 481

(2) INFORMATION FOR SEQ ID NO: 122:

3NSDOCID <WO 9822575A3 IA>

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

CCATATAGTG ACTTCATTGA ACAAAATGTA AATGGAATCT TGCTGGAGAA TGACCCACAT 60

ATATGGATAA AAGCTCTTTC ATTACTTGTT AGTGCAGATC ATAAACGTAG CGAGTTGGCG 120

TTCAATGCTA AAAAATATGC TTGTAAAATT GTAGGTGTCG AGTAAAAAGA TATTTTTATT 180

TAATTGGTGC TATTGAATGT TTAAAAATCG AACTGATTGG TGTTTTAATA TTAATCATAG 240

GTTATGATGC AAAAATATAT TAGGCATTGC CTGCTTCAAT TAACTTGAGA GTGTAAGTTG 300

AATTGAAATA TGGTTATATG ATAAAGCAAT ATATGTTAAT ACATATGTCA ACCGAAAATG 360

CCATTATGTG TTTTTTACTT TATCTGTAAC GACACAATAT ATAAAATAAG GCTAATAATC 420

AAAACGCTTT TTAATTTGAT TGTTTTGAAT CAAGTGACTA AGAAATTCTC TTGCTGCAAA 480

TAACTCCCTT AGTGATTTTT TTTGAGTCTA TTTTATTCTC TGGGCATGGT CATGC 535

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CCGGCCCCAT AATGATGGTT TTATTAAGGT TAGCGCCGAC GGTTTCGATG AACGATTTCA 60

GGTCGGTATC TTTAAAATTA GCGGTGAAAG TGGCTTCTTC CGCCCAGACC GGTGAACTGC 120

ATAATGCCGC TGCCAGCACC AGCGGCAGTA AACGCTTTTT TGTTTTGAGG CCAGTTGTCT 180

TCTTACGCCA GACCGACAAC GTCATATCAC GCCAAAACAC GATGAATGAT TCTCCTGGAT 240

TAAATGCGGT TAGCGCAGCG CGATGGAAAT GTCGTGGCGC GCACCCTTGC GTAAAACCGT 300

AAGTTGAATG GAATCCATTG AAGGTAACTG CCGCATCAGA GCAATCATTG CTCGTGGATC 360

AGTGAAATCC TGCTGATTTA GCGCAAATGC GATATCGCCT TCCTTAAAAC CG 412

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

NSDOCID: <WO__ 9822575A3_IA>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TAGCCTGTTC AGCGTATATT TGGGATGAGA AGCCAAAGTG GCTTTGGTGG TGTCCCAGCC 60

CAGGTTTTTA TTACTGCTGG TTATTTACCT TTCATGTTTT TCAATAAAGT TGTGACTCAG 120

TTGAAATCTG CTGTCAATGC TAATATGGGA CTTTTTTGTT ATAGACAAGT GACTCCTTTT 180

GCAACTTTTA TAGCACGTTT TATGCTAGAA ACAATGGTGG GCATGATTGT CGGTATAATC 240

CTAGTACTAG GATTATTGTG GTTTGGCTTT GATGCAATAC CTGCGGATCC ATTGCAAGTG 300

ATCCTTGGTT ATTCTCTTCT GATGCTGTTT TCTTTTTCTC TTGGTATTGT ATTTTGTGTT 360

ATTTGTAATT KRGCGARAGA GGCAGATAAA TTTCTTAGCT TGTTAATGAT GCCTTTGATG 420

TTTATCTCTT GTGTTATGTT TCCTCTTGCT ACTATTCCCC CTCAATATCA GCATTGGGTT 480

TTTATGGAAT CCACTTGTGC ATGCTGTAGA ACTAATCCGA AGGGCATGGG ATATCTGGGT 540

TATCGTAGTC CTGATGTAAG TTGGGCGTAT CTGTCG 576

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

TTACCAAGCA GGATCTGATG CAACTGGAAG AAGGCTTTGA ATATCGTATC ATTGGCTGCT 60

CCATGTATAA CATGTTGGCC GCCGTACGCG GTGCCTATGA CAGCTTTGAA AATGTCAAAG 120

GGGTGAATTG CT 132

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GATTAGGGGT CACTCAGGAT TATAAAAAAG CGGCAGAATA CTATAAAAAA GGTGATAAAA 60

ATAATGATAT TACAGCACAA TACCGTCTGG CAAAACTTTA TGAACAAGGT AACGGTGTAA 120

AACGTGATTA TCAACAAGCG ATAAACCTTT ACCTTAAACA TATCAACAGA ATGGATCACA 180

TCACTGCCCC CAGTTTTGTG GCTCTGGGTG ATATCTATTC TCTGGGATTS GGGGTAGAGA 240

AAAACCCACA ACTGGCTGAA AAATGGTATC AAAAAGCGAT AGATGCAGCT AATACACAAC 300

ATAACCAGGA AATAAATCAT TAAACGACAA CACTTAATAC CATATTGTGA AGATGTTCAG 360

NSDOCID <WO 9822575A3 IA>

ACATGGCGGA ATTCCCCTAT TCTTTGTTGG CGCTTACAAC AGACTATATT CCGCCATATC 420

TGTCTTTATT GTGTATAAAC CATCGATACT GATGTTTGAT AGTGCTAAAT AATCATTGGC 480

GCAATCACAA AGCCTAATGC CACTCCAGCA ATAATTCCCC CCAACCCAGG CAGCATAAAT 540

GG 542

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GAACCACTTA GCGGCAGCTA TCGGGAATCG CCTGCTGAAA GACGGTCAGA CAGTGATTGT 60

GGTTACCGTG GCTGATGTTA TGAGTGCCCT GCACGCCAGC TATGACGATG GGCAGTCAGG 120

CGAAAAATTT TTGCGGGAAC TGTGCGAAGT GGATCTGCTG GTTCTTGATG AAATTGGCAT 180

TCAGCGCGAG ACGAAAAACG AAGCAGGTGG TACTGCACCA GATTGTTGAT CGCCGGACAG 240

CGTCGATGCG CACGTGGGGA TRCTGACAAA CCTGAACTAT GAGGCCATGA AAACATTGCT 300

CGGCGARCGG ATTATGGATC RCATGACCAT GAACGGCGGG CGATGGGTGA ATTTTAACTG 360

GGAGACTGGC GTCCGAATGT CG 382

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGTCCCGCAC CCGGAAATGG TCAGCGAACC AATCAGCAGG GTCATCGCTA GAAATCATCC 60

TTAGCGAAAG CTAAGGATTT TTTTTATCTG AATTCTAGCC AGATCCCCGC TGATTTATGC 120

TGGTTA 126

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

JSDOCID <WO 9822575A3 IA>

ACCCCCAGCC TAGCTGGGGG TTTTCTGTGC ACAAAAAATC CCGGCATAAT GGCCGGGATT 60

TGCGAGCTTT CCCACTATTT CTTGATTCCT AAACGGAACA TATCAGTTGG GAATAAAGGT 120

TGTATTATCA CTTCATCATT ANAAATGAAT AATTTGGGCG ATAAAGCTGT TACGTCATAG 180

ATATTTTCAG CGATTAATCT TAGANTTGAC CTAAAAACTG GAATACTTGC ATCATCTGCA 240

AAGACAAACA TGTCATCG 258

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AACCAGCGGT TCGCATCATC TCATCCCACT GACTCTCCGC TTTTGACAGA TCTGCATATC 60

CTCGGGCCAA CTTATCCAGT ACTCCGTAGT TTGCCGATTT ATTCACCCGC CAGAACACCG 120

CCTCACCTGC ATCGGCAAGC CGGGGGGAAA ACTGATACCC CAGTAGCCAG AACAGACCGA 180

AAATAATATC GCTGCTACCC GCAGTGTCTG TCATGATTTC AACTGGATTC AGCCCTGTCT 240

GCTGCTCAAG AAGTCCTTCC AGTACAAAAA TCGAATCCCG TAATGTACCG GGTACCACAA 300

TGCCATGGAA CCCAGAGTAC TGATCAGATA CGAATTATAC CAGGTGATGC CTCGTCCAGA 360

ACCAAAATAT TTTCTGTTAG ATCCTGAGTT GATGGTCTT 399

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AAATAACATC AACATACATT TGACTCGCGG GGGAAACGTT TACGGAGTCT TCATACTGGC 60

ACTTTTTTAT GCTGCTGACT ACTCTTCGTC ATCGCCATCA ACATGCGCAC GAATCAGCGC 120

CATAAACGGT TTGCCAAAGC GTTCCAGCTT GCGCATCCCA ACGCCGTTAA CGCTGAGCAT 180

TTCGCTGGCG GTGATCGGCA TCTGTTCAGC CATCTCAATC AAGGTTGCGT CGTTAAACAC 240

CACGTACGGC GGGACATTAC TTTCATCGGC TATCGATTTA CGCAGTTTGC GTAATTNGGC 300

GAACAGTTTG CGATCATAGT TGNCGCCGAN CGATNTCTGC ATCGCTTTCG GTTTGAGCGC 360

CACGATACGC GGCACGGCAA TTGCAAAGAG GATTCGCCGC GCAGCACCGG GCGCGCGGCC 420

TCTGTCAGTT GTAGGGCAGA ATGCTGGGCA ATATTTTGCG TCACCAGGCC GAGGTGAATC 480

NSDOCID: <WO__9822575A3_IA>

AGCTGGCGGA TCACGCTCAC CCAATGTTCA TGGCTTTTAT CACGGCCCAT GCCATAGACT 540

TTCAGTTTGT CATGACCATA GTCGCGGATA CGCTGGTTAT TAGCACCACG AATCACTTCC 600

ACCACATAAC CCATCCCAAA CCGCTGATTC ACACGACCAA TGGTGGAAAG GGCAATCTGA 660

GCATCGGTTG AACCGTCGTA CTGTTTCGGC GGATCGAGGC AGATATCGCA GTTCNCCGCA 720

CGGCTCCTGA CGCCCTTCGC CAAAA 745

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

AGAATGGCGG CTTCTTGCCC CCCTTTGCCC CGGTCCTGAC TAGCATGGCT GGAGTCCAGT 60

GTCCAGGCCA CGACCATGCT CATCATGGAA GCAGCTTTTG TAGTACANTC GCAGCTTATT 120

TTCCTGGAAC GAAATGTCTG GCATCGTGGT GCATAACATA ACCCCCAATG CCCAGCAGAT 180

GCACAGAAGG TTCTAGAATC GCCCACTGAT ATCCCATACA AAATTTACCA AAACGTGTTC 240

GTATTTCTCG TATAAATAAT GTCTCTATGG TGACGTTCTA GACTTCAAAC CCACTTTTTG 300

AATTTGATGA TGTGCTCCTA ATCTCTTCAG GAATGTAACG CCCTTGGTTT ACAGCTACCA 360

ATACACTGGA GGTATACTTA TCTGCAACTG GATGAACTAG ATGTACTTGA GCAAACATTT 420

CATAAGCTCG ACGACAGTT 439

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CTGGAAAGCG ACGTTGATGG ATTAATGCAG TCGGTAAAAC TGAACGCTGC TCAGGCAAGG 60

CAGCAACTTC CTGATGACGC GACGCTGCGC CACCAANTCA TGGAACGTTT GATCATGGAT 120

CAAMTCATCC TGCAGATGGG GCAGAAAATG GGAGTGAAAA TCTCCGATGA GCAGCTGGAT 180

CAGGCGATTG CTAACATCGC GAAACAGNAC AACATGACGC TGGATCAGAT GCGCACCGTC 240

TGGCTTACGA TGGACTGAAC TACAACACCT ATCGTAACCA GATCCGCAAA GAGATGATTA 300

TCTCTGAAGT GCGTAACAAC GAGGTGCGTC GTCGNATCAC CATCCTGCCG 350

(2) INFORMATION FOR SEQ ID NO: 134:

USDOCID <WO 9822575A3 IA>

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCCCAAGATT GCTAACAAAT GCGCGTTGTT CATGCCGGAT GCGGCGTGAC CGCCTTATCC 60

GGCCTACGAA ACCGCAAGAA TTCAATATAT TGCAGGAGCG GTGTAGGCCT GATAAGCGTA 120

GCGAWTCAGG CAGTTTTGCG TTTGCCCGCA ACCTTAGGGG ACATTTAGCG ACCCCATTTA 180

TTTCTCACTT TTCCGCCTCA TCATCGCGCG TTAATTTCTT TCATGAATCA CGCTTTACAA 240

TATCCAGCGC GCGCANAACG GTACTGGCAG GGATCTGAAT TTTCCTCCAG CAGCACAATC 300

AAATCGACAG CCAGTTTGAC ATCGTCAAGG GGCATTTTCC CAGTGACATA ATCTCTCCAT 360

TGCTAAGCGG GTTAAAACGC GCTAACCTGT TTCGATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CTATCCTTAT GACCACCCAA CTACNTCATT TACACCCAAA CCAGCGATCT GAATAAAGAA 60

GCGATTGCCC AGTTACGACT GGGCGGAAAA TGCGCGTAAG GATGAAGTAA AGTTTCAGTT 120

GAGCCTGGCA TTTCCCTGTG GCGTGGGATT TTAGGCCCGA ACTCGGTGTT GGGTGCGTCT 180

TATACGCAAA AATCCTGGTG GCAACTGTCC AATAGCGAAG AGTCTTCACC GTTTCGTGAA 240

ACCAACTACG AACCGCAATT GTTCCTCGGT TTTGCCACCG ATTACCGTTT TGCAGGTTGG 300

ACTGCGCGAT GTGGAGATGG GGTATAACCA CGACTCTAAA CGGGCGTTCC GACCCGACCT 360

CCCGCAGCTG GAACCGCCTT TATACTCGCC TGATGGCAGA AAACGGTAAC TGGCTGGTAG 420

AAGTGAAGCC GNGGTATGTG GTGGGTAATA CTGACGATAA CCC 463

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 584 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

INSDOCID: <WO__9822575A3 IA>

TTGGTCAGCC GTACCTGAAT GGGGGCTGAT GCCCGGCTGG TTAATGGCAG GTGGTCTGAT 60

CGCCTGGTTT GTCGGTTGGC GCAAAACACG CTGATTTTTT CATCGCTCAA GGCGGGCCGT 120

GTAACGTATA ATGCGGCTTT GTTTAATCAT CATCTACCAC AGAGGAACAT GTATGGGTGG 180

TATCAGTATT TGGCAGTTAT TGATTATTGC CGTCATCGTT GTACTGCTTT TTGGCACCAA 240

AAAGCTCGGC TCCATCGGTT CCGATCTTGG TGCGTCGATC AAAGGCTTTA AAAAAGCAAT 300

GAGCGATGAT GAACCAAAGC AGGATAAAAC CAGTCAGGAT GCTGATTTTA CTGCGAAAAC 360

TATCGCCGAT AAGCAGGCGG ATACGAATCA GGAACAGGCT AAAACAGAAG ACGCGAAGCC 420

TACGNTAAAG AGCAGGTGTA ATCCGTGTTT GATATCGGTT TTAGCGNACT GCTATTGGTG 480

TTCATCATCG GCCTCGTCGT TCTGGGGGCG CAACGACTGC CTGTGGCGGT AAAAACGGTA 540

GCGGGCTGGA TTCGCGCGTT GCGTTCACTG GCGACAACGG TGCA 584

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GCAGGCAGGA GGAACTGCCC AGTGATACGG TTATTCGTGA TGGCGGAGGG CAGAGCCTTA 60

ACGGACTGGC GTTGAACACC ACGCTGGATA ACAGAGTTGA GCATTGGNTA CACGGGGGAG 120

GGAAAGCAGA CGTTACAATT ATTAACCAGG ATGTTTACCC AGACCATAAA ACATGGCGGA 180

TTGGCAACCG NAACCATCGT CAACACCGTT GCAGAAGKTG GTCCGGAGTC TGAAAATGTG 240

TCCAGCGGTC AGATGGTCGG AGGGACGGCT GAATCCACCA CCATCAACAA AAATGGCCGG 300

CAGTTATCTG GTCTTCGGGG ATGGCACGGG ACACCCTCAT TTGCGCTGGT GGTGACCAGA 360

CGGTACACGG AGAGGCACAT AACACCCGAC TGGAGGGAGG TTAACCAGTA TGTACACAAC 420

GGTGGCACGG CAACAGAGAC GCTGATAAAC CGTGATGGCT GGCAGGTGAT TAAGGAAGGA 480

GGGAACTGCC GGCGCATTAC CACCATCAAN CCNGAAAAGG GAAANCT 527

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GTCAGTCTCT GGGGGAAGTG CGTGTTCCGA CCGGGGAAAT GTGGTGGAGA AAGTTATTGA 60

ISDOCID: <WO 9822575A3 IA>

AGGGGCTTAC GAGGTGGTGG GGGTTTTTGA CCGGATTGAG GAAAAGCGTG ATGCCATGCA 120

GTCGCTGATT CTGCCGCCAC CGGACGCCAG GCGCTGGCAC AGGCGGCACT GACTTACCGT 180

TATGGTGACG AACMTCARCC CGTCACCACC GCCGACATTC TGACACCACG ACGCCGGGAR 240

GATTACGGTA AGGACCTGTG GAGTGCTTAT CAGACCATTC AGGAGAATAT GCTGAAAGGC 300

GGAATTTCCG GTCGCAGTGC CAGAGGAAAA CGTATCCATA CCCGTGCCAT TCACAGCATC 360

GACACCGACA TTAAGCTCAA CCGCGCATTG TGGGTGATGG CTGAAACGCT GCTGGAGAGT 420

ATGCGCTGAT GCCGTTTCCN T 441

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CGAGCGAGAT GAACTTCGAG GGCGGTGTGA GCCAGTCGGC TTACGAGACA CTGGCGGCGC 60

TTAATCTGCC GAAACCGCAG CAAGGGCCGG AAACCATTAA TCAGGTTACC GAGCATAAGA 120

TGTCAGCTGA GTAAGCCTGT ATGCCGGATA AGGCGCTCGC GCCNATTCCG ATGAAATAAG 180

GCGCATCGGG CCTGAAGGAA AGCCGTATGN ATACACCCGC AGCCCGCATC CGGCAAGTTA 240

CAACAAATAA CCTTTAACCA TGCTTTTTGA TGTTTTTCAG CAATACCCCG CGGCGATGCC 300

CATACTGGCA ACCGTCGGGA GGGATTGATC ATCGGCAGTT TTTTGAATGT GGTGATTTGG 360

GCGTTACCCC ATCATGCTGC GCCAACAAAT GGCGGAGT 398

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

GCCGAACAGA CACAGCAATA TGAACCCTGC CAGCGCAGAC GCTTGCTGAT TAATGCTCTG 60

AACAAAAGGC GAAGAATGGC AAATCCTGCG ATCAGCAAAG TCAGCGCACC GACTATCTGT 120

AACATAGTCA CTCCGTGATG AATATCATGT GTATTGTGAA TGCCAGTGAA TGTGGCACTG 180

AAGCGTTTGC ACCTGTCCGG GTCCCGGTCA TGATGACCGS AACAGAGAGA CAATGCCGAA 240

TTATCAGAAG GTCACATTCA GTGTGGCTTG GCCGTTATAA CCTTCAGCGC TGCTGCCGCT 300

GACGCTGTGG GCATAACCGG CCTGAACGCC CAGGGTGATA TTTTCCCGGA CACGGGCTTC 360

INSDOCID <WO 9822575A3 IA>

CAGTCCGGCC TGCAGCTCCA GTGACGTGCC ATTCCGGGAC GGTGAGAACG TCATGTTACT 420

GCCGGCTGCG GCTGTACCCA TGCTCATGTC TCCCCGGGAG CTGAAGGTGC GGATAACAGA 480

AGGCTGTACC CACCCGTTCA CCGGCAGTTC ACGCACACTG TGTTTTGCAC TGTCACGCAA 540

GGTGTCACGG GATGAGGTGC CTTCANCAAA AGGTCATATT 580

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGCGGACATC CAGCGTTCCG CCATCATCCA CACGGGTTCT GGTGGCTGTG TGTCCGGTCA 60

GCACATCCAG ACGGCCGCCA TTTTCCAGTA CGACATTATC AGCTTTACCC TCCACAACAG 120

AGAATGCTCC CAGGCGGTTT GTGCCGGTGA CGGTTGCAGC AGTGCTGGTA ACCAGTGCTC 180

CGCCCGTGTT CTGGGTGACA TCAGACGCTT TACCGCCGGC ATTCACCTGC AGCTTTCCTT 240

TCTGGTTGAT GGTGGTATGC GCGGCAGTTC CTCCTTCCTT AATCAMCTGC CAGCCATCAC 300

GGTTTATCAG CGTCTCTGTT GCCGTGCCAA CGTTGTGTAC ATACTGGTTA MCTCCCTCCA 360

GTCGGGTGTT AWGTGSCTCT CCGTGTANCG TCTGGTCANC AACAACGCAA ATGANGGTGT 420

CCCGTGCCAT CCCCGAAGAC CAGTAA 446

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGAATACGTT AAGTCAGCAG ACCGGCGGAG ACAGTCTGAC ACAGACAGCG CTGCAGCAGT 60

ATGAGCCGGT GGTGGTTGGC TCTCCGCAAT GGCACGATGA ACTGGCAGGT GCCCTGAATA 120

ATATTGCCGG AGTTCGCCAC TGACCGGTCA GACCGGTATC AGTGATGACT GGCCACTGCC 180

TTCCGTCAAC AATGGATACC TGGTTCCGTC CACGGACCCG GACAGTCCGT ATCTGATTAC 240

GGTGAACCCG AAACTGGATR GTCTCGGACA GGTGGACAGC CATTTGTTTN CCGGACTGTA 300

TGAGCTTCTT GGAGCGAAAC CGGGTCA 327

NSDOCID <WO 9822575A3 IA>

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 8

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet [X]

Name of depositary institution

American Type Culture Collection (ATCC)

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit	Accession Number
September 23, 1996	97726

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet [ ]

DNA plasmid PAI-1

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
[ ] This sheet was received with the international application	[ ] This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

Form PCT/RO/134 (July 1992)

3NSDOCID: <WO 9822575A3 IA>